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

(19) World Intellectual Property Organization
International Bureau

(43) International Publication Date
11 August 2022 (11.08.2022)

WIPO | PCT

(10) International Publication Number
WO 2022/169870 A1

(51) International Patent Classification:
A61K 35/17 (2015.01)

(21) International Application Number:
PCT/US2022/014936

(22) International Filing Date:
02 February 2022 (02.02.2022)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
63/144,860 02 February 2021 (02.02.2021) US

(71) Applicant: **CARISMA THERAPEUTICS INC.** [US/US]; 3675 Market Street, Ste 200, Philadelphia, Pennsylvania 19104 (US).

(72) Inventors: **KLICHINSKY, Michael**; c/o Carisma Therapeutics Inc., 3675 Market Street, Ste 200, Philadelphia, Pennsylvania 19104 (US). **SLOAS, David Christopher**; c/o Carisma Therapeutics Inc., 3675 Market Street, Ste 200, Philadelphia, Pennsylvania 19104 (US). **ANDERSON, Nicholas**; c/o Carisma Therapeutics Inc., 3675 Market Street, Ste 200, Philadelphia, Pennsylvania 19104 (US).

(74) Agent: **BYCHOWSKI, Meaghan E.** et al.; Choate, Hall & Stewart LLP, Two International Place, Boston, Massachusetts 02110 (US).

(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, IT, 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, ST, SV, SY, TH, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, WS, 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,

WO 2022/169870 A1

(54) Title: SELF-POLARIZING IMMUNE CELLS

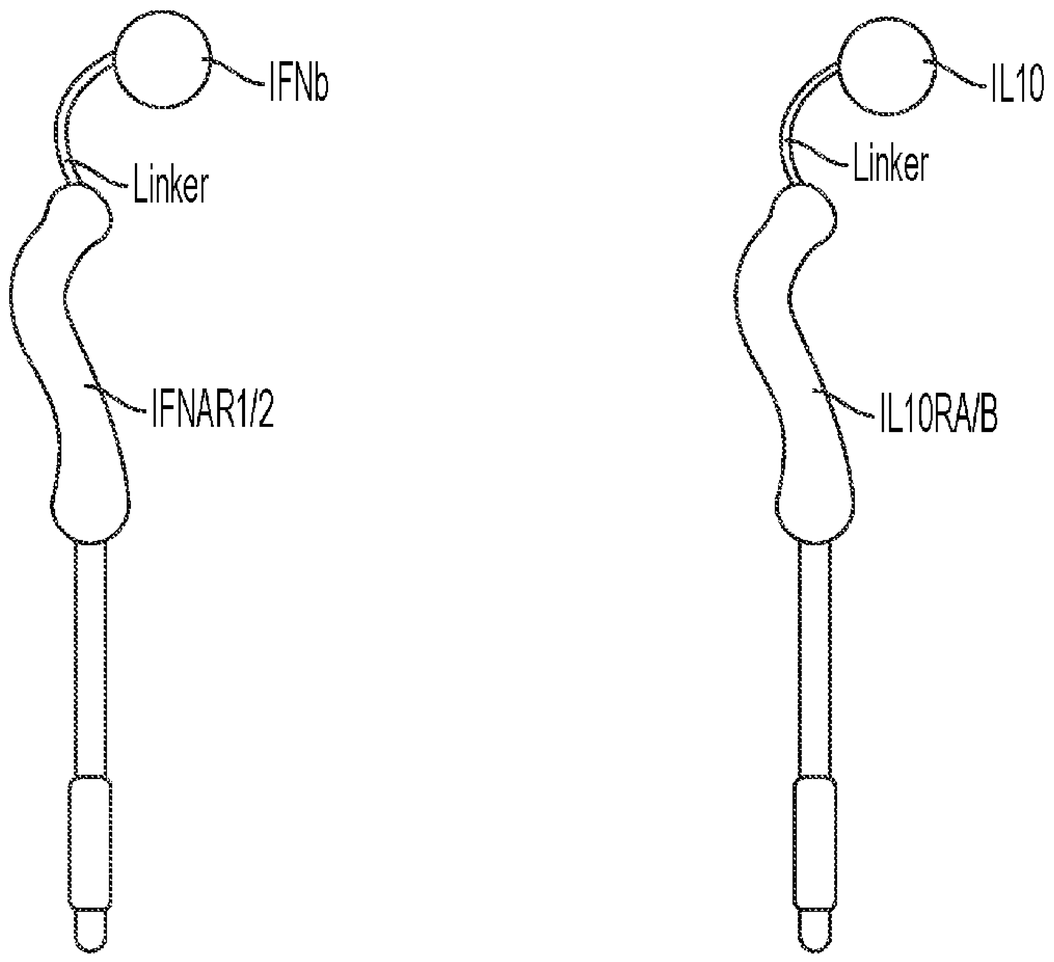


Figure 1

(57) Abstract: The present disclosure pertains to modified immune cells comprising fusion proteins and methods of using and making immune cells comprising fusion proteins. The present disclosure also pertains to modified immune cells comprising exogenous cytokines and chimeric antigen receptors and methods of using and making said immune cells.

[Continued on next page]

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))*

SELF-POLARIZING IMMUNE CELLS

CROSS REFERENCE TO RELATED APPLICATIONS

[0001] This application claims priority to and the benefit of U.S. Provisional Patent Application No. 63/144,860, filed February 2, 2021, the entirety of which is incorporated herein by reference.

SEQUENCE LISTING

[0000] The instant application contains a Sequence Listing which has been submitted electronically in ASCII format and is hereby incorporated by reference in its entirety. Said ASCII copy, created on January 27, 2022, is named 2012851-0124_SL.txt and is 569,792 bytes in size.

BACKGROUND

[0002] Macrophages are powerful modulators of the immune response and can generally adopt either a pro-inflammatory (M1) or an anti-inflammatory (M2) phenotype. A precise balance of M1/M2 macrophages is important in resolving the body's response to disease and injury, and various diseases include dysregulated M1/M2 phenotypes. For example, macrophages in the tumor microenvironment (TME) are often biased toward an M2 phenotype that safeguards the tumor, while M1 macrophages in atherosclerotic tissue promote plaque progression.

[0003] Therefore, a need exists for establish a method to genetically control and/or maintain the M1/M2 polarization of engineered immune cells for cell therapies.

SUMMARY OF THE INVENTION

[0004] The present disclosure encompasses, among other things, compositions comprising modified immune cells (e.g., stem cells, macrophages, monocytes, and/or dendritic cells) comprising exogenous cytokines and methods of producing the same. The present

disclosure also encompasses, among other things, compositions comprising modified immune cells (e.g., stem cells, macrophages, monocytes, and/or dendritic cells) comprising fusion proteins and methods of producing the same.

[0005] The present disclosure provides a system for establishing genetic control over immune cell (e.g., stem cell, macrophage, monocyte, and/or dendritic cell) phenotype using cytokine-based signaling. The present disclosure provides, *inter alia*, co-expression of pro-inflammatory (M1) or anti-inflammatory (M2) promoting exogenous cytokines with a chimeric antigen receptor (CAR) in an immune cell (e.g., stem cell, macrophage, monocyte, and/or dendritic cell), which enables the immune cell to produce large quantities of the expressed exogenous cytokine. Additionally, co-expression of a pro-inflammatory (M1) promoting exogenous cytokine and a CAR in an immune cell (e.g., stem cell, macrophage, monocyte, and/or dendritic cell) enables the immune cell to "self-polarize" to an M1 phenotype. Similarly, co-expression of an anti-inflammatory (M2) promoting exogenous cytokine and a CAR in an immune cell (e.g., stem cell, macrophage, monocyte, and/or dendritic cell) enables the immune cell to "self-polarize" to an M2 phenotype.

[0006] The present disclosure also provides, *inter alia*, fusion proteins in which a pro-inflammatory (M1) or anti-inflammatory (M2) promoting cytokine is directly fused to one of its corresponding receptor subunits, such that the cytokine can intramolecularly bind its tethered receptor and induce downstream signaling. Unlike naturally occurring soluble cytokines, the tethered cytokines of the present disclosure are designed to only stimulate the modified immune cells (e.g., stem cells, macrophages, monocytes, and/or dendritic cells); direct fusion to the receptor can prevent cytokine diffusion from the cell membrane and can encourage rapid binding kinetics due to a high local concentration. This tethered cytokine-cytokine receptor fusion protein design may thereby provide a constitutive pro-inflammatory (M1) or anti-inflammatory (M2) promoting signal to the modified immune cells (e.g., stem cells, macrophages, monocytes, and/or dendritic cells), with minimized risk for cytotoxic effects on surrounding cells.

[0007] In one aspect, the present disclosure provides a modified immune cell comprising a fusion protein comprising a cytokine, a linker, and a cytokine receptor, wherein the modified immune cell is a stem cell, macrophage, monocyte, or dendritic cell and the cytokine binds the

cytokine receptor. In some embodiments, a fusion protein is membrane-bound. In some embodiments, a linker is a flexible linker. In some embodiments, a linker is a cleavable linker.

[0008] In some embodiments, a modified immune cell further comprises a chimeric antigen receptor (CAR).

[0009] In some embodiments, a fusion protein further comprises a signal peptide. In some embodiments, a fusion protein comprises, from N-terminus to C-terminus: a signal peptide, a cytokine, a linker, and a cytokine receptor. In some embodiments, a fusion protein comprises an amino acid sequence at least 80% identical to a sequence selected from Table 2a, Table 2b, Table 3a, Table 3b, Table 6, Table 8, or Table 9.

[0010] In another aspect, the present disclosure provides a modified immune cell comprising one or more nucleic acids encoding a fusion protein comprising a cytokine, a linker, and a cytokine receptor, wherein the modified immune cell is a stem cell, macrophage, monocyte or dendritic cell and the cytokine binds the cytokine receptor. In some embodiments, a fusion protein is membrane-bound. In some embodiments, a linker is a flexible linker. In some embodiments, a linker is a cleavable linker.

[0011] In some embodiments, a modified immune cell further comprises a chimeric antigen receptor (CAR).

[0012] In some embodiments, a fusion protein further comprises a signal peptide. In some embodiments, a fusion protein comprises, from N-terminus to C-terminus: a signal peptide, a cytokine, a linker, and a cytokine receptor. In some embodiments, one or more nucleic acids encoding a fusion protein comprise a sequence at least 80% identical to a sequence selected from Table 10. In some embodiments, one or more nucleic acids encoding a fusion protein comprise a sequence at least 80% identical to a sequence selected from Table 11a or 11b. In some embodiments, one or more nucleic acids comprise a sequence at least 80% identical to a sequence selected from Table 4a, Table 4b, or Table 7. In some embodiments, one or more nucleic acids comprise a sequence at least 80% identical to a sequence selected from Table 5a or Table 5b. In some embodiments, one or more nucleic acids comprise a sequence at least 80% identical to a signal peptide sequence selected from Table 8. In some embodiments, one or more nucleic acids comprise a sequence at least 80% identical to a linker sequence selected from Table 8.

[0013] In some embodiments, a signal peptide is or comprises a CD8a, IgG κ, PDGFR-β, Type I Interferon (IFN-α1, IFN-α2, IFN-α4, IFN-α5, IFN-α6, IFN-α7, IFN-α8, IFN-α10, IFN-α13, IFN-α14, IFN-α16, IFN-α17, IFN-α21, IFN-β, IFN-ω, IFN-ε, or IFN-κ), Type II Interferon (IFN-γ), Type III Interferon (IFN-λ1, IFN-λ2, IFN-λ3, or IFN-λ4), TNF-α, IL-1β, IL-6, IL-12, IL-17, IL-23, GM-CSF, IL-4, IL-10, IL-13, IL-18, M-CSF, TGF-β, IFNAR1, IFNAR2, IFNGR1, IFNGR2, IFNLR1, TNFR1, TNFR2, IL-1R1, IL-1R3, IL-6Rα, gp130, IL-12Rβ1, IL-12Rβ2, IL-17RA, IL-17RB, IL-17RC, IL-23R, CSF2-Rα, CSF2-Rβ, IL-4Rα, IL-4Rα1, IL-2Rγc, IL-10R1, IL-10R2, IL-13Rα1, IL-18Rα, IL-18Rβ, CSF1-R, TGF-βR1, or TGF-βR2 signal peptide.

[0014] In some embodiments, a cytokine is or comprises a pro-inflammatory cytokine. In some embodiments, a cytokine is or comprises an anti-inflammatory cytokine. In some embodiments, a cytokine is or comprises a Type I Inteferon (IFN-α1, IFN-α2, IFN-α4, IFN-α5, IFN-α6, IFN-α7, IFN-α8, IFN-α10, IFN-α13, IFN-α14, IFN-α16, IFN-α17, IFN-α21, IFN-β, IFN-ω, IFN-ε, or IFN-κ), Type II Interferon (IFN-γ), Type III Interferon (IFN-λ1, IFN-λ2, IFN-λ3, or IFN-λ4), TNF-α, IL-1β, IL-6, IL-12, IL-17, IL-23, or GM-CSF. In some embodiments, a cytokine is or comprises IL-4, IL-10, IL-13, IL-18, M-CSF, or TGF-β. In some embodiments, a cytokine is or comprises a Type I Inteferon (IFN-α1, IFN-α2, IFN-α4, IFN-α5, IFN-α6, IFN-α7, IFN-α8, IFN-α10, IFN-α13, IFN-α14, IFN-α16, IFN-α17, IFN-α21, IFN-β, IFN-ω, IFN-ε, or IFN-κ), Type II Interferon (IFN-γ), Type III Interferon (IFN-λ1, IFN-λ2, IFN-λ3, or IFN-λ4), TNF-α, IL-1β, IL-6, IL-12, IL-17, IL-23, GM-CSF, IL-4, IL-10, IL-13, IL-18, M-CSF, or TGF-β.

[0015] In some embodiments, a cytokine receptor is or comprises a pro-inflammatory cytokine receptor. In some embodiments, a cytokine receptor is or comprises an anti-inflammatory cytokine receptor. In some embodiments, a cytokine receptor is or comprises IFNAR1, IFNAR2, IFNGR1, IFNGR2, IFNLR1, TNFR1, TNFR2, IL-1R1, IL-1R3, IL-6Rα, gp130, IL-12Rβ1, IL-12Rβ2, IL-17RA, IL-17RB, IL-17RC, IL-23R, CSF2-Rα, or CSF2-Rβ. In some embodiments, a cytokine receptor is or comprises IL-4Rα, IL-4Rα1, IL-2Rγc, IL-10R1, IL-10R2, IL-13Rα1, IL-18Rα, IL-18Rβ, CSF1-R, TGF-βR1, or TGF-βR2. In some embodiments, a cytokine receptor is or comprises IFNAR1, IFNAR2, IFNGR1, IFNGR2, IFNLR1, TNFR1, TNFR2, IL-1R1, IL-1R3, IL-6Rα, gp130, IL-12Rβ1, IL-12Rβ2, IL-17RA, IL-17RB, IL-17RC,

IL-23R, CSF2-Rα, CSF2-Rβ, IL-4Rα, IL-4Rα1, IL-2Rγc, IL-10R1, IL-10R2, IL-13Rα1, IL-18Rα, IL-18Rβ, CSF1-R, TGF-βR1, or TGF-βR2.

[0016] In some embodiments, a linker is or comprises a linker selected from a group consisting of: a $(G4S)_n$ linker, wherein n = 1-5 **(SEQ ID NO: 170)**, a Whitlow linker, and Linker 26.

[0017] In another aspect, the present disclosure provides a modified immune cell comprising a fusion protein comprising interleukin 10 (IL-10), a linker, and interleukin-10 receptor (IL10R). In another aspect, the present disclosure provides a modified immune cell comprising a fusion protein comprising interferon beta (IFNβ), a linker, and interferon-α/β receptor (IFNAR).

[0018] In some embodiments, a fusion protein is membrane-bound. In some embodiments, a linker is a flexible linker. In some embodiments, a linker is a cleavable linker.

[0019] In some embodiments, a modified immune cell further comprises a chimeric antigen receptor (CAR).

[0020] In another aspect, the present disclosure provides a pharmaceutical composition comprising a modified immune cell of the present disclosure. In some embodiments, a pharmaceutical composition comprises a pharmaceutically acceptable carrier.

[0021] In another aspect, the present disclosure provides a nucleic acid construct comprising one or more nucleic acids encoding a fusion protein comprising a cytokine and a cytokine receptor. In some embodiments, a nucleic acid construct further comprises one or more nucleic acids encoding a chimeric antigen receptor (CAR).

[0022] In another aspect, the present disclosure provides a pharmaceutical composition comprising a nucleic acid construct of the present disclosure. In some embodiments, a pharmaceutical composition comprises a pharmaceutically acceptable carrier.

[0023] In another aspect, the present disclosure provides a method of treating or preventing a disease or disorder in a subject, comprising delivering to the subject a therapeutically effective amount of a pharmaceutical composition of the present disclosure.

[0024] In another aspect, the present disclosure provides a method of modifying an immune cell, the method comprising delivering to the immune cell a nucleic acid construct comprising one or more nucleic acids encoding a fusion protein comprising a cytokine, a linker, and a cytokine receptor. In some embodiments, a linker is a flexible linker. In some embodiments, a linker is a cleavable linker. In some embodiments, a nucleic acid construct further comprises one or more nucleic acids encoding a chimeric antigen receptor (CAR). In some embodiments, delivering comprises electroporation or transfection with DNA, mRNA, or chemically modified mRNA. In some embodiments, delivering comprises transduction with an adeno-associated viral (AAV) vector, an adenoviral vector, or a retroviral vector. In some embodiments, a retroviral vector comprises a lentiviral vector or a gammaretroviral vector. In some embodiments, a lentiviral vector is packaged with a Vpx protein. In some embodiments, an adenoviral vector comprises an Ad2 vector or an Ad5 vector. In some embodiments, an Ad5 vector comprises an Ad5f35 adenoviral vector. In some embodiments, delivery comprises transposon-based delivery or CRISPR-based targeted integration.

[0025] In another aspect, the present disclosure provides a modified immune cell comprising an exogenous cytokine and a chimeric antigen receptor (CAR), wherein the modified immune cell is a stem cell, macrophage, monocyte, or dendritic cell and the exogenous cytokine is or comprises a pro-inflammatory cytokine, an anti-inflammatory cytokine, or a chemoattractant chemokine. In some embodiments, an exogenous cytokine comprises a signal peptide. In some embodiments, an exogenous cytokine comprises an amino acid sequence at least 80% identical to a sequence selected from Table 2a, Table 2b, Table 6, or Table 8.

[0026] In another aspect, the present disclosure provides a modified immune cell comprising one or more nucleic acids encoding an exogenous cytokine and a chimeric antigen receptor (CAR), wherein the modified immune cell is a stem cell, macrophage, monocyte or dendritic cell and the exogenous cytokine is or comprises a pro-inflammatory cytokine, an anti-inflammatory cytokine, or a chemoattractant chemokine. In some embodiments, an exogenous cytokine further comprises a signal peptide. In some embodiments, one or more nucleic acids comprise a sequence at least 80% identical to a sequence selected from Table 4a, Table 4b, Table 7, or Table 11b. In some embodiments, one or more nucleic acids comprise a sequence at least 80% identical to a sequence selected from Table 8.

[0027] In some embodiments, one or more nucleic acids encode a signal peptide. In some embodiments, a signal peptide is or comprises a CD8a, IgG κ, PDGFR-β, Type I Interferon (IFN-α1, IFN-α2, IFN-α4, IFN-α5, IFN-α6, IFN-α7, IFN-α8, IFN-α10, IFN-α13, IFN-α14, IFN-α16, IFN-α17, IFN-α21, IFN-β, IFN-ω, IFN-ε, or IFN-κ), Type II Interferon (IFN-γ), Type III Interferon (IFN-λ1, IFN-λ2, IFN-λ3, or IFN-λ4), TNF-α, IL-1β, IL-6, IL-12, IL-17, IL-23, GM-CSF, IL-4, IL-10, IL-13, IL-18, M-CSF, TGF-β, IFNAR1, IFNAR2, IFNGR1, IFNGR2, IFNLR1, TNFR1, TNFR2, IL-1R1, IL-1R3, IL-6Rα, gp130, IL-12Rβ1, IL-12Rβ2, IL-17RA, IL-17RB, IL-17RC, IL-23R, CSF2-Rα, CSF2-Rβ, IL-4Rα, IL-4Rα1, IL-2Rγc, IL-10R1, IL-10R2, IL-13Rα1, IL-18Rα, IL-18Rβ, CSF1-R, TGF-βR1, or TGF-βR2 signal peptide.

[0028] In some embodiments, an exogenous cytokine is or comprises a Type I Inteferon (IFN-α1, IFN-α2, IFN-α4, IFN-α5, IFN-α6, IFN-α7, IFN-α8, IFN-α10, IFN-α13, IFN-α14, IFN-α16, IFN-α17, IFN-α21, IFN-β, IFN-ω, IFN-ε, or IFN-κ), Type II Interferon (IFN-γ), Type III Interferon (IFN-λ1, IFN-λ2, IFN-λ3, or IFN-λ4), TNF-α, IL-1β, IL-6, IL-12, IL-17, IL-23, GM-CSF, IL-4, IL-10, IL-13, IL-18, M-CSF, TGF-β, CCL19, or CXCL12. In some embodiments, an exogenous cytokine is or comprises IFN-γ, IL-10, CCL19, or CXCL12.

[0029] In another aspect, the present disclosure provides a pharmaceutical composition comprising a modified immune cell of the present disclosure comprising an exogenous cytokine and a CAR. In some embodiments, a pharmaceutical composition comprises a pharmaceutically acceptable carrier.

[0030] In another aspect, the present disclosure provides a nucleic acid construct comprising one or more nucleic acids encoding an exogenous cytokine and a chimeric antigen receptor (CAR).

[0031] In another aspect, the present disclosure provides a pharmaceutical composition comprising a nucleic acid construct of the present disclosure comprising one or more nucleic acids encoding an exogenous cytokine and a CAR. In some embodiments, a pharmaceutical composition comprises a pharmaceutically acceptable carrier.

[0032] In another aspect, the present disclosure provides a method of treating or preventing a disease or disorder in a subject, comprising delivering to the subject a therapeutically effective amount of a pharmaceutical composition of the present disclosure, wherein the pharmaceutical composition comprises a modified immune cell of the present

disclosure comprising an exogenous cytokine and a CAR or a nucleic acid construct of the present disclosure comprising one or more nucleic acids encoding an exogenous cytokine and a CAR.

[0033] In another aspect, the present disclosure provides a method of modifying an immune cell, the method comprising delivering to the immune cell a nucleic acid construct comprising one or more nucleic acids encoding an exogenous cytokine and a chimeric antigen receptor (CAR). In some embodiments, the delivering comprises electroporation or transfection with DNA, mRNA, or chemically modified mRNA. In some embodiments, delivering comprises transduction with an adeno-associated viral (AAV) vector, an adenoviral vector, or a retroviral vector. In some embodiments, a retroviral vector comprises a lentiviral vector or a gammaretroviral vector. In some embodiments, a lentiviral vector is packaged with a Vpx protein. In some embodiments, an adenoviral vector comprises an Ad2 vector or an Ad5 vector. In some embodiments, an Ad5 vector comprises an Ad5f35 adenoviral vector. In some embodiments, delivery comprises transposon-based delivery or CRISPR-based targeted integration.

BRIEF DESCRIPTION OF THE DRAWING

[0034] The drawings are for illustration purposes only, not for limitation.

[0035] **Figure 1** shows exemplary fusion proteins comprising IFN-β and IFNAR1/2 and IL10 and IL10RA/B.

[0036] **Figure 2** shows exemplary fusion protein designs comprising a signal peptide, a cytokine, a linker and a cytokine receptor, wherein the cytokine binds the cytokine receptor. Figure discloses "(GGGGS)x" as SEQ ID NO: 175.

[0037] **Figure 3A** and **Figure 3B** show illustrations of an exemplary method of the present disclosure, comprising gene delivery of constructs encoding a fusion protein (and optionally a CAR, see **Figure 3B**) to an immune cell (e.g., a macrophage), dimerization of the fusion protein with an endogenous receptor and polarization of a macrophage to a pro-inflammatory (i.e., M1) state.

[0038] **Figure 4A** and **Figure 4B** show illustrations of an exemplary method of the present disclosure, comprising gene delivery of constructs encoding a fusion protein (and optionally a CAR, see Figure 4B) to an immune cell (e.g., a macrophage), dimerization of the fusion protein with an endogenous receptor and polarization of a macrophage to an anti-inflammatory (i.e., M2) state.

[0039] **Figure 5A** and **Figure 5B** show exemplary constructs comprising a signal peptide, a FLAG tag, a cytokine, a linker, a cytokine receptor, a P2A peptide and mCherry. In **Figure 5A**, an antibody binds the FLAG tag and in **Figure 5B**, an antibody binds the cytokine.

[0040] **Figure 6A** and **Figure 6B** show exemplary graphs illustrating viability of HEK293T cells (**Figure 6A**) and surface expression of fusion proteins in HEK293T cells (**Figure 6B**) transfected with plasmid DNA.

[0041] **Figure 7** shows exemplary graphs illustrating a correlation between detection of a FLAG tag by an antibody and mCherry expression in the IFNβ-IFNAR1 and IL4-IL13Rα groups.

[0042] **Figure 8** shows exemplary Western blots illustrating expression of the fusion proteins in HEK293T cells.

[0043] **Figure 9** shows an exemplary construct comprising a signal peptide, a FLAG tag, a cytokine, a linker, a cytokine receptor, a P2A peptide and mCherry. This figure also illustrates an antibody that binds the FLAG tag.

[0044] **Figure 10A** and **Figure 10B** show exemplary graphs illustrating viability of macrophages (**Figure 10A**) and surface expression of fusion proteins in macrophages (**Figure 10B**) transduced with VPX-Lentivirus comprising a fusion protein.

[0045] **Figure 11A** and **Figure 11B** show exemplary graphs illustrating viability, P2A-mCherry expression, and surface expression of fusion proteins in macrophages transduced with VPX-Lentivirus comprising a fusion protein.

[0046] **Figure 12A** and **Figure 12B** show exemplary graphs illustrating expression of pro-inflammatory (M1) and anti-inflammatory (M2) markers from macrophages that were transduced with VPX-Lentivirus comprising a fusion protein.

[0047] **Figure 13** shows an exemplary graph illustrating viability of macrophages after transfection with mRNA encoding cytokines and a CAR.

[0048] **Figure 14** shows an exemplary graph illustrating CAR expression in macrophages after transfection with mRNA encoding cytokines and a CAR.

[0049] **Figure 15** shows an exemplary graph illustrating IFN-γ levels from macrophages after transfection with mRNA encoding cytokines and a CAR.

[0050] **Figure 16** shows an exemplary graph illustrating IL-10 levels from macrophages after transfection with mRNA encoding cytokines and a CAR.

[0051] **Figure 17** shows an exemplary graph illustrating CCL19 levels from macrophages after transfection with mRNA encoding cytokines and a CAR.

[0052] **Figure 18** shows an exemplary graph illustrating CXCL12 levels from macrophages after transfection with mRNA encoding cytokines and a CAR.

[0053] **Figure 19** shows exemplary graphs illustrating levels of pro-inflammatory (M1) markers CD80 and CD86 from macrophages after transfection with mRNA encoding cytokines and a CAR.

[0054] **Figure 20** shows exemplary graphs illustrating levels of anti-inflammatory (M2) markers CD163 and CD206 from macrophages after transfection with mRNA encoding cytokines and a CAR.

DEFINITIONS

[0055] In order for the present invention to be more readily understood, certain terms are first defined below. Additional definitions for the following terms and other terms are set forth throughout the specification. The publications and other reference materials referenced herein to describe the background of the invention and to provide additional detail regarding its practice are hereby incorporated by reference.

[0056] The articles “a” and “an” are used herein to refer to one or to more than one (i.e., to at least one) of the grammatical object of the article. By way of example, “an element” means one element or more than one element.

[0057] *Approximately or about:* As used herein, the term "approximately" or "about," as applied to one or more values of interest, refers to a value that is similar to a stated reference value. In certain embodiments, the term "approximately" or "about" refers to a range of values that fall within 25%, 20%, 19%, 18%, 17%, 16%, 15%, 14%, 13%, 12%, 11%, 10%, 9%, 8%, 7%, 6%, 5%, 4%, 3%, 2%, 1 %, or less in either direction (greater than or less than) of the stated reference value unless otherwise stated or otherwise evident from the context (except where such number would exceed 100% of a possible value).

[0058] *Activation:* As used herein, the term "activation" refers to the state of a cell, for example a monocyte, macrophage, or dendritic cell that has been sufficiently stimulated to induce detectable cellular proliferation or has been stimulated to exert its effector function. Activation can also be associated with induced cytokine production, phagocytosis, cell signaling, target cell killing, and/or antigen processing and presentation.

[0059] *Activated monocytes/macrophages/dendritic cells*: As used herein, the term "activated monocytes/macrophages/dendritic cells" refers to, among other things, monocyte/macrophage/dendritic cells that are undergoing cell division or exerting effector function. The term "activated monocytes/macrophages/dendritic cells" refers to, among others thing, cells that are performing an effector function or exerting any activity not seen in the resting state, including phagocytosis, cytokine secretion, proliferation, gene expression changes, metabolic changes, and other functions.

[0060] *Agent*: As used herein, the term "agent" (or "biological agent" or "therapeutic agent"), refers to a molecule that may be expressed, released, secreted or delivered to a target by a modified cell described herein. An agent includes, but is not limited to, a nucleic acid, an antibiotic, an anti-inflammatory agent, an antibody or fragments thereof, an antibody agent or fragments thereof, a growth factor, a cytokine, an enzyme, a protein (e.g., an RNAse inhibitor), a peptide, a fusion protein, a synthetic molecule, an organic molecule (e.g., a small molecule), a carbohydrate, a lipid, a hormone, a microsome, a derivative or a variation thereof, and any combinations thereof. An agent may bind any cell moiety, such as a receptor, an antigenic determinant, or other binding site present on a target or target cell. An agent may diffuse or be transported into a cell, where it may act intracellularly.

[0061] *Antibody*: As used herein, the term "antibody" refers to a polypeptide that includes canonical immunoglobulin sequence elements sufficient to confer specific binding to a particular target antigen. As is known in the art, intact antibodies as produced in nature are approximately 150 kD tetrameric agents comprising two identical heavy chain polypeptides (about 50 kD each) and two identical light chain polypeptides (about 25 kD each) that associate with each other into what is commonly referred to as a "Y-shaped" structure. Each heavy chain comprises at least four domains (each about 110 amino acids long) – an amino-terminal variable (VH) domain (located at the tips of the Y structure), followed by three constant domains: CH1, CH2, and the carboxy-terminal CH3 (located at the base of the Y's stem). A short region, known as the "switch", connects the heavy chain variable and constant regions. The "hinge" connects CH2 and CH3 domains to the rest of the antibody. Two disulfide bonds in this hinge region connect the two heavy chain polypeptides to one another in an intact antibody. Each light chain comprises two domains – an amino-terminal variable (VL) domain, followed by a carboxy-terminal constant (CL) domain, separated from one another by another "switch". Intact antibody tetramers comprise two heavy chain-light chain dimers in which the heavy and light chains are linked to one another by a single disulfide bond; two other disulfide bonds connect the heavy chain hinge regions to one another, so that the dimers are connected to one another and a tetramer is formed. Naturally-produced antibodies are also glycosylated, typically on the CH2 domain. Each domain in a natural antibody has a structure characterized by an "immunoglobulin fold" formed from two beta sheets (e.g., 3-, 4-, or 5-stranded sheets) packed against each other in a compressed antiparallel beta barrel. Each variable domain contains three hypervariable loops known as "complementarity determining regions" (CDR1, CDR2, and CDR3) and four somewhat invariant "framework" regions (FR1, FR2, FR3, and FR4). When natural antibodies fold, the FR regions form the beta sheets that provide the structural framework for the domains, and the CDR loop regions from both the heavy and light chains are brought together in three-dimensional space so that they create a single hypervariable antigen binding site located at the tip of the Y structure. The Fc region of naturally-occurring antibodies binds to elements of the complement system, and also to receptors on effector cells, including, for example, effector cells that mediate cytotoxicity. Affinity and/or other binding attributes of Fc regions for Fc receptors can be modulated through glycosylation or other modification. In some embodiments, antibodies produced and/or utilized in accordance with the present invention (e.g., as a component of a

CAR) include glycosylated Fc domains, including Fc domains with modified or engineered glycosylation. In some embodiments, any polypeptide or complex of polypeptides that includes sufficient immunoglobulin domain sequences as found in natural antibodies can be referred to and/or used as an "antibody", whether such polypeptide is naturally produced (e.g., generated by an organism reacting to an antigen), or produced by recombinant engineering, chemical synthesis, or other artificial system or methodology. In some embodiments, an antibody is polyclonal. In some embodiments, an antibody is monoclonal. In some embodiments, an antibody has constant region sequences that are characteristic of mouse, rabbit, primate, or human antibodies. In some embodiments, antibody sequence elements are humanized, primatized, chimeric, etc, as is known in the art. Moreover, the term "antibody", as used herein, can refer in appropriate embodiments (unless otherwise stated or clear from context) to any of the art-known or developed constructs or formats for utilizing antibody structural and functional features in alternative presentation. For example, in some embodiments, an antibody utilized in accordance with the present invention is in a format selected from, but not limited to, intact IgA, IgG, IgE or IgM antibodies; bi- or multi- specific antibodies (e.g., Zybodies®, etc); antibody fragments such as Fab fragments, Fab' fragments, F(ab')2 fragments, Fd' fragments, Fd fragments, and isolated CDRs or sets thereof; single chain Fvs; polypeptide-Fc fusions; single domain antibodies (e.g., shark single domain antibodies such as IgNAR or fragments thereof); cameloid antibodies; masked antibodies (e.g., Probodies®); Small Modular ImmunoPharmaceuticals ("SMIPs™"); single chain or Tandem diabodies (TandAb®); VHHs; Anticalins®; Nanobodies® minibodies; BiTE®s; ankyrin repeat proteins or DARPINs®; Avimers®; DARTs; TCR-like antibodies;, Adnectins®; Affilins®; Trans-bodies®; Affibodies®; TrimerX®; MicroProteins; Fynomers®, Centyrins®; and KALBITOR®s. In some embodiments, an antibody may lack a covalent modification (e.g., attachment of a glycan) that it would have if produced naturally. In some embodiments, an antibody may contain a covalent modification (e.g., attachment of a glycan, a payload [e.g., a detectable moiety, a therapeutic moiety, a catalytic moiety, etc], or other pendant group [e.g., poly-ethylene glycol, etc.].

[0062] *Antibody agent*: As used herein, the term "antibody agent" refers to an agent that specifically binds to a particular antigen. In some embodiments, the term encompasses any polypeptide or polypeptide complex that includes immunoglobulin structural elements sufficient to confer specific binding. Exemplary antibody agents include, but are not limited to monoclonal

antibodies or polyclonal antibodies. In some embodiments, an antibody agent may include one or more constant region sequences that are characteristic of mouse, rabbit, primate, or human antibodies. In some embodiments, an antibody agent may include one or more sequence elements are humanized, primatized, chimeric, etc., as is known in the art. In many embodiments, the term "antibody agent" is used to refer to one or more of the art-known or developed constructs or formats for utilizing antibody structural and functional features in alternative presentation. For example, in some embodiments, an antibody agent utilized in accordance with the present invention is in a format selected from, but not limited to, intact IgA, IgG, IgE or IgM antibodies; bi- or multi- specific antibodies (e.g., Zybodies®, etc); antibody fragments such as Fab fragments, Fab' fragments, F(ab')2 fragments, Fd' fragments, Fd fragments, and isolated CDRs or sets thereof; single chain Fvs; polypeptide-Fc fusions; single domain antibodies (e.g., shark single domain antibodies such as IgNAR or fragments thereof); cameloid antibodies; masked antibodies (e.g., Probodies®); Small Modular ImmunoPharmaceuticals ("SMIPsTM"); single chain or Tandem diabodies (TandAb®); VHHs; Anticalins®; Nanobodies® minibodies; BiTE®s; ankyrin repeat proteins or DARPINs®; Avimers®; DARTs; TCR-like antibodies;, Adnectins®; Affilins®; Trans-bodies®; Affibodies®; TrimerX®; MicroProteins; Fynomers®, Centyrins®; and KALBITOR®s. In some embodiments, an antibody agent may lack a covalent modification (e.g., attachment of a glycan) that it would have if produced naturally. In some embodiments, an antibody agent may contain a covalent modification (e.g., attachment of a glycan, a payload [e.g., a detectable moiety, a therapeutic moiety, a catalytic moiety, etc], or other pendant group [e.g., poly-ethylene glycol, etc.]. In many embodiments, an antibody agent is or comprises a polypeptide whose amino acid sequence includes one or more structural elements recognized by those skilled in the art as a complementarity determining region (CDR); in some embodiments an antibody agent is or comprises a polypeptide whose amino acid sequence includes at least one CDR (e.g., at least one heavy chain CDR and/or at least one light chain CDR) that is substantially identical to one found in a reference antibody. In some embodiments an included CDR is substantially identical to a reference CDR in that it is either identical in sequence or contains between 1-5 amino acid substitutions as compared with the reference CDR. In some embodiments an included CDR is substantially identical to a reference CDR in that it shows at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity with the

reference CDR. In some embodiments an included CDR is substantially identical to a reference CDR in that it shows at least 96%, 96%, 97%, 98%, 99%, or 100% sequence identity with the reference CDR. In some embodiments an included CDR is substantially identical to a reference CDR in that at least one amino acid within the included CDR is deleted, added, or substituted as compared with the reference CDR but the included CDR has an amino acid sequence that is otherwise identical with that of the reference CDR. In some embodiments an included CDR is substantially identical to a reference CDR in that 1-5 amino acids within the included CDR are deleted, added, or substituted as compared with the reference CDR but the included CDR has an amino acid sequence that is otherwise identical to the reference CDR. In some embodiments an included CDR is substantially identical to a reference CDR in that at least one amino acid within the included CDR is substituted as compared with the reference CDR but the included CDR has an amino acid sequence that is otherwise identical with that of the reference CDR. In some embodiments an included CDR is substantially identical to a reference CDR in that 1-5 amino acids within the included CDR are deleted, added, or substituted as compared with the reference CDR but the included CDR has an amino acid sequence that is otherwise identical to the reference CDR. In some embodiments, an antibody agent is or comprises a polypeptide whose amino acid sequence includes structural elements recognized by those skilled in the art as an immunoglobulin variable domain. In some embodiments, an antibody agent is a polypeptide protein having a binding domain which is homologous or largely homologous to an immunoglobulin-binding domain. In some embodiments, an antibody agent is not and/or does not comprise a polypeptide whose amino acid sequence includes structural elements recognized by those skilled in the art as an immunoglobulin variable domain. In some embodiments, an antibody agent may be or comprise a molecule or composition which does not include immunoglobulin structural elements (e.g., a receptor or other naturally occurring molecule which includes at least one antigen binding domain).

[0063] *Antibody fragment*: As used herein, the term "antibody fragment" refers to a portion of an intact antibody and refers to the antigenic determining variable regions of an intact antibody. Examples of antibody fragments include, but are not limited to, Fab, Fab', F(ab')2, and Fv fragments, linear antibodies, scFv antibodies, and multispecific antibodies formed from antibody fragments and human and humanized versions thereof.

[0064] *Antibody heavy chain*: As used herein, the term "antibody heavy chain" refers to the larger of the two types of polypeptide chains present in all antibody molecules in their naturally occurring conformations.

[0065] *Antibody light chain:* As used herein, the term "antibody light chain" refers to the smaller of the two types of polypeptide chains present in all antibody molecules in their naturally occurring conformations.

[0066] *Synthetic antibody:* As used herein, the term "synthetic antibody" refers to an antibody that is generated using recombinant DNA technology, such as, for example, an antibody expressed by a bacteriophage as described herein. The term should also be construed to mean an antibody which has been generated by the synthesis of a DNA molecule encoding the antibody and which DNA molecule expresses an antibody protein, or an amino acid sequence specifying the antibody, wherein the DNA or amino acid sequence has been obtained using synthetic DNA or amino acid sequence technology which is available and well known in the art.

[0067] *Antigen:* As used herein, the term "antigen" or "Ag" refers to a molecule that is capable of provoking an immune response. This immune response may involve either antibody production, the activation of specific immunologically-competent cells, or both. A skilled artisan will understand that any macromolecule, including virtually all proteins or peptides, can serve as an antigen. Furthermore, antigens can be derived from recombinant or genomic DNA. A skilled artisan will understand that any DNA that comprises a nucleotide sequences or a partial nucleotide sequence encoding a protein that elicits an immune response encodes an "antigen" as that term is used herein. Furthermore, one skilled in the art will understand that an antigen need not be encoded solely by a full length nucleotide sequence of a gene. It is readily apparent that the present invention includes, but is not limited to, the use of partial nucleotide sequences of more than one gene and that these nucleotide sequences are arranged in various combinations to elicit the desired immune response. Moreover, a skilled artisan will understand that an antigen need not be encoded by a "gene" at all. It is readily apparent that an antigen can be generated synthesized or can be derived from a biological sample. Such a biological sample can include, but is not limited to a tissue sample, a tumor sample, a cell or a biological fluid.

[0068] *Anti-tumor effect:* As used herein, the term "anti-tumor effect" refers to a biological effect which can be manifested by a decrease in tumor volume, a decrease in the

number of tumor cells, a decrease in the number of metastases, an increase in life expectancy, or amelioration of various physiological symptoms associated with the cancerous condition. An "anti-tumor effect" can also be manifested by the ability of the peptides, polynucleotides, cells and antibodies of the invention in prevention of the occurrence of a tumor in the first place.

[0069] *Autologous:* As used herein, the term "autologous" refers to any material derived from an individual to which it is later to be re-introduced into the same individual.

[0070] *Allogeneic:* As used herein, the term "allogeneic" refers to any material (e.g., a population of cells) derived from a different animal of the same species.

[0071] *Xenogenic:* As used herein, the term "xenogeneic" refers to any material (e.g., a population of cells) derived from an animal of a different species.

[0072] *Cancer:* As used herein, the term "cancer" refers to a disease characterized by the rapid and uncontrolled growth of aberrant cells. Cancer cells can spread locally or through the bloodstream and lymphatic system to other parts of the body. Examples of various cancers include but are not limited to, breast cancer, prostate cancer, ovarian cancer, cervical cancer, skin cancer, pancreatic cancer, colorectal cancer, renal cancer, liver cancer, brain cancer, lymphoma, leukemia, lung cancer and the like. In certain embodiments, the cancer is medullary thyroid carcinoma.

[0073] *Conservative sequence modifications:* As used herein, the term "conservative sequence modifications" refers to amino acid modifications that do not significantly affect or alter the binding characteristics of an antibody containing the amino acid sequence. Such conservative modifications include amino acid substitutions, additions and deletions. Modifications can be introduced into an antibody compatible with various embodiments by standard techniques known in the art, such as site-directed mutagenesis and PCR-mediated mutagenesis. Conservative amino acid substitutions are ones in which an amino acid residue is replaced with an amino acid residue having a similar side chain. Families of amino acid residues having similar side chains have been defined in the art. These families include amino acids with basic side chains (e.g., lysine, arginine, histidine), acidic side chains (e.g., aspartic acid, glutamic acid), uncharged polar side chains (e.g., glycine, asparagine, glutamine, serine, threonine, tyrosine, cysteine, tryptophan), nonpolar side chains (e.g., alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine), beta-branched side chains (e.g., threonine, valine,

isoleucine) and aromatic side chains (e.g., tyrosine, phenylalanine, tryptophan, histidine). Thus, one or more amino acid residues within the CDR regions of an antibody can be replaced with other amino acid residues from the same side chain family and the altered antibody can be tested for the ability to bind antigens using the functional assays described herein.

[0074] *Co-stimulatory ligand:* As used herein, the term "co-stimulatory ligand" refers to a molecule on an antigen presenting cell (e.g., an APC, dendritic cell, B cell, and the like) that specifically binds a cognate co-stimulatory molecule on a monocyte/macrophage/dendritic cell, thereby providing a signal which mediates a monocyte/macrophage/dendritic 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, MICB, HVEM, lymphotoxin beta receptor, 3/TR6, ILT3, ILT4, HVEM, 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 monocyte/macrophage/dendritic cell, such as, but not limited to, CD27, CD28, 4-1BB, 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.

[0075] *Cytotoxic:* As used herein, the term "cytotoxic" or "cytotoxicity" refers to killing or damaging cells. In one embodiment, cytotoxicity of the metabolically enhanced cells is improved, e.g. increased cytolytic activity of macrophages.

[0076] *Effective amount*: As used herein, "effective amount" and "therapeutically effective amount" are interchangeable, and refer to an amount of a compound, formulation, material, or composition, as described herein effective to achieve a particular biological result or provides a manufacturing, therapeutic or prophylactic benefit. Such results may include, but are not limited to, anti-tumor activity as determined by any means suitable in the art.

[0077] *Effector function*: As used herein, "effector function" or "effector activity" refers to a specific activity carried out by an immune cell in response to stimulation of the immune cell. For example, an effector function of macrophages to engulf and digest cellular debris, foreign substances, microbes, cancer cells and other unhealthy cells by phagocytosis.

[0078] *Encoding:* As used herein, "encoding" refers to the inherent property of specific sequences of nucleotides in a polynucleotide, such as a gene, a cDNA, or an mRNA, to serve as templates for synthesis of other polymers and macromolecules in biological processes having either a defined sequence of nucleotides (i.e., rRNA, tRNA and mRNA) or a defined sequence of amino acids and the biological properties resulting therefrom. Thus, a gene encodes a protein if transcription and translation of mRNA corresponding to that gene produces the protein in a cell or other biological system. Both the coding strand, the nucleotide sequence of which is identical to the mRNA sequence and is usually provided in sequence listings, and the non-coding strand, used as the template for transcription of a gene or cDNA, can be referred to as encoding the protein or other product of that gene or cDNA.

[0079] *Endogenous:* As used herein "endogenous" refers to any material from or produced inside a particular organism, cell, tissue or system.

[0080] *Exogenous:* As used herein, the term "exogenous" refers to any material introduced from or produced outside a particular organism, cell, tissue or system.

[0081] *Expand:* As used herein, the term "expand" refers to increasing in number, as in an increase in the number of cells, for example, monocytes, macrophages, and/or dendritic cells. In one embodiment, monocytes, macrophages, or dendritic cells that are expanded ex vivo increase in number relative to the number originally present in a culture. In another embodiment, monocytes, macrophages, or dendritic cells that are expanded ex vivo increase in number relative to other cell types in a culture. In some embodiments, expansion may occur *in vivo*. The term "ex vivo," as used herein, refers to cells that have been removed from a living organism, (e.g., a human) and propagated outside the organism (e.g., in a culture dish, test tube, or bioreactor).

[0082] *Expression:* As used herein, the term "expression" of a nucleic acid sequence refers to generation of any gene product from a nucleic acid sequence. In some embodiments, a gene product can be a transcript. In some embodiments, a gene product can be a polypeptide. In some embodiments, expression of a nucleic acid sequence involves one or more of the following: (1) production of an RNA template from a DNA sequence (*e.g.*, by transcription); (2) processing of an RNA transcript (e.g., by splicing, editing, 5' cap formation, and/or 3' end formation); (3)

translation of an RNA into a polypeptide or protein; and/or (4) post-translational modification of a polypeptide or protein.

[0083] *Expression vector:* As used herein, the term "expression vector" refers to a vector comprising a recombinant polynucleotide comprising expression control sequences operatively linked to a nucleotide sequence to be expressed. An expression vector comprises sufficient cis-acting elements for expression; other elements for expression can be supplied by the host cell or in an in vitro expression system. Expression vectors include all those known in the art, such as cosmids, plasmids (e.g., naked or contained in liposomes) and viruses (e.g., lentiviruses, retroviruses, adenoviruses, and adeno-associated viruses).

[0084] *Fragment:* As used herein, the terms "fragment" or "portion" refers to a structure that includes a discrete portion of the whole, but lacks one or more moieties found in the whole structure. In some embodiments, a fragment consists of such a discrete portion. In some embodiments, a fragment consists of or comprises a characteristic structural element or moiety found in the whole. In some embodiments, a nucleotide fragment comprises or consists of at least 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, 200, 210, 220, 230, 240, 250, 275, 300, 325, 350, 375, 400, 425, 450, 475, 500, or more monomeric units (e.g., nucleic acids) as found in the whole nucleotide. In some embodiments, a nucleotide fragment comprises or consists of at least about 5%, 10%, 15%, 20%, 25%, 30%, 25%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or more of the monomeric units (e.g., residues) found in the whole nucleotide. The whole material or entity may in some embodiments be referred to as the "parent" of the whole.

[0085] *Homology:* As used herein, the term "homology" refers to the overall relatedness between polymeric molecules, e.g., between nucleic acid molecules (*e.g.*, DNA molecules and/or RNA molecules) and/or between polypeptide molecules. In some embodiments, polymeric molecules are considered to be "homologous" to one another if their sequences are at least 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or 99% identical. In some embodiments, polymeric molecules are considered to be "homologous" to one another if their sequences are at least 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or 99% similar (e.g., containing residues with related chemical

properties at corresponding positions). As will be understood by those skilled in the art, a variety of algorithms are available that permit comparison of sequences in order to determine their degree of homology, including by permitting gaps of designated length in one sequence relative to another when considering which residues "correspond" to one another in different sequences. Calculation of the percent homology between two nucleic acid sequences, for example, can be performed by aligning the two sequences for optimal comparison purposes (e.g., gaps can be introduced in one or both of a first and a second nucleic acid sequences for optimal alignment and non-corresponding sequences can be disregarded for comparison purposes). In certain embodiments, the length of a sequence aligned for comparison purposes is at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95%, or substantially 100% of the length of the reference sequence. The nucleotides at corresponding nucleotide positions are then compared. When a position in the first sequence is occupied by the same nucleotide as the corresponding position in the second sequence, then the molecules are identical at that position; when a position in the first sequence is occupied by a similar nucleotide as the corresponding position in the second sequence, then the molecules are similar at that position. The percent homology between the two sequences is a function of the number of identical and similar positions shared by the sequences, taking into account the number of gaps, and the length of each gap, which needs to be introduced for optimal alignment of the two sequences.

[0086] *Identity:* As used herein, the term "identity" refers to the subunit sequence identity between two polymeric molecules particularly between two amino acid molecules, such as, between two polypeptide molecules. When two amino acid sequences have the same residues at the same positions; e.g., if a position in each of two polypeptide molecules is occupied by an Arginine, then they are identical at that position. The identity or extent to which two amino acid sequences have the same residues at the same positions in an alignment is often expressed as a percentage. The identity between two amino acid sequences is a direct function of the number of matching or identical positions; e.g., if half (e.g., five positions in a polymer ten amino acids in length) of the positions in two sequences are identical, the two sequences are 50% identical; if 90% of the positions (e.g., 9 of 10), are matched or identical, the two amino acids sequences are 90% identical.

[0087] *Substantial identity:* As used herein, the term "substantial identity" refers to a comparison between amino acid or nucleic acid sequences. As will be appreciated by those of ordinary skill in the art, two sequences are generally considered to be "substantially identical" if they contain identical residues in corresponding positions. As is well known in this art, amino acid or nucleic acid sequences may be compared using any of a variety of algorithms, including those available in commercial computer programs such as BLASTN for nucleotide sequences and BLASTP, gapped BLAST, and PSI-BLAST for amino acid sequences. In some embodiments, two sequences are considered to be substantially identical if at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or more of their corresponding residues are identical over a relevant stretch of residues. In some embodiments, the relevant stretch is a complete sequence. In some embodiments, the relevant stretch is at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 125, 150, 175, 200, 225, 250, 275, 300, 325, 350, 375, 400, 425, 450, 475, 500 or more residues. In the context of a CDR, reference to "substantial identity" typically refers to a CDR having an amino acid sequence at least 80%, preferably at least 85%, at least 90%, at least 95%, at least 98% or at least 99% identical to that of a reference CDR.

[0088] *Immune cell*: As used herein, the term "immune cell," refers to a cell that is involved in an immune response, e.g., promotion of an immune response. Examples of immune cells include, but are not limited to, macrophages, monocytes, dendritic cells, neutrophils, eosinophils, mast cells, platelets, large granular lymphocytes, Langerhans' cells, natural killer (NK) cells, T-lymphocytes, or B-lymphocytes. A source of immune cells (e.g., macrophages, monocytes, or dendritic cells) can be obtained from a subject.

[0089] *Immune response:* As used herein the term "immune response" refers to a cellular and/or systemic response to an antigen that occurs when lymphocytes identify antigenic molecules as foreign and induce the formation of antibodies and/or activate lymphocytes to remove the antigen.

[0090] *Immunoglobulin:* As used herein, the term "immunoglobulin" or "Ig," refers to a class of proteins that function as antibodies. Antibodies expressed by B cells are sometimes referred to as a BCR (B cell receptor) or antigen receptor. The five members included in this class of proteins are IgA, IgG, IgM, IgD, and IgE. IgA is the primary antibody that is present in

body secretions, such as saliva, tears, breast milk, gastrointestinal secretions and mucus secretions of the respiratory and genitourinary tracts. IgG is the most common circulating antibody. IgM is the main immunoglobulin produced in the primary immune response in most subjects. It is the most efficient immunoglobulin in agglutination, complement fixation, and other antibody responses, and is important in defense against bacteria and viruses. IgD is an immunoglobulin that has no known antibody function, but may serve as an antigen receptor. IgE is an immunoglobulin that mediates immediate hypersensitivity by causing release of mediators from mast cells and basophils upon exposure to allergen.

[0091] *Isolated:* As used herein, the term "isolated" refers to something altered or removed from the natural state. For example, a nucleic acid or a peptide naturally present in a living animal is not "isolated," but the same nucleic acid or peptide partially or completely separated from the coexisting materials of its natural state is "isolated." An isolated nucleic acid or protein can exist in substantially purified form, or can exist in a non-native environment such as, for example, a host cell.

[0092] *Modified:* As used herein, the term "modified" refers to a changed state or structure of a molecule or cell of the invention. Molecules may be modified in many ways, including chemically, structurally, and functionally. Cells may be modified through the introduction of nucleic acids.

[0093] *Modulating:* As used herein the term "modulating," refers to mediating a detectable increase or decrease in the level of a response and/or a change in the nature of a response in a subject compared with the level and/or nature of a response in the subject in the absence of a treatment or compound, and/or compared with the level and/or nature of a response in an otherwise identical but untreated subject. The term encompasses perturbing and/or affecting a native signal or response thereby mediating a beneficial therapeutic response in a subject, preferably, a human.

[0094] *Nucleic acid*: As used herein, the term "nucleic acid" refers to a polymer of at least three nucleotides. In some embodiments, a nucleic acid comprises DNA. In some embodiments, a nucleic acid comprises RNA. In some embodiments, a nucleic acid is single stranded. In some embodiments, a nucleic acid is double stranded. In some embodiments, a nucleic acid comprises both single and double stranded portions. In some embodiments, a

nucleic acid comprises a backbone that comprises one or more phosphodiester linkages. In some embodiments, a nucleic acid comprises a backbone that comprises both phosphodiester and non-phosphodiester linkages. For example, in some embodiments, a nucleic acid may comprise a backbone that comprises one or more phosphorothioate or 5'-N-phosphoramidite linkages and/or one or more peptide bonds, e.g., as in a "peptide nucleic acid". In some embodiments, a nucleic acid comprises one or more, or all, natural residues (*e.g.,* adenine, cytosine, deoxyadenosine, deoxycytidine, deoxyguanosine, deoxythymidine, guanine, thymine, uracil). In some embodiments, a nucleic acid comprises one or more, or all, non-natural residues. In some embodiments, a non-natural residue comprises a nucleoside analog (e.g., 2-aminoadenosine, 2-thiothymidine, inosine, pyrrolo-pyrimidine, 3 -methyl adenosine, 5-methylcytidine, C-5 propynyl-cytidine, C-5 propynyl-uridine, 2-aminoadenosine, C5-bromouridine, C5-fluorouridine, C5-iodouridine, C5-propynyl-uridine, C5 -propynyl-cytidine, C5-methylcytidine, 2-aminoadenosine, 7-deazaadenosine, 7-deazaguanosine, 8-oxoadenosine, 8-oxoguanosine, 0(6)-methylguanine, 2-thiocytidine, methylated bases, intercalated bases, and combinations thereof). In some embodiments, a non-natural residue comprises one or more modified sugars (e.g., 2'-fluororibose, ribose, 2'-deoxyribose, arabinose, and hexose) as compared to those in natural residues. In some embodiments, a nucleic acid has a nucleotide sequence that encodes a functional gene product such as an RNA or polypeptide. In some embodiments, a nucleic acid has a nucleotide sequence that comprises one or more introns. In some embodiments, a nucleic acid may be prepared by isolation from a natural source, enzymatic synthesis (e.g., by polymerization based on a complementary template, e.g., *in vivo* or *in vitro*, reproduction in a recombinant cell or system, or chemical synthesis. In some embodiments, a nucleic acid is at least 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, 20, 225, 250, 275, 300, 325, 350, 375, 400, 425, 450, 475, 500, 600, 700, 800, 900, 1000, 1500, 2000, 2500, 3000, 3500, 4000, 4500, 5000 or more residues long.

[0095] *Operably linked:* As used herein, the term "operably linked" refers to functional linkage between, for example, a regulatory sequence and a heterologous nucleic acid sequence resulting in expression of the latter. For example, a first nucleic acid sequence is operably linked with a second nucleic acid sequence when the first nucleic acid sequence is placed in a functional relationship with the second nucleic acid sequence. For instance, a promoter is operably linked

to a coding sequence if the promoter affects the transcription or expression of the coding sequence. Generally, operably linked DNA sequences are contiguous and, where necessary to join two protein coding regions, in the same reading frame.

[0096] *Overexpressed tumor antigen:* As used herein, the term "overexpressed" tumor antigen or "overexpression" of a tumor antigen refers to an abnormal level of expression of a tumor antigen in a cell from a disease area like a solid tumor within a specific tissue or organ of the patient relative to the level of expression in a normal cell from that tissue or organ. Patients having solid tumors or a hematological malignancy characterized by overexpression of the tumor antigen can be determined by standard assays known in the art.

[0097] *Polynucleotide:* As used herein, the term "polynucleotide" refers to a chain of nucleotides. Furthermore, nucleic acids are polymers of nucleotides. Thus, nucleic acids and polynucleotides as used herein are interchangeable. One skilled in the art has the general knowledge that nucleic acids are polynucleotides, which can be hydrolyzed into the monomeric "nucleotides." The monomeric nucleotides can be hydrolyzed into nucleosides. As used herein polynucleotides include, but are not limited to, all nucleic acid sequences which are obtained by any means available in the art, including, without limitation, recombinant means, i.e., the cloning of nucleic acid sequences from a recombinant library or a cell genome, using ordinary cloning technology and PCR™, and the like, and by synthetic means.

[0098] *Polypeptide:* As used herein, the term "polypeptide" refers to any polymeric chain of residues (e.g., amino acids) that are typically linked by peptide bonds. In some embodiments, a polypeptide has an amino acid sequence that occurs in nature. In some embodiments, a polypeptide has an amino acid sequence that does not occur in nature. In some embodiments, a polypeptide has an amino acid sequence that is engineered in that it is designed and/or produced through action of the hand of man. In some embodiments, a polypeptide may comprise or consist of natural amino acids, non-natural amino acids, or both. In some embodiments, a polypeptide may comprise or consist of only natural amino acids or only non-natural amino acids. In some embodiments, a polypeptide may comprise D-amino acids, L-amino acids, or both. In some embodiments, a polypeptide may comprise only D-amino acids. In some embodiments, a polypeptide may comprise only L-amino acids. In some embodiments, a polypeptide may include one or more pendant groups or other modifications, e.g., modifying or

attached to one or more amino acid side chains, at the polypeptide's N-terminus, at the polypeptide's C-terminus, or any combination thereof. In some embodiments, such pendant groups or modifications may be selected from the group consisting of acetylation, amidation, lipidation, methylation, pegylation, etc., including combinations thereof. In some embodiments, a polypeptide may be cyclic, and/or may comprise a cyclic portion. In some embodiments, a polypeptide is not cyclic and/or does not comprise any cyclic portion. In some embodiments, a polypeptide is linear. In some embodiments, a polypeptide may be or comprise a stapled polypeptide. In some embodiments, the term "polypeptide" may be appended to a name of a reference polypeptide, activity, or structure; in such instances it is used herein to refer to polypeptides that share the relevant activity or structure and thus can be considered to be members of the same class or family of polypeptides. For each such class, the present specification provides and/or those skilled in the art will be aware of exemplary polypeptides within the class whose amino acid sequences and/or functions are known; in some embodiments, such exemplary polypeptides are reference polypeptides for the polypeptide class or family. In some embodiments, a member of a polypeptide class or family shows significant sequence homology or identity with, shares a common sequence motif (e.g., a characteristic sequence element) with, and/or shares a common activity (in some embodiments at a comparable level or within a designated range) with a reference polypeptide of the class; in some embodiments with all polypeptides within the class). For example, in some embodiments, a member polypeptide shows an overall degree of sequence homology or identity with a reference polypeptide that is at least about 30-40%, and is often greater than about 50%, 60%, 70%, 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or more and/or includes at least one region (e.g., a conserved region that may in some embodiments be or comprise a characteristic sequence element) that shows very high sequence identity, often greater than 90% or even 95%, 96%, 97%, 98%, or 99%. Such a conserved region usually encompasses at least 3-4 and often up to 20 or more amino acids; in some embodiments, a conserved region encompasses at least one stretch of at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15 or more contiguous amino acids. In some embodiments, a useful polypeptide may comprise or consist of a fragment of a parent polypeptide. In some embodiments, a useful polypeptide as may comprise or consist of a plurality of fragments, each of which is found in the same parent polypeptide in a different spatial arrangement relative to one another than is found in the polypeptide of interest (e.g.,

fragments that are directly linked in the parent may be spatially separated in the polypeptide of interest or vice versa, and/or fragments may be present in a different order in the polypeptide of interest than in the parent), so that the polypeptide of interest is a derivative of its parent polypeptide.

[0099] *Protein:* As used herein, the term "protein" refers to a polypeptide (i.e., a string of at least two amino acids linked to one another by peptide bonds). Proteins may include moieties other than amino acids (*e.g.*, may be glycoproteins, proteoglycans, etc.) and/or may be otherwise processed or modified. Those of ordinary skill in the art will appreciate that a "protein" can be a complete polypeptide chain as produced by a cell (with or without a signal sequence), or can be a characteristic portion thereof. Those of ordinary skill will appreciate that a protein can sometimes include more than one polypeptide chain, for example linked by one or more disulfide bonds or associated by other means. Polypeptides may contain L-amino acids, D-amino acids, or both and may contain any of a variety of amino acid modifications or analogs known in the art. Useful modifications include, e.g., terminal acetylation, amidation, methylation, etc. In some embodiments, proteins may comprise natural amino acids, non-natural amino acids, synthetic amino acids, and combinations thereof. The term "peptide" is generally used to refer to a polypeptide having a length of less than about 100 amino acids, less than about 50 amino acids, less than 20 amino acids, or less than 10 amino acids. In some embodiments, proteins are antibodies, antibody fragments, biologically active portions thereof, and/or characteristic portions thereof.

[0100] *Signal transduction pathway:* As used herein, the term "signal transduction pathway" refers to the biochemical relationship between a variety of signal transduction molecules that play a role in the transmission of a signal from one portion of a cell to another portion of a cell. The phrase "cell surface receptor" includes molecules and complexes of molecules capable of receiving a signal and transmitting signal across the plasma membrane of a cell.

[0101] *Single chain antibodies:* As used herein, the term "single chain antibodies" refers to antibodies formed by recombinant DNA techniques in which immunoglobulin heavy and light chain fragments are linked to the Fv region via an engineered span of amino acids. Various methods of generating single chain antibodies are known, including those described in U.S. Pat.

No. 4,694,778; Bird (1988) Science 242:423-442; Huston et al. (1988) Proc. Natl. Acad. Sci. USA 85:5879-5883; Ward et al. (1989) Nature 334:54454; Skerra et al. (1988) Science 242:1038-1041.

[0102] *Specifically binds:* As used herein, the term "specifically binds," with respect to an antigen binding domain, such as an antibody agent, refers to an antigen binding domain or antibody agent which recognizes a specific antigen, but does not substantially recognize or bind other molecules in a sample. For example, an antigen binding domain or antibody agent that specifically binds to an antigen from one species may also bind to that antigen from one or more species. But, such cross-species reactivity does not itself alter the classification of an antigen binding domain or antibody agent as specific. In another example, an antigen binding domain or antibody agent that specifically binds to an antigen may also bind to different allelic forms of the antigen. However, such cross reactivity does not itself alter the classification of an antigen binding domain or antibody agent as specific. In some instances, the terms "specific binding" or "specifically binding," can be used in reference to the interaction of an antigen binding domain or antibody agent, a protein, or a peptide with a second chemical species, to mean that the interaction is dependent upon the presence of a particular structure (e.g., an antigenic determinant or epitope) on the chemical species; for example, an antigen binding domain or antibody agent recognizes and binds to a specific protein structure rather than to proteins generally. If an antigen binding domain or antibody agent is specific for epitope "A", the presence of a molecule containing epitope A (or free, unlabeled A), in a reaction containing labeled "A" and the antigen binding domain or antibody agent, will reduce the amount of labeled A bound to the antibody.

[0103] *Stimulation:* As used herein, the term "stimulation," refers to a primary response induced by binding of a stimulatory molecule (e.g., an FcR complex, a TLR complex, or a TCR/CD3 complex), for example, with its cognate ligand thereby mediating a signal transduction event, such as, but not limited to, signal transduction via Fc receptor machinery or via a synthetic CAR. Stimulation can mediate altered expression of certain molecules, such as downregulation of TGF-beta, and/or reorganization of cytoskeletal structures, and the like. As used herein, the term "stimulatory molecule," refers to a molecule of a monocyte, macrophage, or dendritic cell that specifically binds with a cognate stimulatory ligand present on an antigen

presenting cell. In some embodiments, a stimulatory molecule comprises an FcR extracellular domain comprising a CD64 (FcγRI), CD32a (FcγRIIa), CD32b (FcγRIIb), CD32c, CD16a (FcγRIIIa), CD16b (FcγRIIIb), FcεRI, FcεRII, FcαRI (CD89) or CD40 domain. In some embodiments, a stimulatory molecule comprises a TLR extracellular domain comprising a TLR1, TLR2, TLR3, TLR4, TLR5, TLR6, TLR7, TLR8, or TLR9 domain. As used herein, the term "stimulatory ligand," refers to a ligand that when present on an antigen presenting cell (e.g., an aAPC, a macrophage, a dendritic cell, a B-cell, and the like) or tumor cell can specifically bind with a cognate binding partner (referred to herein as a "stimulatory molecule") on a monocyte, macrophage, or dendritic cell thereby mediating a response by the immune cell, including, but not limited to, activation, initiation of an immune response, proliferation, and the like. Stimulatory ligands are well-known in the art and encompass, *inter alia*, Toll-like receptor (TLR) ligand, an anti-toll-like receptor antibody, an agonist, and an antibody for a monocyte/macrophage receptor. In addition, cytokines, such as interferon-gamma, are potent stimulants of macrophages.

[0104] *Subject:* As used herein, the term "subject" refers to an organism, for example, a mammal (e.g., a human, a non-human mammal, a non-human primate, a primate, a laboratory animal, a mouse, a rat, a hamster, a gerbil, a cat, or a dog). In some embodiments a human subject is an adult, adolescent, or pediatric subject. In some embodiments, a subject is suffering from a disease, disorder or condition, e.g., a disease, disorder, or condition that can be treated as provided herein, e.g., a cancer or a tumor listed herein. In some embodiments, a subject is susceptible to a disease, disorder, or condition; in some embodiments, a susceptible subject is predisposed to and/or shows an increased risk (as compared to the average risk observed in a reference subject or population) of developing the disease, disorder, or condition. In some embodiments, a subject displays one or more symptoms of a disease, disorder, or condition. In some embodiments, a subject does not display a particular symptom (e.g., clinical manifestation of disease) or characteristic of a disease, disorder, or condition. In some embodiments, a subject does not display any symptom or characteristic of a disease, disorder, or condition. In some embodiments, a subject is a patient. In some embodiments, a subject is an individual to whom diagnosis and/or therapy is and/or has been administered.

[0105] *Substantially purified:* As used herein, the term "substantially purified", for example as applied to a cell, refers to a cell that is essentially free of other cell types. A substantially purified cell also refers to a cell which has been separated from other cell types with which it is normally associated in its naturally occurring state. In some instances, a population of substantially purified cells refers to a homogenous population of cells. In other instances, this term refers simply to cell that have been separated from the cells with which they are naturally associated in their natural state. In some embodiments, the cells are cultured *in vitro*. In other embodiments, the cells are not cultured *in vitro*.

[0106] *Target:* As used herein, the term "target" refers to a cell, tissue, organ, or site within the body that is the subject of provided methods, systems, and /or compositions, for example, a cell, tissue, organ or site within a body that is in need of treatment or is preferentially bound by, for example, an antibody (or fragment thereof) or a CAR.

[0107] *Target site:* As used herein, the term "target site" or "target sequence" refers to a genomic nucleic acid sequence that defines a portion of a nucleic acid to which a binding molecule may specifically bind under conditions sufficient for binding to occur.

[0108] *T cell receptor:* As used herein, the term "T cell receptor" or "TCR" refers to a complex of membrane proteins that participate in the activation of T cells in response to the presentation of antigen. A TCR is responsible for recognizing antigens bound to major histocompatibility complex molecules. A TCR comprises a heterodimer of an alpha (a) and beta (β) chain, although in some cells the TCR comprises gamma and delta (γ/δ) chains. TCRs may exist in alpha/beta and gamma/delta forms, which are structurally similar but have distinct anatomical locations and functions. Each chain comprises two extracellular domains, a variable and constant domain. In some embodiments, a TCR may be modified on any cell comprising a TCR, including, for example, a helper T cell, a cytotoxic T cell, a memory T cell, regulatory T cell, natural killer T cell, and gamma delta T cell.

[0109] *Therapeutic:* As used herein, the term "therapeutic" refers to a treatment and/or prophylaxis. A therapeutic effect is obtained by suppression, remission, or eradication of a disease state.

[0110] *Transfected:* As used herein, the term "transfected" or "transformed" or "transduced" refers to a process by which exogenous nucleic acid is transferred or introduced

into the host cell. A "transfected" or "transformed" or "transduced" cell is one which has been transfected, transformed or transduced with exogenous nucleic acid. The cell includes the primary subject cell and its progeny.

[0111] *Treat:* As used herein, the term "treat," "treatment," or "treating" refers to partial or complete alleviation, amelioration, delay of onset of, inhibition, prevention, relief, and/or reduction in incidence and/or severity of one or more symptoms or features of a disease, disorder, and/or condition. In some embodiments, treatment may be administered to a subject who does not exhibit signs or features of a disease, disorder, and/or condition (e.g., may be prophylactic). In some embodiments, treatment may be administered to a subject who exhibits only early or mild signs or features of the disease, disorder, and/or condition, for example for the purpose of decreasing the risk of developing pathology associated with the disease, disorder, and/or condition. In some embodiments, treatment may be administered to a subject who exhibits established, severe, and/or late-stage signs of the disease, disorder, or condition. In some embodiments, treating may comprise administering to an immune cell (e.g., a monocyte, macrophage, or dendritic cell) or contacting an immune cell with a modulator of a pathway activated by *in vitro* transcribed mRNA.

[0112] *Tumor:* As used herein, the term "tumor" refers to an abnormal growth of cells or tissue. In some embodiments, a tumor may comprise cells that are precancerous (*e.g.*, benign), malignant, pre-metastatic, metastatic, and/or non-metastatic. In some embodiments, a tumor is associated with, or is a manifestation of, a cancer. In some embodiments, a tumor may be a disperse tumor or a liquid tumor. In some embodiments, a tumor may be a solid tumor.

[0113] *Vector:* As used herein, the term "vector" refers to a composition of matter that comprises an isolated nucleic acid and which can be used to deliver the isolated nucleic acid to the interior of a cell. Numerous vectors are known in the art including, but not limited to, linear polynucleotides, polynucleotides associated with ionic or amphiphilic compounds, plasmids, and viruses. Thus, the term "vector" includes an autonomously replicating plasmid or a virus. The term should also be construed to include non-plasmid and non-viral compounds which facilitate transfer of nucleic acid into cells, such as, for example, polylysine compounds, liposomes, and the like. Examples of viral vectors include, but are not limited to, adenoviral vectors, adeno-associated virus vectors, retroviral vectors, lentiviral vectors, and the like.

[0114] Throughout this disclosure, various aspects of the invention can be presented in a range format. It should be understood that the description in range format is merely for convenience and brevity and should not be construed as an inflexible limitation on the scope of the invention. Accordingly, the description of a range should be considered to have specifically disclosed all the possible subranges as well as individual numerical values within that range. For example, description of a range such as from 1 to 6 should be considered to have specifically disclosed subranges such as from 1 to 3, from 1 to 4, from 1 to 5, from 2 to 4, from 2 to 6, from 3 to 6 etc., as well as individual numbers within that range, for example, 1, 2, 2.7, 3, 4, 5, 5.3, and 6. This applies regardless of the breadth of the range.

DETAILED DESCIPTION

[0115] Macrophages are powerful modulators of the immune response and can generally adopt either a pro-inflammatory (M1) or an anti-inflammatory (M2) phenotype. A precise balance of M1/M2 macrophages is important in the body's response to disease and injury, and various diseases include dysregulated M1/M2 phenotypes. For example, macrophages in the tumor microenvironment (TME) are often biased toward an M2 phenotype that safeguards the tumor, while M1 macrophages in atherosclerotic tissue typically promote plaque progression. Methods that allow external control over macrophage phenotype are thus promising therapeutic strategies, whether by repolarizing existing macrophages or by delivering macrophages of a desired phenotype (e.g. the delivery of M1 macrophages to the TME or M2 macrophages to atherosclerotic tissue).

[0116] Natural systems use cytokines as potent regulators of M1/M2 phenotype, and thus manipulated cytokine signaling networks represent an appealing system for engineering macrophages. However, cytokines have pleiotropic effects on various immune cells, creating the challenges of avoiding off-target signaling and exclusively activating macrophages of interest. Furthermore, uncontrolled cytokine expression can lead to cytokine release syndrome and other adverse side effects. In order to control an immune cell (e.g., macrophage, monocyte, or dendritic cell) phenotype by harnessing endogenous cytokine signaling pathways, an ideal technology would (i) specify a desired M1/M2 phenotype, (ii) maintain this phenotype in a

disease microenvironment, and (iii) have minimal cytotoxic off-target effects. The present disclosure provides, *inter alia*, such technology.

Immune Cells

[0117] The present disclosure, among other things, provides modified immune cells (e.g., stem cells, macrophages, monocytes, or dendritic cells) comprising an exogenous cytokine as described herein and a chimeric antigen receptor (CAR) as described herein. Accordingly, in some embodiments, at least one CAR comprises: (a) an extracellular domain (e.g., an extracellular domain as described herein), (b) a transmembrane domain (e.g., a transmembrane domain as described herein), and (c) an intracellular domain (e.g., an intracellular domain as described herein).

[0118] The present disclosure, among other things, also provides modified immune cells (e.g., stem cells, macrophages, monocytes, or dendritic cells) comprising at least one fusion protein as described herein. Accordingly, in some embodiments, an immune cell comprising fusion protein comprises: a cytokine ((e.g., a cytokine as described herein), a linker (e.g., a linker as described herein), and a cytokine receptor (e.g., a cytokine receptor as described herein), wherein the cytokine binds the cytokine receptor (see **Figures 3A** and **4A**). In some embodiments, an immune cell further comprises at least one chimeric antigen receptor (CAR) (see **Figures 3B** and **4B**). Accordingly, in some embodiments, at least one CAR comprises: (a) an extracellular domain (e.g., an extracellular domain as described herein), (b) a transmembrane domain (e.g., a transmembrane domain as described herein), and (c) an intracellular domain (e.g., an intracellular domain as described herein).

[0119] In some embodiments, a population of immune cells as described herein comprises stem cells, monocytes, macrophages, dendritic cells, and/or precursors thereof. In some embodiments, a population of immune cells comprises a substantially purified population of stem cells, monocytes, macrophages, or dendritic cells, or a cell line.

[0120] In some embodiments, an immune cell is activated, e.g., an immune cell exhibits increased cytokine production, chemokine production, phagocytosis, cell signaling, target cell killing, and/or antigen presentation, e.g., relative to an inactive cell. In some embodiments, an

activated immune cell exhibits changes in gene expression, e.g., an induction of pro-inflammatory gene expression (e.g., one, two, three, four, five, six, or seven of TNF, IL-12, IFN, GM-CSF, G-CSF, M-CSF, or IL-1), e.g., relative to an inactive cell. In some embodiments, an activated immune cell exhibits changes in gene expression, e.g., an induction of anti-inflammatory gene expression, e.g., relative to an inactive cell. In certain embodiments, activated immune cells are undergoing cell division. In some embodiments, targeted effector activity of an immune cell is enhanced by inhibition of CD47 and/or SIRPα activity. CD47 and/or SIRPα activity may be inhibited by treating an immune cell with an anti-CD47 or anti-SIRPα antibody or by any method known to those skilled in the art.

[0121] In some embodiments, immune cells (e.g., stem cells, macrophages, monocytes, or dendritic cells) are obtained (e.g., isolated) from a subject. Immune cells may be autologous or sourced from allogeneic or universal donors. Cells can be obtained from a number of sources including peripheral blood mononuclear cells, bone marrow, lymph node tissue, spleen tissue, umbilical cord, tumors, and/or induced pluripotent stem cells, such as embryonic stem cells (ESCs). In certain embodiments, cells can be obtained from a unit of blood collected from a subject using any number of separation techniques known to a skilled artisan, such as Ficoll separation. In some embodiments, cells from circulating blood of a subject are obtained by apheresis or leukapheresis. Cells collected by apheresis may be washed to remove a plasma fraction and resuspended in a variety of buffers (e.g., phosphate buffered saline (PBS)) or culture media). In some embodiments, enrichment of immune cells (e.g. monocytes) comprises plastic adherence. In some embodiments, following enrichment, differentiation of immune cells (e.g. monocytes) comprises stimulation with GM-CSF. In some embodiments, a composition comprising blood cells (e.g., monocytes, lymphocytes, platelets, plasma, and/or red blood cells), such as a leukapheresis composition (e.g., a leukopak) is used for enrichment. In some embodiments, a leukapheresis composition (e.g., a leukopak) comprises a sample from a healthy human donor. In certain embodiments, apheresis of immune cells (e.g. monocytes) is followed by mobilization with GM-CSF. In certain embodiments, selection of immune cells (e.g., monocytes) comprises CD14 positive selection using microbeads (e.g., MACS® MicroBeads on a CliniMACS Prodigy device). In some embodiments, an immune cell precursor (e.g., precursors to macrophages, monocytes, or dendritic cells including, but not limited to induced pluripotent stem cells, or iPSCs) is used in compositions and methods described herein. Immune

cell precursors may be differentiated *in vivo* or *ex vivo* into immune cells. Non-limiting examples of precursor immune cells include hematopoietic stem cells, common myeloid progenitors, myeloblasts, monoblasts, promonocytes, or intermediates thereof. For example, induced pluripotent stem cells may be used to generate monocytes, macrophages, and/or dendritic cells. Induced pluripotent stem cells (iPSCs) may be derived from normal human tissue, such as peripheral blood, fibroblasts, skin, keratinocytes, or renal epithelial cells. Autologous, allogeneic, or universal donor iPSCs could be differentiated toward a myeloid lineage (e.g., a monocyte, macrophage, dendritic cell, or precursor thereof).

[0122] Immune cells (e.g., stem cells, macrophages, monocytes, or dendritic cells) as described herein can be isolated from peripheral blood, for example, by lysing red blood cells and depleting lymphocytes and red blood cells, such as by centrifugation through a PERCOLL™ gradient. Alternatively, immune cells can be isolated from umbilical cord tissue. A specific subpopulation of immune cells can be further isolated by positive or negative selection techniques. In some embodiments, immune cells can be depleted of cells expressing certain antigens, including, but not limited to, CD34, CD3, CD4, CD8, CD56, CD66b, CD19, or CD20. In some embodiments, enrichment of an immune cell population, for example, by negative selection can be accomplished using a combination of antibodies directed to surface markers unique to the negatively selected cells. By way of non-limiting example, cell selection can also comprise negative magnetic immunoadherence or flow cytometry that uses a cocktail of monoclonal antibodies directed to cell surface markers present on negatively selected cells.

[0123] During isolation of a desired population of immune cells (e.g., stem cells, macrophages, monocytes, or dendritic cells) as described herein by positive or negative selection, immune cell concentration and surface (e.g., particles, such as beads) can be varied. It may be desirable to significantly decrease volume in which beads and cells are mixed together to ensure maximum contact area of cells and beads.

[0124] In some embodiments, prior to administration, immune cells (e.g., stem cells, macrophages, monocytes, or dendritic cells) as described herein (e.g., comprising an exogenous cytokine described herein or a fusion protein described herein) are treated with a pro-inflammatory agent. In some embodiments, treatment with a pro-inflammatory agent increases anti-tumor activity of immune cells described herein. In some embodiments, treatment with a

pro-inflammatory agent promotes a pro-inflammatory (i.e., M1) phenotype (e.g., a switch from an anti-inflammatory (M2) to a pro-inflammatory (M1) phenotype) in immune cells described herein. In some embodiments, a pro-inflammatory agent comprises or is a CD40 agonist (e.g., CD40L). In some embodiments, a pro-inflammatory agent comprises or is a 41BB-ligand agonist (e.g., 4-1BB).

[0125] In some embodiments, prior to administration, immune cells (e.g., stem cells, macrophages, monocytes, or dendritic cells) as described herein (e.g., comprising an exogenous cytokine described herein or a fusion protein described herein) are treated with an anti-inflammatory agent. In some embodiments, treatment with an anti-inflammatory agent increases anti-inflammatory activity of immune cells described herein. In some embodiments, treatment with an anti-inflammatory agent promotes an anti-inflammatory (i.e., M2) phenotype (e.g., a switch from a pro-inflammatory (M1) to an anti-inflammatory (M2) phenotype) in immune cells described herein. In some embodiments, an anti-inflammatory agent comprises or is an IL-10 agonist. In some embodiments, an anti-inflammatory agent comprises or is a TGFβ agonist.

[0126] In some embodiments, immune cells (e.g., stem cells, macrophages, monocytes, or dendritic cells) as described herein (e.g., comprising an exogenous cytokine described herein or a fusion protein described herein) are administered to a subject in combination with a pro-inflammatory agent. In some embodiments, immune cells (e.g., stem cells, macrophages, monocytes, or dendritic cells) as described herein (e.g., comprising an exogenous cytokine described herein or a fusion protein described herein) are administered to a subject substantially simultaneously, before, or after a pro-inflammatory agent. In some embodiments, administration with a pro-inflammatory agent increases anti-tumor activity of immune cells described herein. In some embodiments, administration with a pro-inflammatory agent promotes a pro-inflammatory (i.e., M1) phenotype (e.g., a switch from an anti-inflammatory (M2) to pro-inflammatory (M1) phenotype) in immune cells described herein. In some embodiments, a pro-inflammatory agent comprises or is a CD40 agonist (e.g., CD40L). In some embodiments, a pro-inflammatory agent comprises or is a 41BB-ligand agonists (e.g., 4-1BB).

Macrophages

[0127] Macrophages are immune cells specialized for detection, phagocytosis, and destruction of target cells, such as pathogens or tumor cells. Macrophages are potent effectors of the innate immune system and are capable of at least three distinct anti-tumor functions: 1) phagocytosis of dead and dying cells, microorganisms, cancer cells, cellular debris, or other foreign substances; 2) cytotoxicity against tumor cells; and 3) presentation of tumor antigens to orchestrate an adaptive anti-tumor immune response.

[0128] Accumulating evidence suggests that macrophages are abundant in the tumor microenvironment of numerous cancers and can adopt a number of phenotypes that are collectively referred to as tumor-associated macrophages (TAMs). The immunosuppressive nature of the tumor microenvironment typically results in more M2-like TAMs, which further contribute to the general suppression of anti-tumor immune responses. Recent studies, however, have identified that TAMs are able to be "reprogrammed" via pro-inflammatory signals, and that the switch from a M2 phenotype to a more M1 phenotype is associated with productive anti-tumor immune responses. Inducing endogenous TAMs to switch to M1-type cells and engineering macrophages that cannot be subverted into M2 would greatly enhance anti-tumor immunotherapy and represent a significant advance in the field.

[0129] In some embodiments, a macrophage comprises or is an undifferentiated or M0 macrophage. In certain embodiments, a macrophage comprises or expresses one, two, three, four, five, or six of CD14, CD16, CD64, CD68, CD71, or CCR5. Exposure to various stimuli can induce M0 macrophages to polarize into several distinct populations, which may be identified by macrophage phenotype markers, cytokine production, and/or chemokine secretion.

[0130] In some embodiments, a macrophage comprises or is a polarized macrophage. Under classical conditions of activation, M0 macrophages can be exposed to pro-inflammatory signals, such as LPS, IFNγ, and GM-CSF, and polarize into pro-inflammatory (i.e., M1) macrophages. Generally, pro-inflammatory (M1) macrophages are associated with pro-inflammatory immune responses, such as Th1 and Th17 T cell responses. Exposure to other stimuli can polarize macrophages into a diverse group of "alternatively activated" or anti-inflammatory (i.e., M2) macrophages.

[0131] In some embodiments, a macrophage comprises or is a pro-inflammatory (M1) macrophage. In some embodiments, a macrophage expresses one or more markers of pro-inflammatory (M1) macrophages (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, or 18 of CD86, CD80, MHC II, IL-1R, TLR2, TLR4, iNOS, SOCS3, CD83, PD-L1, CD69, MHC I, CD64, CD32, CD16, IL1R, a IFIT family member, or an ISG family member).

[0132] In some embodiments, a macrophage comprising or expressing at least one exogenous cytokine described herein or at least one fusion protein described herein secretes relatively high levels of one or more inflammatory cytokines (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, or 12 of IL-1, TNF, IL-12, IL-18, IL-23, IFNα, IFNβ, IFNγ, IL-2, IL-6, IL-8, or IL33) or chemokines (e.g., one or both of CC or CXC chemokines) (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, or 16 of the CXC chemokines; e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, or 28 of the CC chemokines; eg., one of the CX3C chemokines, e.g., one or both of the C chemokines), e.g., relative to a macrophage without an exogenous cytokine as described herein or a fusion protein as described herein. In some embodiments, a macrophage comprising or expressing at least one exogenous cytokine described herein or at least one fusion protein described herein stimulates an immune response and/or inflammation, e.g., relative to a macrophage without an exogenous cytokine as described herein or a fusion protein as described herein.

[0133] In some embodiments, a macrophage comprises or is an anti-inflammatory (M2) macrophage (e.g., an M2a, M2b, M2c, and M2d macrophage). An M2a macrophage can be induced by IL-4, IL-13, and/or fungal infection. An M2b macrophage can be induced by IL-1R ligands, an immune complex, and/or LPS. An M2c macrophage can be induced by IL-10 and/or TGFβ. An M2d macrophage can be induced by IL-6 and/or adenosine. In some embodiments, a macrophage comprising or expressing at least one exogenous cytokine described herein or at least one fusion protein described herein decreases an immune response in a subject, e.g., relative to a macrophage without an exogenous cytokine described herein or a fusion protein as described herein. In some embodiments, a macrophage expresses one or more markers of anti-inflammatory (M2) macrophages (e.g., one, two, or three of CD206, CD163, or CD209). In some embodiments, a macrophage comprising or expressing at least one exogenous cytokine described herein or at least one fusion protein described herein exhibits increased secretion of

one or more anti-inflammatory cytokines (e.g., one or both of IL-10 or TGFβ), e.g., relative to a macrophage without an exogenous cytokine described as herein or a fusion protein as described herein.

[0134] In some embodiments, a macrophage comprises at least one upregulated pro-inflammatory (M1) marker and/or at least one downregulated anti-inflammatory (M2) marker as compared to a control macrophage that does not comprise an exogenous cytokine as provided herein or a fusion protein as provided herein and/or the same macrophage before delivery of an exogenous cytokine described herein or a fusion protein as described herein. In some embodiments, at least one pro-inflammatory (M1) marker (e.g., HLA DR, CD86, CD80, PD-L1, CD83, CD69, MHC I, CD64, CD32, CD16, IL1R, an IFIT family member, and/or an ISG family member) is upregulated in a macrophage. In some embodiments, at least one anti-inflammatory (M2) marker (e.g., CD206, CD163, and/or CD209) is downregulated in a macrophage.

[0135] In some embodiments, a macrophage comprising or expressing at least one exogenous cytokine described herein or at least one fusion protein described herein exhibits increased phagocytosis, e.g., relative to a macrophage without an exogenous cytokine as described herein or a fusion protein as described herein. In some embodiments, a macrophage comprising or expressing at least one exogenous cytokine described herein or at least one fusion protein described herein exhibits increased cytotoxicity against a tumor cell, e.g., relative to a macrophage without an exogenous cytokine as described herein or a fusion protein as described herein. In some embodiments, a macrophage comprising or expressing at least one exogenous cytokine described herein or at least one fusion protein described herein exhibits increased tumor antigen presentation (e.g., post-phagocytosis presentation) and/or increased antigen processing, e.g., relative to a macrophage without an exogenous cytokine as described herein or a fusion protein as described herein. In some embodiments, a macrophage comprising or expressing at least one exogenous cytokine described herein or at least one fusion protein described herein exhibits increased tumor killing (e.g., by phagocytosis, lysis, apoptosis, or production of tumor killing cytokines (e.g., TNFα), e.g., relative to a macrophage without an exogenous cytokine as described herein or a fusion protein as described herein.

[0136] In some embodiments, a macrophage comprising or expressing at least one exogenous cytokine described herein or at least one fusion protein described herein exhibits one

or both of increased expression of one or more genes typically associated with increased effector function (e.g., phagocytosis, targeted cellular cytotoxicity, antigen presentation, or cytokine secretion) (e.g., CD80, CD86, MHC-I, MHC-II, CD40, 41BBL, TNF, IFN-α, IFN-β, IFN-γ, IL2, IL12, IL6, IL8, IL1b, and/or CXCL12) or decreased expression of one or more genes typically associated with decreased effector function (e.g., phagocytosis, targeted cellular cytotoxicity, antigen presentation, or cytokine secretion) (e.g., CD163, CD206, TGFβ, IL-10, and/or IL4), e.g., relative to a macrophage without an exogenous cytokine as described herein or a fusion protein as described herein. In some embodiments, a macrophage comprising or expressing at least one exogenous cytokine described herein or at least one fusion protein described herein exhibits increased production of ROS, e.g., relative to a macrophage without an exogenous cytokine as described herein or a fusion protein as described herein. In some embodiments, a macrophage comprising or expressing at least one exogenous cytokine described herein or at least one fusion protein described herein exhibits metabolic reprogramming (e.g., of an interferon signaling pathway, TH1 pathway, PTEN signaling, PI3K signaling, MTOR signaling, TLR signaling, CD40 signaling, 41BB signaling, 41BBL signaling, macrophage maturation signaling, dendritic cell maturation signaling, CD3-zeta signaling, FcR γ signaling, CD64 signaling, CD32a signaling, CD32c signaling, CD16a signaling, TLR1 signaling, TLR2 signaling, TLR3 signaling, TLR4 signaling, TLR5 signaling, TLR6 signaling, TLR7 signaling, TLR8 signaling, TLR9 signaling, ALK signaling, AXL signaling, DDR2 signaling, EGFR signaling, EphA1 signaling, INSR signaling, cMET signaling, MUSK signaling, PDGFR signaling, PTK7 signaling, RET signaling, ROR1 signaling, ROS1 signaling, RYK signaling, TIE2 signaling, TRK signaling, VEGFR signaling, CD40 signaling, CD19 signaling, CD20 signaling, 41BB signaling, CD28 signaling, OX40 signaling, GITR signaling, TREM-1 signaling, TREM-2 signaling, DAP12 signaling, MR signaling, ICOS signaling, MyD88 signaling, V/I/LxYxxL/V signaling, SIRPα signaling, CD45 signaling, Siglec-10 signaling, PD1 signaling, SHP-1 signaling, SHP-2 signaling, KIR-2DL signaling, KIR-3DL signaling, NKG2A signaling, CD170 signaling, CD33 signaling, BTLA signaling, CD32b signaling, SIRPβ signaling, CD22 signaling, PIR-B signaling, and/or LILRB1 signaling), e.g., relative to a macrophage without an exogenous cytokine as described herein or a fusion protein as described herein. In some embodiments, a macrophage comprising or expressing at least one exogenous cytokine described herein or at least one fusion protein described herein exhibits induction of cell

survival mechanisms, e.g., relative to a macrophage without an exogenous cytokine described herein or a fusion protein as described herein. In some embodiments, a macrophage comprising or expressing at least one exogenous cytokine described herein or at least one fusion protein described herein exhibits induction of cell death mechanisms, e.g., relative to a macrophage without an exogenous cytokine as described herein or a fusion protein as described herein. In some embodiments, a macrophage comprising or expressing at least one exogenous cytokine described herein or at least one fusion protein described herein exhibits one, two, three, four, or five of increased resistance to phagocytic checkpoints, increased expression of chemokine receptors to aid in trafficking, increased expression of chemokines to recruit other immune cells, increased expression of ECM degrading enzymes (e.g., MMPs to degrade tumor ECM and/or exhibit anti fibrotic activity), and/or increased proliferation, e.g., relative to a macrophage without an exogenous cytokine as described herein or a fusion protein as described herein. In some embodiments, a macrophage comprising or expressing at least one exogenous cytokine described herein and at least one CAR as described herein exhibits one, two, three, or four of improved duration of exogenous cytokine expression, improved stability of the CAR on the cell surface, increased level of exogenous cytokine expression, and/or decreased background activity of the exogenous cytokine, e.g., relative to a macrophage without an exogenous cytokine as described herein. In some embodiments, a macrophage comprising or expressing at least one fusion protein described herein exhibits one, two, three, or four of improved duration of fusion protein expression, improved stability of the fusion protein on the cell surface, increased level of fusion protein expression, and/or decreased background activity of the fusion protein, e.g., relative to a macrophage without a fusion protein as described herein.

[0137] In some embodiments, a macrophage comprising or expressing at least one exogenous cytokine described herein or at least one fusion protein described herein decreases one or more signs and/or symptoms of an infection (e.g., of an infectious agent) in a subject, e.g., relative to a macrophage without an exogenous cytokine as described herein or a fusion protein as described herein. In some embodiments, an infectious agent comprises or is a virus, a protozoa (e.g., trypanosome, malaria, or toxoplasma), a bacteria (e.g., mycobacterium, salmonella, or listeria), a fungi (e.g., Candida), or a combination thereof. In some embodiments, a virus comprises hepatitis virus (e.g., hepatitis A, hepatitis B, hepatitis C, or hepatitis E), retrovirus, human immunodeficiency virus (e.g., HIV1 or HIV2), T cell leukemia virus, a

Lymphotropic virus (e.g., HTLV1 or HTLV2), herpes simplex virus (e.g., herpes simplex virus type 1 or type 2), Epstein-Barr virus, cytomegalovirus, varicella-zoster virus, poliovirus, measles virus, Rubella virus, Japanese encephalitis virus, mumps virus, influenza virus, adenovirus, enterovirus, rhinovirus, coronavirus (e.g., severe acute respiratory syndrome (SARS) virus, Middle East respiratory syndrome (MERS) virus, or severe acute respiratory syndrome coronavirus 2 (SARS-CoV2)), Ebola virus, West Nile virus, or a variant or combination thereof.

[0138] In some embodiments, a macrophage comprising or expressing at least one exogenous cytokine described herein or at least one fusion protein described herein decreases formation and/or degrades existing aggregates via phagocytosis of at least one protein aggregate in a subject (e.g., a subject having a neurodegenerative disease, an inflammatory disease, a cardiovascular disease, a fibrotic disease, amyloidosis, or a combination thereof), e.g., relative to a macrophage without an exogenous cytokine as described herein or a fusion protein as described herein. In some embodiments, a neurodegenerative disease is selected from the group consisting of tauopathy, a-synucleopathy, presenile dementia, senile dementia, Alzheimer's disease, progressive supranuclear palsy (PSP), Pick's disease, primary progressive aphasia, frontotemporal dementia, corticobasal dementia, Parkinson's disease, dementia with Lewy bodies, Down's syndrome, multiple system atrophy, amyotrophic lateral sclerosis (ALS), Hallervorden-Spatz syndrome, polyglutamine disease, trinucleotide repeat disease, and prion disease. In some embodiments, an inflammatory disease is selected from the group consisting of systemic lupus erythematosus, vasculitis, rheumatoid arthritis, periodontitis, ulcerative colitis, sinusitis, asthma, tuberculosis, Crohn’s disease, chronic infection, hereditary periodic fever, a malignancy, systemic vasculitides, cystic fibrosis, bronchiectasis, epidermolysis bullosa, cyclic neutropenia, an immunodeficiency, Muckle-Wells (MWS) disease, and Familiar Mediterranean Fever (FMF). In some embodiments, amyloidosis is selected from the group consisting of Primary Amyloidosis (AL), Secondary Amyloidosis (AA), Familial Amyloidosis (ATTR) , Beta-2 Microglobulin Amyloidosis, Localized Amyloidosis, Heavy Chain Amyloidosis (AH), Light Chain Amyloidosis (AL), Primary Systemic Amyloidosis, ApoAI Amyloidosis, ApoAII Amyloidosis, ApoAIV Amyloidosis, Apolipoprotein C2 Amyloidosis, Apolipoprotein C3 Amyloidosis, Corneal lactoferrin amyloidosis, Transthyretin-Related Amyloidosis, Dialysis amyloidosis, Fibrinogen amyloidosis, Lect2 amyloidosis (ALECT2), and Lysozyme amyloidosis. In some embodiments, a cardiovascular disease is selected from the group consisting of

atherosclerosis, coronary artery disease, peripheral artery disease, hypertensive heart disease, metabolic syndrome, hypertension, cerebrovascular disease, and heart failure. In some embodiments, a fibrotic disease is selected from the group consisting of pulmonary fibrosis, idiopathic pulmonary fibrosis, cirrhosis, cystic fibrosis, scleroderma, cardiac fibrosis, radiation-induced lung injury, steatohepatitis, glomerulosclerosis, interstitial lung disease, liver fibrosis, mediastinal fibrosis, retroperitoneal cavity fibrosis, bone marrow fibrosis, and skin fibrosis.

Monocytes

[0139] Monocytes are multipotent cells that circulate in the blood, bone marrow, and spleen, and generally do not proliferate when in a steady state. Monocytes can vary in size significantly in the range of about 10-30 μm in diameter. A ratio of nucleus to cytoplasm for a monocyte can range from about 2:1 to about 1:1. Typically, monocytes comprise chemokine receptors and pathogen recognition receptors that mediate migration from blood to tissues, such as during an infection. Monocytes can produce inflammatory cytokines, take up cells and/or toxic molecules, and differentiate into dendritic cells or macrophages.

[0140] In some embodiments, a monocyte comprises or expresses one or more phenotypic markers. Exemplarily phenotypic markers for human monocyte cells include, but are not limited to, CD9, CD11b, CD11c, CDw12, CD13, CD15, CDw17, CD31, CD32, CD33, CD35, CD36, CD38, CD43, CD49b, CD49e, CD49f, CD63, CD64, CD65s, CD68, CD84, CD85, CD86, CD87, CD89, CD91, CDw92, CD93, CD98, CD101, CD102, CD111, CD112, CD115, CD116, CD119, CDwl2lb, CDw123, CD127, CDw128, CDw131, CD147, CD155, CD156a, CD157, CD162 CD163, CD164, CD168, CD171, CD172a, CD180, CD206, CD131a1, CD213 2, CDw210, CD226, CD281, CD282, CD284, and CD286. Exemplarily phenotypic markers for mouse monocyte cells include, but are not limited to, CD11a, CD11b, CD16, CD18, CD29, CD31, CD32, CD44, CD45, CD49d, CD115, CD116, Cdw131, CD281, CD282, CD284, CD286, F4/80, and CD49b. In certain embodiments monocytes comprise one, two, or three of CD11b, CD14, or CD16. In certain embodiments, monocytes comprise CD14+ CD16- monocytes, CD14+ CD16+ monocytes, or CD14- CD16+ monocytes.

[0141] In some embodiments, a monocyte differentiates into a macrophage. In some embodiments, a monocyte differentiates into a dendritic cell (DC). Monocytes can be

differentiated into macrophages or DCs by any technique known in the art. For example, differentiation of monocytes into macrophages can be induced by macrophage colony stimulating factor (M-CSF). Differentiation of monocytes into DCs can be induced by granulocyte-macrophage colony stimulating factor (GM-CSF) in combination with IL-4.

[0142] In some embodiments, a monocyte comprising or expressing at least one exogenous cytokine described herein or at least one fusion protein described herein exhibits increased secretion of one or more cytokines (e.g., one, two, three, four, five, six, or seven of TNF, IL-12, IFN, GM-CSF, G-CSF, M-CSF, or IL-1), e.g., relative to a monocyte without an exogenous cytokine described herein or a fusion protein as described herein. In some embodiments, a monocyte comprising or expressing at least one exogenous cytokine described herein or at least one fusion protein described herein exhibits increased phagocytosis, e.g., relative to a monocyte without an exogenous cytokine described as herein or a fusion protein as described herein. In some embodiments, a monocyte comprising or expressing at least one exogenous cytokine described herein or at least one fusion protein described herein exhibits enhanced survival, e.g., relative to a monocyte without an exogenous cytokine as described herein or a fusion protein as described herein. In some embodiments, a monocyte comprising or expressing at least one exogenous cytokine described herein or at least one fusion protein described herein exhibits enhanced differentiation into macrophages (e.g., M1 or M2 macrophages), e.g., relative to a monocyte without an exogenous cytokine as described herein or a fusion protein as described herein. In some embodiments, a monocyte comprising or expressing at least one exogenous cytokine described herein or at least one fusion protein described herein exhibits enhanced differentiation into DCs (e.g., resident or migrating DCs and/or in lymphoid and non-lymphoid tissue), e.g., relative to a monocyte without an exogenous cytokine as described herein or a fusion protein as described herein. In some embodiments, a monocyte comprising or expressing at least one exogenous cytokine described herein or at least one fusion protein described herein exhibits increased cytotoxicity against a tumor cell, e.g., relative to a monocyte without an exogenous cytokine as described herein or a fusion protein as described herein. In some embodiments, a monocyte comprising or expressing at least one exogenous cytokine described herein or at least one fusion protein described herein exhibits increased tumor antigen presentation (e.g., post-phagocytosis presentation) and/or increased antigen processing, e.g., relative to a monocyte without an exogenous cytokine as described

herein or a fusion protein as described herein. In some embodiments, a monocyte comprising or expressing at least one exogenous cytokine described herein or at least one fusion protein described herein exhibits increased tumor killing (e.g., by phagocytosis, lysis, apoptosis, or production of tumor killing cytokines (e.g., TNFα), e.g., relative to a monocyte without an exogenous cytokine described herein or a fusion protein as described herein.

[0143] In some embodiments, a monocyte comprising or expressing at least one exogenous cytokine described herein or at least one fusion protein described herein exhibits one or both of increased expression of one or more genes typically associated with increased effector function (e.g., phagocytosis, targeted cellular cytotoxicity, antigen presentation, or cytokine secretion) or decreased expression of one or more genes typically associated with decreased effector function (e.g., phagocytosis, targeted cellular cytotoxicity, antigen presentation, or cytokine secretion), e.g., relative to a monocyte without an exogenous cytokine as described herein or a fusion protein as described herein. In some embodiments, a monocyte comprising or expressing at least one exogenous cytokine described herein or at least one fusion protein described herein exhibits increased production of ROS, e.g., relative to a monocyte without an exogenous cytokine as described herein or a fusion protein as described herein. In some embodiments, a monocyte comprising or expressing at least one exogenous cytokine described herein or at least one fusion protein described herein exhibits metabolic reprogramming, e.g., relative to a monocyte without an exogenous cytokine as described herein or a fusion protein as described herein. In some embodiments, a monocyte comprising or expressing at least one exogenous cytokine described herein or at least one fusion protein described herein exhibits induction of cell survival mechanisms, e.g., relative to a monocyte without an exogenous cytokine as described herein or a fusion protein as described herein. In some embodiments, a monocyte comprising or expressing at least one exogenous cytokine described herein or at least one fusion protein described herein exhibits induction of cell death mechanisms, e.g., relative to a monocyte without an exogenous cytokine as described herein or a fusion protein as described herein. In some embodiments, a monocyte comprising or expressing at least one exogenous cytokine described herein or at least one fusion protein described herein exhibits one, two, three, four, or five of increased resistance to phagocytic checkpoints, increased expression of chemokine receptors to aid in trafficking, increased expression of chemokines to recruit other immune cells, increased expression of ECM degrading enzymes (e.g., MMPs to degrade tumor

ECM and/or exhibit anti fibrotic activity), or increased proliferation, e.g., relative to a monocyte without an exogenous cytokine as described herein or a fusion protein as described herein. In some embodiments, a monocyte comprising or expressing at least one exogenous cytokine described herein and at least one CAR as described herein exhibits one, two, three, or four of improved duration of exogenous cytokine expression, improved stability of the CAR on the cell surface, increased level of exogenous cytokine expression, and/or decreased background activity of the exogenous cytokine, e.g., relative to a monocyte without an exogenous cytokine as described herein. In some embodiments, a monocyte comprising or expressing at least one fusion protein described herein exhibits one, two, three, or four of improved duration of fusion protein expression, improved stability of the fusion protein on the cell surface, increased level of fusion protein expression, or decreased background activity of the fusion protein, e.g., relative to a monocyte without a fusion protein as described herein.

Dendritic Cells

[0144] Dendritic cells (DCs) are bone marrow-derived, specialized antigen presenting cells that are involved in initiating immune responses and maintaining tolerance of the immune system to self-antigens. Dendritic cells may be found in both lymphoid and non-lymphoid organs and are generally thought to arise from lymphoid or myeloid lineages.

[0145] In some embodiments, a DC comprises or expresses one or more phenotypic markers. Exemplarily phenotypic markers for DCs include, but are not limited to, CD11c, CD83, CD1a, CD1c, CD141, CD207, CLEC9a, CD123, CD85, CD180, CD187, CD205, CD281, CD282, CD284, CD286 and partially CD206, CD207, CD208 and CD209.

[0146] Immature DCs can be characterized by a high capacity for antigen capture, but relatively low T cell stimulatory capability. Inflammatory mediators promote DC maturation. Once DCs reach the mature stage, there is a dramatic change in properties relative to immature DCs, such as a decrease in antigen capture ability and/or an increased ability to stimulate T cells. In some embodiments, a DC comprises or is an immature DC. In other embodiments, a DC comprises or is a mature DC.

[0147] Without wishing to be bound by theory, it is believed that modification of a DC cell to comprise or express at least one exogenous cytokine described herein or at least one fusion protein described herein can allow mature DCs to simultaneously exhibit increased antigen capture ability and T cell stimulation, e.g., relative to a DC without an exogenous cytokine described herein or a fusion protein described herein. In some embodiments, a DC comprising or expressing at least one exogenous cytokine described herein or at least one fusion protein described herein mediates tumor antigen presentation, e.g., increased tumor antigen presentation relative to a DC without an exogenous cytokine as described herein or a fusion protein as described herein. In some embodiments, a DC comprising or expressing at least one exogenous cytokine described herein or at least one fusion protein described herein mediates tumor T cell stimulation, e.g., increased T cell stimulation relative to a DC without an exogenous cytokine as described herein or a fusion protein as described herein.

[0148] In some embodiments, a DC comprising or expressing at least one exogenous cytokine described herein or at least one fusion protein described herein exhibits increased secretion of one or more cytokines (e.g., one, two, three, four, five, six, or seven of TNF, IL-12, IFN, GM-CSF, G-CSF, M-CSF, or IL-1), e.g., relative to a DC without an exogenous cytokine as described herein or a fusion protein as described herein. In some embodiments, a DC comprising or expressing at least one exogenous cytokine described herein or at least one fusion protein described herein exhibits increased phagocytosis, e.g., relative to a DC without an exogenous cytokine as described herein or a fusion protein as described herein. In some embodiments, a DC comprising or expressing at least one exogenous cytokine described herein or at least one fusion protein described herein exhibits increased tumor antigen presentation (e.g., post-phagocytosis presentation), increased antigen processing, increased antigen cross presentation, increased T cell priming, and/or stimulation of T cells, e.g., relative to a DC without an exogenous cytokine as described herein or a fusion protein as described herein.

[0149] In some embodiments, a DC comprising or expressing at least one exogenous cytokine described herein or at least one fusion protein described herein exhibits one or both of increased expression of favorable genes or decreased expression of unfavorable genes, e.g., relative to a DC without an exogenous cytokine as described herein or a fusion protein as described herein. In some embodiments, a DC comprising or expressing at least one exogenous

cytokine described herein or at least one fusion protein described herein exhibits increased production of ROS, e.g., relative to a DC without an exogenous cytokine as described herein or a fusion protein as described herein. In some embodiments, a DC comprising or expressing at least one exogenous cytokine described herein or at least one fusion protein described herein exhibits metabolic reprogramming, e.g., relative to a DC without an exogenous cytokine described herein or a fusion protein as described herein. In some embodiments, a DC comprising or expressing at least one exogenous cytokine described herein or at least one fusion protein described herein exhibits induction of cell survival mechanisms, e.g., relative to a DC without an exogenous cytokine as described herein or a fusion protein as described herein.

[0150] In some embodiments, a DC comprising or expressing at least one exogenous cytokine described herein or at least one fusion protein described herein exhibits induction of cell death mechanisms, e.g., relative to a DC without an exogenous cytokine as described herein or a fusion protein as described herein. In some embodiments, a DC comprising or expressing at least one exogenous cytokine described herein or at least one fusion protein described herein exhibits one, two, three, four, or five of increased resistance to phagocytic checkpoints, increased expression of chemokine receptors to aid in trafficking, increased expression of chemokines to recruit other immune cells, increased expression of ECM degrading enzymes (e.g., MMPs to degrade tumor ECM and/or exhibit anti fibrotic activity), or increased proliferation, e.g., relative to a DC without an exogenous cytokine as described herein or a fusion protein as described herein. In some embodiments, a DC comprising or expressing at least one exogenous cytokine described herein and at least one CAR as described herein exhibits one, two, three, or four of improved duration of exogenous cytokine expression, improved stability of the CAR on the cell surface, increased level of exogenous cytokine expression, and/or decreased background activity of the exogenous cytokine, e.g., relative to a DC without an exogenous cytokine as described herein. In some embodiments, a DC comprising or expressing at least one fusion protein described herein exhibits one, two, three, or four of improved duration of fusion protein expression, improved stability of the fusion protein on the cell surface, increased level of fusion protein expression, or decreased background activity of the fusion protein, e.g., relative to a DC without a fusion protein as described herein.

Methods of Immune Cell Modification

[0151] The present disclosure provides, among other things, methods for modifying an immune cell (e.g., a stem cell, monocyte, macrophage, or dendritic cell) comprising delivering to the immune cell a nucleic acid construct comprising one or more nucleic acids encoding an exogenous cytokine and a chimeric antigen receptor (CAR) into an immune cell. Methods can comprise delivering to an immune cell (e.g., a stem cell, monocyte, macrophage, or dendritic cell), a nucleic acid construct comprising one or more nucleic acids encoding an exogenous cytokine and a CAR.

[0152] The present disclosure also provides, among other things, methods for modifying an immune cell (e.g., a stem cell, monocyte, macrophage, or dendritic cell) comprising delivering to the immune cell a nucleic acid construct comprising one or more nucleic acids encoding a fusion protein or a fragment thereof into an immune cell. Methods can comprise delivering to an immune cell (e.g., a stem cell, monocyte, macrophage, or dendritic cell), a nucleic acid construct comprising one or more nucleic acids encoding: a fusion protein comprising a cytokine, a linker, and a cytokine receptor.

[0153] A nucleic acid construct comprising one or more nucleic acid sequences encoding at least one exogenous cytokine as described herein or at least one fusion protein as described herein can be introduced into an immune cell (e.g., a stem cell, macrophage, monocyte, or dendritic cell) by physical, chemical, or biological methods. Physical methods for introducing a nucleic acid construct as described herein into an immune cell (e.g., a stem cell, macrophage, monocyte, or dendritic cell) can comprise electroporation, calcium phosphate precipitation, lipofection, particle bombardment, microinjection, or a combination thereof. A nucleic acid construct can be introduced into immune cells using commercially available methods, including electroporation (Amaxa Nucleofector-II® (Amaxa Biosystems, Cologne, Germany), ECM 830 BTX (Harvard Instruments, Boston, Mass.) Gene Pulser II® (BioRad, Denver, Colo.), or Multiporator® (Eppendort, Hamburg Germany)). A nucleic acid construct can also be introduced into immune cells using mRNA transfection, e.g., cationic liposome-mediated transfection, lipofection, polymer encapsulation, peptide-mediated transfection, or biolistic particle delivery systems, such as "gene guns" (See, e.g., Nishikawa, et al. Hum Gene Ther., 12(8):861-70 (2001), which is hereby incorporated by reference in its entirety).

[0154] Biological methods for introducing a nucleic acid construct as described herein into an immune cell (e.g., a stem cell, macrophage, monocyte, or dendritic cell) include use of DNA and RNA vectors. Viral vectors, and especially retroviral vectors, have become widely used for inserting genes into mammalian cells (e.g., human cells). Viral vectors can also be derived from lentivirus, poxviruses, herpes simplex virus I, adenoviruses (e.g. Ad5f35), or adeno-associated viruses (See, e.g., U.S. Patent Nos. 5,350,674 and 5,585,362, which are hereby incorporated by reference in their entirety). Retroviral vectors, such as lentivirus, are suitable tools to achieve long-term gene transfer that allow for long-term, stable integration of a transgene and its propagation in daughter cells. In some embodiments, a lentiviral vector is packaged with a Vpx protein (e.g., as described in International Publication No. WO 2017/044487, which is hereby incorporated by reference in its entirety). In some embodiments, Vpx comprises a virion-associated protein (e.g., an accessory protein for viral replication). In some embodiments, a Vpx protein is encoded by human immunodeficiency virus type 2 (HIV-2). In some embodiments, a Vpx protein is encoded by simian immunodeficiency virus (SIV). In some embodiments, an immune cell as described herein (e.g., a stem cell, macrophage, monocyte, or dendritic cell) is transfected with a lentiviral vector packaged with a Vpx protein. In some embodiments, Vpx inhibits at least one antiviral factor of an immune cell as described herein (e.g., a stem cell, macrophage, monocyte, or dendritic cell). In some embodiments, a lentiviral vector packaged with a Vpx protein exhibits increased transfection efficiency of an immune cell as described herein (e.g., a stem cell, macrophage, monocyte, or dendritic cell), e.g., relative to a lentiviral vector not packaged with a Vpx protein. In some embodiments, an immune cell as described herein (e.g., a stem cell, macrophage, monocyte, or dendritic cell) is one or both of electroporated or transfected with at least one VPX mRNA prior to transfection with a viral vector (e.g., an adenoviral vector, e.g., an Ad2 vector or an Ad5 vector (e.g., Ad5f35 adenoviral vector, e.g., a helper-dependent Ad5F35 adenoviral vector)).

[0155] Chemical means for introducing a nucleic acid construct as described herein into an immune cell (e.g., a stem cell, macrophage, monocyte, or dendritic cell) include colloidal dispersion systems, macromolecule complexes, nanocapsules, microspheres, beads, and lipid-based systems (e.g., oil-in-water emulsions, micelles, mixed micelles, nanoparticles, liposomes, and lipofectamine-nucleic acid complexes).

[0156] An exemplary system for delivery of a nucleic acid construct as described herein is a lipid-based system. A nucleic acid construct as described herein may be encapsulated in an aqueous interior of a liposome, interspersed within a lipid bilayer, attached to a liposome via a linking molecule, entrapped in a liposome, complexed with a liposome, dispersed in a solution or suspension comprising a lipid, mixed with a lipid, complexed with a micelle, or otherwise associated with a lipid. Lipids for use in methods described herein may be naturally occurring or synthetic lipids. Lipids can also be obtained from commercial sources. For example, dimyristyl phosphatidylcholine can be obtained from Sigma (St. Louis, MO); dicetyl phosphate can be obtained from K & K Laboratories (Plainview, NY); cholesterol can be obtained from Calbiochem-Behring; and dimyristyl phosphatidylglycerol can be obtained from Avanti Polar Lipids, Inc. (Birmingham, AL.). Stock solutions of lipids in chloroform or chloroform/methanol can be stored at about -20°C.

[0157] In some embodiments of the present disclosure, a nucleic acid construct is or comprises an mRNA. In some embodiments, mRNA according to the present disclosure may be synthesized as unmodified or modified mRNA. Typically, mRNAs are modified to enhance stability. Modifications of mRNA can include, for example, modifications of the nucleotides of the RNA. A modified mRNA according to the present disclosure can thus include, for example, backbone modifications, sugar modifications or base modifications. In some embodiments, a step of modifying an mRNA comprises causing the mRNA to include a modified nucleotide, an alteration to the 5' or 3' untranslated region (UTR), a cap structure, and/or a poly(A) tail.

[0158] In some embodiments, mRNAs of the present disclosure (e.g., mRNAs encoding exogenous cytokines, mRNAs encoding CARs, or mRNAs encoding fusion proteins) may contain RNA backbone modifications. Typically, a backbone modification is a modification in which the phosphates of the backbone of the nucleotides contained in the RNA are modified chemically. Exemplary backbone modifications typically include, but are not limited to, modifications from the group consisting of methylphosphonates, methylphosphoramidates, phosphoramidates, phosphorothioates (e.g. cytidine 5'-O-(1-thiophosphate)), boranophosphates, positively charged guanidinium groups etc., which comprises replacing the phosphodiester linkage by other anionic, cationic or neutral groups.

[0159] In some embodiments, mRNAs of the present disclosure (e.g., mRNAs encoding exogenous cytokines, mRNAs encoding CARs, or mRNAs encoding fusion proteins) may contain sugar modifications. A typical sugar modification is a chemical modification of the sugar of the nucleotides it contains including, but not limited to, sugar modifications chosen from the group consisting of 2'-deoxy-2'-fluoro-oligoribonucleotide (2'-fluoro-2'-deoxycytidine 5'-triphosphate, 2'-fluoro-2'-deoxyuridine 5'-triphosphate), 2'-deoxy-2'-deamine-oligoribonucleotide (2'-amino-2'-deoxycytidine 5'-triphosphate, 2'-amino-2'-deoxyuridine 5'-triphosphate), 2'-O-alkyloligoribonucleotide, 2'-deoxy-2'-C-alkyloligoribonucleotide (2'-O-methylcytidine 5'-triphosphate, 2'-methyluridine 5'-triphosphate), 2'-C-alkyloligoribonucleotide, and isomers thereof (2'-aracytidine 5'-triphosphate, 2'-arauridine 5'-triphosphate), or azidotriphosphates (2'-azido-2'-deoxycytidine 5'-triphosphate, 2'-azido-2'-deoxyuridine 5'-triphosphate).

[0160] In some embodiments, mRNAs of the present disclosure (e.g., mRNAs encoding exogenous cytokines, mRNAs encoding CARs, or mRNAs encoding fusion proteins) may contain modifications of the bases of the nucleotides (base modifications). A modified nucleotide which contains a base modification is also called a base-modified nucleotide.

[0161] Typically, mRNA synthesis includes the addition of a “cap” on the N-terminal (5’) end, and a “tail” on the C-terminal (3’) end. The presence of the cap is important in providing resistance to nucleases found in most eukaryotic cells. The presence of a “tail” serves to protect the mRNA from exonuclease degradation.

[0162] Thus, in some embodiments, mRNAs of the present disclosure (e.g., mRNAs encoding exogenous cytokines, mRNAs encoding CARs, or mRNAs encoding fusion proteins) include a 5’ cap structure. A 5’ cap is typically added as follows: first, an RNA terminal phosphatase removes one of the terminal phosphate groups from the 5’ nucleotide, leaving two terminal phosphates; guanosine triphosphate (GTP) is then added to the terminal phosphates via a guanylyl transferase, producing a 5’ triphosphate linkage; and the 7-nitrogen of guanine is then methylated by a methyltransferase. Examples of cap structures include, but are not limited to, m7G(5')ppp (5'(A,G(5')ppp(5')A and G(5')ppp(5')G. In some embodiments, a cap comprises a Cap0 structure. A cap0 structures lack a 2'-O-methyl residue of the ribose attached to bases 1 and 2. In some embodiments, a cap comprises an AGCap1 structure. An AGCap1 structures has a 2'-O-methyl residue at base 2. In some embodiments, a cap comprises a Cap2 structure. Cap2

structures have a 2'-O-methyl residue attached to both bases 2 and 3. In some embodiments, a cap structure comprises AGCap1, m6AGCap1, or Anti-Reverse Cap Analog (ARCA). In some embodiments, a modified mRNA of the present disclosure comprises an m6AGCap1 and modified nucleotides comprising pseudouridine (PsU).

[0163] In some embodiments, mRNAs of the present disclosure (e.g., mRNAs encoding exogenous cytokines, mRNAs encoding CARs, or mRNAs encoding fusion proteins) include a 3' poly(A) tail structure. A poly(A) tail on the 3' terminus of mRNA typically includes about 10 to 400 adenosine nucleotides (SEQ ID NO: 176) (e.g., about 100 to 400 adenosine nucleotides, about 10 to 200 adenosine nucleotides, about 10 to 150 adenosine nucleotides, about 10 to 100 adenosine nucleotides, about 20 to 70 adenosine nucleotides, or about 20 to 60 adenosine nucleotides). In some embodiments, mRNAs include a 3' poly(C) tail structure. A suitable poly(C) tail on the 3' terminus of mRNA typically include about 10 to 200 cytosine nucleotides (SEQ ID NO: 177) (e.g., about 10 to 150 cytosine nucleotides, about 10 to 100 cytosine nucleotides, about 20 to 70 cytosine nucleotides, about 20 to 60 cytosine nucleotides, or about 10 to 40 cytosine nucleotides). A poly(C) tail may be added to a poly(A) tail or may be a substitute for the poly(A) tail.

[0164] In some embodiments, mRNAs of the present disclosure (e.g., mRNAs encoding exogenous cytokines, mRNAs encoding CARs, or mRNAs encoding fusion proteins) include a 5' and/or 3' untranslated region. In some embodiments, a 5' untranslated region includes one or more elements that affect an mRNA's stability or translation, for example, an iron responsive element. In some embodiments, a 5' untranslated region may be between about 50 and 500 nucleotides in length.

[0165] In some embodiments, a 3' untranslated region includes one or more of a polyadenylation signal, a binding site for proteins that affect an mRNA's stability of location in a cell, or one or more binding sites for miRNAs. In some embodiments, a 3' untranslated region may be between 50 and 500 nucleotides in length or longer.

Treatment and Culturing of Immune Cells During Modification

[0166] In some embodiments, methods of the present disclosure comprise one or more steps of treating an immune cell (e.g., a stem cell, macrophage, monocyte, or dendritic cell) during the process of modifying the immune cell.

[0167] In some embodiments, methods of the present disclosure comprise a step of treating an immune cell (e.g., a stem cell, macrophage, monocyte, or dendritic cell) with a modulator of a pathway activated by in vitro transcribed mRNA. In vitro transcribed (IVT) mRNA is recognized by various endosomal innate immune receptors (Toll-like receptor 3 (TLR3), TLR7 and TLR8) and cytoplasmic innate immune receptors (protein kinase RNA-activated (PKR), retinoic acid-inducible gene I protein (RIG-I), melanoma differentiation-associated protein 5 (MDA5) and 2′-5′-oligoadenylate synthase (OAS)). Signaling through these different pathways results in inflammation associated with type 1 interferon (IFN), tumor necrosis factor (TNF), interleukin-6 (IL-6), IL-12 and the activation of cascades of transcriptional programs. Overall, these create a pro-inflammatory microenvironment poised for inducing specific immune responses. Moreover, downstream effects such as slow-down of translation by eukaryotic translation initiation factor 2α (eIF2α) phosphorylation, enhanced RNA degradation by ribonuclease L (RNaseL), and overexpression and inhibition of replication of self-amplifying mRNA are of relevance for the pharmacokinetics and pharmacodynamics of IVT mRNA.

[0168] In some embodiments, a modulator of a pathway activated by in vitro transcribed mRNA comprises an RNase inhibitor. In some embodiments, a modulator of a pathway activated by in vitro transcribed mRNA comprises an RNaseL, RNase T2 or RNase1 inhibitor. In some embodiments, a modulator of a pathway activated by in vitro transcribed mRNA comprises an RNaseL inhibitor. In some embodiments, an RNaseL inhibitor comprises sunitinib. In some embodiments, an RNaseL inhibitor comprises ABCE1.

[0169] In some embodiments, treating an immune cell (e.g., a stem cell, macrophage, monocyte, or dendritic cell) with an RNaseL inhibitor increases mRNA stability in a modified immune cell relative to mRNA stability in a modified immune cell of the same type that was not treated with an RNaseL inhibitor. In some embodiments, treating an immune cell (e.g., a stem cell, macrophage, monocyte, or dendritic cell) with an RNaseL inhibitor increases exogenous

cytokine expression in a modified immune cell relative to exogenous cytokine expression in a modified immune cell of the same type that was not treated with an RNaseL inhibitor. In some embodiments, treating an immune cell (e.g., a stem cell, macrophage, monocyte, or dendritic cell) with an RNaseL inhibitor increases fusion protein expression in a modified immune cell relative to fusion protein expression in a modified immune cell of the same type that was not treated with an RNaseL inhibitor. In some embodiments, treating an immune cell (e.g., a stem cell, macrophage, monocyte, or dendritic cell) with an RNaseL inhibitor increases effector activity in a modified immune cell relative to effector activity in a modified immune cell of the same type that was not treated with an RNaseL inhibitor.

[0170] In some embodiments of the present disclosure, a step of treating an immune cell (e.g., a stem cell, macrophage, monocyte, or dendritic cell) occurs before a step of delivering an mRNA to the immune cell.

[0171] In some embodiments, methods of the present disclosure comprise a step of culturing an immune cell (e.g., a stem cell, macrophage, monocyte, or dendritic cell) with a cytokine or immune stimulating recombinant protein. In some embodiments, a cytokine comprises IFN-α, IFN-β, IFN-γ, TNFα, IL-6, STNGL, LPS, a CD40 agonist, a 4-1BB ligand, recombinant 4-1BB, a CD19 agonist, a TLR agonist (e.g., TLR-1, TLR-2, TLR-3, TLR-4, TLR-5, TLR-6, TLR-7, TLR-8 or TLR-9), TGF-β (e.g., TGF-β1, TGF- β2, or TGF-β3), a glucocorticoid, an immune complex, interleukin-1 alpha (IL-1α), IL-1β, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-9, IL-10, IL-12, IL-13, IL-14, IL-15, IL-16, IL-17, IL-18, IL-20, granulocyte-macrophage colony-stimulating factor (GM-CSF), granulocyte colony-stimulating factor (G-CSF), Leukemia inhibitory factor (LIF), oncostatin M (OSM), TNF-β, CD154, lymphotoxin beta (LT-β), an A proliferation-inducing ligand (APRIL), CD70, CD153, glucocorticoid-induced TNF receptor ligand (GITRL), tumor necrosis factor superfamily member 14 (TNFSF14), OX40L (CD252), TALL-1 (Tumor necrosis factor ligand superfamily member 13B - TNFSF13B), TNF-related apoptosis-inducing ligand (TRAIL), TNF-related weak inducer of apoptosis (TWEAK), TNF-related activation-induced cytokine (TRANCE), erythropoietin (Epo), thyroid peroxidase precursor (Tpo), FMS-related tyrosine kinase 3 ligand (FLT-3L), stem cell factor (SCF), macrophage colony-stimulating factor (M-CSF), merozoite surface protein (MSP), a Nucleotide-binding oligomerization domain-containing protein (NOD) ligand (e.g., NOD1, NOD2, or

NOD1/2 agonists), a RIG-I-like receptor (RLR) ligand (e.g., 5'ppp-dsRNA, 3p-hpRNA, Poly(I:C), or Poly(dA:dT)), a C-type lectin receptor (CLR) ligand (e.g., curdlan, β-glucan, HKCA, laminarin, pustulan, scleroglucan, WGP dispersible, WGP soluble, zymosan, zymosan depleted, furfurman, b-GlcCer, GlcC14C18, HKMT, TDB, TDB-HS15, or TDM), a cyclic dinucleotide sensor ligand (e.g., C-Gas agonist or stimulator of interferon gene (STING) ligand), an inflammasome inducer (e.g., alum, ATP, CPPD crystals, hemozoin, MSU crystals, Nano-SiO2, Nigericin, or TDB), an aryl hydrocarbon (AhR) ligand (e.g., FICZ, indirubin, ITE, or L-kynurenine), an alpha-protein kinase 1 (ALPK1) ligand, a multi-PRR ligand, an NFKB/NFAT activator (e.g., concavalin A, ionomycin, PHA-P, or PMA) or a combination thereof. In some embodiments, a cytokine comprises IFN-β.

[0172] In some embodiments of the present disclosure, a step of culturing an immune cell (e.g., a stem cell, macrophage, monocyte, or dendritic cell) occurs after a step of delivering an mRNA to the immune cell.

[0173] In some embodiments, culturing a modified immune cell (e.g., a stem cell, macrophage, monocyte, or dendritic cell) with a cytokine or immune stimulating recombinant protein increases the viability of the modified immune cell relative to a modified immune cell of the same type that was not cultured with the cytokine or immune stimulating recombinant protein. In some embodiments, culturing a modified immune cell (e.g., a stem cell, macrophage, monocyte, or dendritic cell) with a cytokine or immune stimulating recombinant protein increases protein (e.g., exogenous cytokine, CAR, or fusion protein) expression of the modified immune cell relative to a modified immune cell of the same type that was not cultured with the cytokine or immune stimulating recombinant protein. In some embodiments, culturing a modified immune cell (e.g., a stem cell, macrophage, monocyte, or dendritic cell) with a cytokine or immune stimulating recombinant protein increases longevity of protein (e.g., exogenous cytokine, CAR, or fusion protein) expression relative to a modified immune cell of the same type that was not cultured with the cytokine or immune stimulating recombinant protein. In some embodiments, culturing a modified immune cell (e.g., a stem cell, macrophage, monocyte, or dendritic cell) with a cytokine or immune stimulating recombinant protein increases effector activity of the modified immune cell relative to a modified immune cell of the same type that was not cultured with the cytokine or immune stimulating recombinant protein.

In some embodiments, culturing a modified immune cell (e.g., a stem cell, macrophage, monocyte, or dendritic cell) with a cytokine or immune stimulating recombinant protein increases pro-inflammatory (M1) polarization of the modified immune cell relative to a modified immune cell of the same type that was not cultured with the cytokine or immune stimulating recombinant protein.

Modified Immune Cells

[0174] In some embodiments, a modified immune cell (e.g., a stem cell, macrophage, monocyte, or dendritic cell) is made by methods of the present disclosure. In some embodiments, a modified immune cell (e.g., a stem cell, macrophage, monocyte, or dendritic cell) comprising a modified mRNA encoding an exogenous cytokine and/or CAR as provided herein exhibits increased viability relative to a modified immune cell of the same type comprising unmodified mRNA encoding an exogenous cytokine and/or CAR. In some embodiments, a modified immune cell (e.g., a stem cell, macrophage, monocyte, or dendritic cell) comprising a modified mRNA encoding an exogenous cytokine and/or CAR as provided herein exhibits increased expression of an mRNA encoding an exogenous cytokine and/or CAR relative to a modified immune cell of the same type comprising unmodified mRNA encoding the exogenous cytokine and/or CAR. In some embodiments, a modified immune cell (e.g., a stem cell, macrophage, monocyte, or dendritic cell) comprising a modified mRNA encoding an exogenous cytokine and/or CAR as provided herein exhibits increased exogenous cytokine and/or CAR expression relative to a modified immune cell of the same type comprising unmodified mRNA encoding the exogenous cytokine and/or CAR. In some embodiments, a modified immune cell (e.g., a stem cell, macrophage, monocyte, or dendritic cell) comprising a modified mRNA encoding an exogenous cytokine and/or CAR as provided herein exhibits increased longevity of an mRNA encoding an exogenous cytokine and/or CAR relative to a modified immune cell of the same type comprising unmodified mRNA encoding the exogenous cytokine and/or CAR. In some embodiments, a modified immune cell (e.g., a stem cell, macrophage, monocyte, or dendritic cell) comprising a modified mRNA encoding an exogenous cytokine and/or CAR as provided herein exhibits increased longevity of an exogenous cytokine and/or CAR relative to a modified immune cell of the same type comprising unmodified mRNA

encoding the exogenous cytokine and/or CAR. In some embodiments, a modified immune cell (e.g., a stem cell, macrophage, monocyte, or dendritic cell) comprising a modified mRNA encoding an exogenous cytokine and/or CAR as provided herein exhibits increased effector activity relative to a modified immune cell of the same type comprising unmodified mRNA encoding an exogenous cytokine and/or CAR. In some embodiments, a modified immune cell (e.g., a stem cell, macrophage, monocyte, or dendritic cell) comprising a modified mRNA encoding an exogenous cytokine and/or CAR as provided herein exhibits increased pro-inflammatory (M1) polarization relative to a modified immune cell of the same type comprising unmodified mRNA encoding an exogenous cytokine and/or CAR.

[0175] In some embodiments, a modified immune cell (e.g., a stem cell, macrophage, monocyte, or dendritic cell) is made by methods of the present disclosure. In some embodiments, a modified immune cell (e.g., a stem cell, macrophage, monocyte, or dendritic cell) comprising a modified mRNA encoding a fusion protein as provided herein exhibits increased viability relative to a modified immune cell of the same type comprising unmodified mRNA encoding a fusion protein. In some embodiments, a modified immune cell (e.g., a stem cell, macrophage, monocyte, or dendritic cell) comprising a modified mRNA encoding a fusion protein as provided herein exhibits increased expression of an mRNA encoding a fusion protein relative to a modified immune cell of the same type comprising unmodified mRNA encoding the fusion protein. In some embodiments, a modified immune cell (e.g., a stem cell, macrophage, monocyte, or dendritic cell) comprising a modified mRNA encoding a fusion protein as provided herein exhibits increased fusion protein expression relative to a modified immune cell of the same type comprising unmodified mRNA encoding the fusion protein. In some embodiments, a modified immune cell (e.g., a stem cell, macrophage, monocyte, or dendritic cell) comprising a modified mRNA encoding a fusion protein as provided herein exhibits increased longevity of an mRNA encoding a fusion protein relative to a modified immune cell of the same type comprising unmodified mRNA encoding the fusion protein. In some embodiments, a modified immune cell (e.g., a stem cell, macrophage, monocyte, or dendritic cell) comprising a modified mRNA encoding a fusion protein as provided herein exhibits increased longevity of a fusion protein relative to a modified immune cell of the same type comprising unmodified mRNA encoding the fusion protein. In some embodiments, a modified immune cell (e.g., a stem cell, macrophage, monocyte, or dendritic cell) comprising a modified mRNA encoding a fusion protein as provided

herein exhibits increased effector activity relative to a modified immune cell of the same type comprising unmodified mRNA encoding a fusion protein. In some embodiments, a modified immune cell (e.g., a stem cell, macrophage, monocyte, or dendritic cell) comprising a modified mRNA encoding a fusion protein as provided herein exhibits increased pro-inflammatory (M1) polarization relative to a modified immune cell of the same type comprising unmodified mRNA encoding a fusion protein.

Assays

[0176] A variety of assays may be performed to confirm the presence of a nucleic acid construct as described herein in an immune cell (e.g., a stem cell, macrophage, monocyte, or dendritic cell). For example, such assays include molecular biological assays well known to those of skill in the art, such as Southern and Northern blotting, RT-PCR, and PCR; and biochemical assays, such as detecting the presence or absence of a particular peptide, e.g., by immunological means (ELISAs and Western blots). Other assays of the present disclosure, include, for example, fluorescence-activated cell sorting (FACS), immunofluorescent microscopy, MSD cytokine analysis, mass spectrometry (MS), RNA-Seq and functional assays.

[0177] A variety of assays may be performed to determine various characteristics of a modified immune cell (e.g., a stem cell, macrophage, monocyte, or dendritic cell), such as, but not limited to, immune cell viability, nucleic acid expression, nucleic acid longevity, protein (e.g., exogenous cytokine, CAR, or fusion protein) expression, protein (e.g., exogenous cytokine, CAR, or fusion protein) longevity, effector activity, and pro-inflammatory (M1) polarization. For example, such assays include flow cytometry, quantitative PCR, and in vitro functional assays such as cytokine/chemokine secretion, phagocytosis, and specific lysis assays of target tumor cells.

Exogenous Cytokines

[0178] In some embodiments, immune cells (e.g., stem cells, macrophages, monocytes, or dendritic cells) of the present disclosure do not comprise fusion proteins. In some embodiments, immune cells (e.g., stem cells, macrophages, monocytes, or dendritic cells) of the

present disclosure comprise at least one exogenous cytokine and at least one chimeric antigen receptor (CAR). As used herein, the term "exogenous cytokine" refers to a cytokine produced as a result of the introduction of an exogenous nucleic acid material (e.g., DNA or RNA) encoding the cytokine into an immune cell. In some embodiments, an exogenous cytokine is or comprises a pro-inflammatory (M1) cytokine. In some embodiments, a pro-inflammatory cytokine is or comprises a Type I Inteferon (IFN-α1, IFN-α2, IFN-α4, IFN-α5, IFN-α6, IFN-α7, IFN-α8, IFN-α10, IFN-α13, IFN-α14, IFN-α16, IFN-α17, IFN-α21, IFN-β, IFN-ω, IFN-ε, or IFN-κ), Type II Interferon (IFN-γ), Type III Interferon (IFN-λ1, IFN-λ2, IFN-λ3, or IFN-λ4), TNF-α, IL-1β, IL-6, IL-12, IL-17, IL-23, or GM-CSF. In some embodiments, an exogenous cytokine is or comprises an anti-inflammatory (M2) cytokine. In some embodiments, an anti-inflammatory cytokine is or comprises IL-4, IL-10, IL-13, IL-18, M-CSF, or TGF-β. In some embodiments, a cytokine is or comprises a Type I Inteferon (IFN-α1, IFN-α2, IFN-α4, IFN-α5, IFN-α6, IFN-α7, IFN-α8, IFN-α10, IFN-α13, IFN-α14, IFN-α16, IFN-α17, IFN-α21, IFN-β, IFN-ω, IFN-ε, or IFN-κ), Type II Interferon (IFN-γ), Type III Interferon (IFN-λ1, IFN-λ2, IFN-λ3, or IFN-λ4), TNF-α, IL-1β, IL-6, IL-12, IL-17, IL-23, GM-CSF, IL-4, IL-10, IL-13, IL-18, M-CSF, or TGF-β. In some embodiments, a cytokine is selected from **Table 1**.

[0179] In some embodiments, an exogenous cytokine of the present invention comprises the same linear amino acid sequence as an endogenous cytokine (e.g., sequences in **Table 2a** and **Table 2b**). In some embodiments, an exogenous cytokine of the present invention comprises a cytokine comprising an engineered amino acid sequence (e.g., sequences in **Table 6**). In some embodiments, an engineered cytokine amino acid sequence is derived from an endogenous cytokine sequence.

[0180] In some embodiments, an exogenous cytokine is or comprises a circular permutation. A circular permutation is a version of a protein wherein sections of amino acids are rearranged such that a region of amino acids in the middle of an endogenous protein is instead at the N-terminal or C-terminal end, but with the resulting protein still having an overall three-dimensional shape similar to the endogenous protein. In some embodiments, an exogenous cytokine comprising a circular permutation of the cytokine will have increased binding between the cytokine and its corresponding cytokine receptor relative to an exogenous cytokine comprising the same linear amino acid sequence as an endogenous cytokine. In some

embodiments, an exogenous cytokine comprising a circular permutation of the cytokine will have increased signaling relative to an exogenous cytokine comprising the same linear amino acid sequence as an endogenous cytokine. In some embodiments, an exogenous cytokine of the present invention comprises a circular permutation of IL-1β, IL-4, IL-10, or IL-13.

[0181] In some embodiments, an exogenous cytokine is or comprises a single-chain cytokine. As used herein, a single-chain cytokine comprises two or more copies of a cytokine fused together. In some embodiments, the two or more copies of a cytokine in a single-chain cytokine are separated by a linker. In some embodiments, a single-chain cytokine allows an exogenous cytokine of the present disclosure to mimic an endogenous cytokine that acts as a multimer when binding to its corresponding cytokine receptor. In some embodiments, an exogenous cytokine of the present invention comprises a single-chain cytokine comprising two or more copies of IFN-γ, TNF-α, IL-12, or IL-10.

[0182] In some embodiments, an exogenous cytokine is or comprises a monomeric cytokine. As used herein, a monomeric cytokine has been engineered so that it does not need to multimerize (e.g., dimerize or trimerize) in order to bind to its corresponding cytokine receptor. In some embodiments, an exogenous cytokine of the present invention comprises a monomeric cytokine comprising an engineered version of IFN-γ, TNF-α, IL-12, or IL-10.

[0183] In some embodiments, an exogenous cytokine of the present disclosure comprises an amino acid sequence at least 80% identical to a sequence selected from **Table 2a**, **Table 2b**, or **Table 6**. In some embodiments, an exogenous cytokine of the present disclosure comprises an amino acid sequence at least 85% identical to a sequence selected from **Table 2a**, **Table 2b**, or **Table 6**. In some embodiments, an exogenous cytokine of the present disclosure comprises an amino acid sequence at least 90% identical to a sequence selected from **Table 2a**, **Table 2b**, or **Table 6**. In some embodiments, an exogenous cytokine of the present disclosure comprises an amino acid sequence at least 95% identical to a sequence selected from **Table 2a**, **Table 2b**, or **Table 6**. In some embodiments, an exogenous cytokine of the present disclosure comprises an amino acid sequence at least 96% identical to a sequence selected from **Table 2a**, **Table 2b**, or **Table 6**. In some embodiments, an exogenous cytokine of the present disclosure comprises an amino acid sequence at least 97% identical to a sequence selected from **Table 2a**, **Table 2b**, or **Table 6**. In some embodiments, an exogenous cytokine of the present disclosure comprises

an amino acid sequence at least 98% identical to a sequence selected from **Table 2a**, **Table 2b**, or **Table 6**. In some embodiments, an exogenous cytokine of the present disclosure comprises an amino acid sequence at least 99% identical to a sequence selected from **Table 2a**, **Table 2b**, or **Table 6**. In some embodiments, an exogenous cytokine of the present disclosure comprises an amino acid sequence identical to a sequence selected from **Table 2a**, **Table 2b**, or **Table 6**.

[0184] In some embodiments, an exogenous cytokine of the present disclosure is encoded by one or more nucleic acids comprise a sequence at least 80% identical to a sequence selected from **Table 4a**, **Table 4b**, or **Table 7**. In some embodiments, an exogenous cytokine of the present disclosure is encoded by one or more nucleic acids comprising a sequence at least 85% identical to a sequence selected from **Table 4a**, **Table 4b**, or **Table 7**. In some embodiments, an exogenous cytokine of the present disclosure is encoded by one or more nucleic acids comprising a sequence at least 90% identical to a sequence selected from **Table 4a**, **Table 4b**, or **Table 7**. In some embodiments, an exogenous cytokine of the present disclosure is encoded by one or more nucleic acids comprising a sequence at least 95% identical to a sequence selected from **Table 4a**, **Table 4b**, or **Table 7**. In some embodiments, an exogenous cytokine of the present disclosure is encoded by one or more nucleic acids comprising a sequence at least 96% identical to a sequence selected from **Table 4a**, **Table 4b**, or **Table 7**. In some embodiments, an exogenous cytokine of the present disclosure is encoded by one or more nucleic acids comprising a sequence at least 97% identical to a sequence selected from **Table 4a**, **Table 4b**, or **Table 7**. In some embodiments, an exogenous cytokine of the present disclosure is encoded by one or more nucleic acids comprising a sequence at least 98% identical to a sequence selected from **Table 4a**, **Table 4b**, or **Table 7**. In some embodiments, an exogenous cytokine of the present disclosure is encoded by one or more nucleic acids comprising a sequence at least 99% identical to a sequence selected from **Table 4a**, **Table 4b**, or **Table 7**. In some embodiments, an exogenous cytokine of the present disclosure is encoded by one or more nucleic acids comprising a sequence identical to a sequence selected from **Table 4a**, **Table 4b**, or **Table 7**.

Fusion Proteins

[0185] The term “fusion protein”, as used herein, refers to an artificial chimeric protein comprising a cytokine fused to at least one of its corresponding receptor subunits, such that the

cytokine can intramolecularly bind its tethered receptor and induce downstream signaling. Fusion proteins may be used, for example, as a therapy with adoptive cell transfer. For example, in some embodiments, immune cells (e.g., stem cells, macrophages, monocytes, and/or dendritic cells are removed from a patient (e.g., from blood, tumor or ascites fluid) and modified so that they express a fusion protein. In some embodiments, such modified immune cells are then reintroduced to the same or a different patient as a therapeutic.

[0186] In some embodiments, a fusion protein may comprise one or more of: one or more cytokines, one or more linkers and one or more cytokine receptors (see **Figure 1**). In some embodiments, fusion proteins of the present disclosure are membrane-bound. In some embodiments, fusion proteins of the present disclosure are not membrane-bound.

[0187] In embodiments, a fusion protein of the present disclosure further comprises a signal peptide. In some embodiments, a fusion protein comprises, from N-terminus to C-terminus: a signal peptide, a cytokine, a linker, and a cytokine receptor (see Figure 2).

[0188] In some embodiments, a fusion protein comprises a linker between cytokine and a cytokine receptor. As used herein, the term "linker" refers to any oligo- or polypeptide that functions to link a cytokine to a cytokine receptor in a polypeptide chain in a fusion protein of the present disclosure. In some embodiments, a linker may comprise up to 300 amino acids, preferably 5 to 100 amino acids and most preferably 5 to 30 amino acids.

[0189] In some embodiments, an immune cell (e.g., a stem cell, macrophage, monocyte, or dendritic cell) comprising a fusion protein may comprise one or more control systems including, but not limited to: a safety switch (e.g., an on switch, an off switch, a suicide switch), transcriptional control (e.g. cell-specific promoters, cell-state specific promoters, promoters downstream of fusion protein activation, promoters downstream of endogenous signaling pathways, or drug-inducible transcription), post-transcriptional control of fusion protein mRNA (e.g. RNA-based inhibition with endogenous or recombinant miRNA), or post-translational control of a fusion protein's structure or stability (e.g. a fusion protein whose intracellular domain conditionally associates with the full structure by drug/light-inducible association (to allow signaling) or dissociation (to inhibit signaling), or whose stability is drug-regulated for inducible stabilization (to allow signaling) or degradation (to inhibit signaling)). These control systems can be combined to create logic gates, for example an AND gate (e.g. a fusion protein

with a fusion protein-inducible promoter and cytosolic domain that associates in a drug-dependent manner, thus requiring fusion protein activation and the presence of a small molecule), an OR gate (e.g. a fusion protein under control of a promoter that is transcriptionally active following either fusion protein activation or small molecule addition), and/or a NOT gate (e.g. a fusion protein whose mRNA is degraded by endogenous miRNA's expressed in natural immune cell signaling states (such as miRNA's upregulated by a particular cytokine signaling pathway, thus only expressing fusion protein in the absence of this cytokine)).In some embodiments, a modified immune cell, for example, a modified stem cell, macrophage, monocyte, or dendritic cell, is generated by expressing a fusion protein therein. In some embodiments, an immune cell comprises a fusion protein comprising a cytokine, a linker, and a cytokine receptor, wherein the immune cell comprises a stem cell, macrophage, monocyte, or dendritic cell, and wherein the cytokine binds the cytokine receptor.

[0190] In some embodiments, a fusion protein of the present disclosure comprises a cytokine selected from **Table 1** and the corresponding Receptor 1 selected from the same row in **Table 1**. In some embodiments, a fusion protein of the present disclosure comprises a cytokine selected from **Table 1** and the corresponding Receptor 2/Co-Receptor selected from the same row in **Table 1**.

Table 1 - Cytokines and Corresponding Receptors

Cytokine	M1/M2	Receptor 1	Receptor 2 or Co-Receptor
IFN-α2	M1	IFNAR1	IFNAR2
IFN-β	M1	IFNAR1	IFNAR2
IFN-γ	M1	IFNGR1	IFNGR2
TNF-α	M1	TNFR1	TNFR2
IL-1β	M1	IL-1R1	IL-1R3
IL-6	M1	IL-6Rα	gp130
IL-12	M1	IL-12-Rβ1	IL-12-Rβ2
IL-4	M2	IL-4Rα	IL-2Rγc or IL-13Rα1
IL-10	M2	IL-10R1	IL-10R2
IL-13	M2	IL-13Rα1	IL-4Rα
IL-18	M2	IL-18Rα	IL-18Rβ

[0191] In some embodiments, a fusion protein of the present disclosure comprises interleukin 10 (IL-10), a linker, and interleukin-10 receptor (IL10R).

[0192] In some embodiments, a fusion protein of the present disclosure comprises interferon beta (IFNβ), a linker, and interferon-α/β receptor (IFNAR).

[0193] In some embodiments, a modified immune cell (e.g., stem cell, macrophage, monocyte, or dendritic cell) further comprises a chimeric antigen receptor (CAR) of the present disclosure.

[0194] The present disclosure also provides immune cells (e.g., stem cells, macrophages, monocytes, or dendritic cells) comprising a nucleic acid sequence (e.g., an isolated nucleic acid sequence) encoding a fusion protein, wherein the nucleic acid sequence comprises a nucleic acid sequence encoding a cytokine, a nucleic acid sequence encoding a linker and a nucleic acid sequence encoding a cytokine receptor, wherein the cell is a stem cell, macrophage, monocyte or dendritic cell that expresses the fusion protein.

[0195] In some embodiments, a fusion protein comprises a cytokine that is operably linked to another domain of the fusion protein, such as a cytokine receptor, for expression in an immune cell (e.g., a stem cell, macrophage, monocyte, or dendritic cell).

[0196] In some embodiments, a fusion protein of the present disclosure is expressed at the surface of a modified immune cell (e.g., a stem cell, macrophage, monocyte, or dendritic cell). In some embodiments, a fusion protein of the present disclosure induces a pro-inflammatory phenotype, as indicated by cytokine production, gene expression changes, cell surface markers, and/or functional assays. In some embodiments, a fusion protein of the present disclosure induces an anti-inflammatory phenotype, as indicated by cytokine production, gene expression changes, cell surface markers, and/or functional assays.

[0197] In some embodiments, a fusion protein of the present disclosure comprises an amino acid sequence at least 80% identical to a sequence selected from Table 9. In some embodiments, a fusion protein of the present disclosure comprises an amino acid sequence at least 85% identical to a sequence selected from Table 9. In some embodiments, a fusion protein of the present disclosure comprises an amino acid sequence at least 90% identical to a sequence selected from Table 9. In some embodiments, a fusion protein of the present disclosure

comprises an amino acid sequence at least 95% identical to a sequence selected from Table 9. In some embodiments, a fusion protein of the present disclosure comprises an amino acid sequence at least 96% identical to a sequence selected from Table 9. In some embodiments, a fusion protein of the present disclosure comprises an amino acid sequence at least 97% identical to a sequence selected from Table 9. In some embodiments, a fusion protein of the present disclosure comprises an amino acid sequence at least 98% identical to a sequence selected from Table 9. In some embodiments, a fusion protein of the present disclosure comprises an amino acid sequence at least 99% identical to a sequence selected from Table 9. In some embodiments, a fusion protein of the present disclosure comprises an amino acid sequence identical to a sequence selected from Table 9.

[0198] In some embodiments, a fusion protein of the present disclosure is encoded by one or more nucleic acids comprise a sequence at least 80% identical to a sequence selected from Table 10. In some embodiments, a fusion protein of the present disclosure is encoded by one or more nucleic acids comprising a sequence at least 85% identical to a sequence selected from Table 10. In some embodiments, a fusion protein of the present disclosure is encoded by one or more nucleic acids comprising a sequence at least 90% identical to a sequence selected from Table 10. In some embodiments, a fusion protein of the present disclosure is encoded by one or more nucleic acids comprising a sequence at least 95% identical to a sequence selected from Table 10. In some embodiments, a fusion protein of the present disclosure is encoded by one or more nucleic acids comprising a sequence at least 96% identical to a sequence selected from Table 10. In some embodiments, a fusion protein of the present disclosure is encoded by one or more nucleic acids comprising a sequence at least 97% identical to a sequence selected from Table 10. In some embodiments, a fusion protein of the present disclosure is encoded by one or more nucleic acids comprising a sequence at least 98% identical to a sequence selected from Table 10. In some embodiments, a fusion protein of the present disclosure is encoded by one or more nucleic acids comprising a sequence at least 99% identical to a sequence selected from Table 10. In some embodiments, a fusion protein of the present disclosure is encoded by one or more nucleic acids comprising a sequence identical to a sequence selected from Table 10.

[0199] In some embodiments, a modified immune cell (e.g., a stem cell, macrophage, monocyte, or dendritic cell) comprising a fusion protein of the present disclosure maintains a

pro-inflammatory phenotype over time. In some embodiments, a modified immune cell (e.g., a stem cell, macrophage, monocyte, or dendritic cell) comprising a fusion protein of the present disclosure maintains a pro-inflammatory phenotype at least 4 hours, 2 days, 4 days, 7 days, 14 days, and/or 28 days after an immune cell is modified with a nucleic acid encoding the fusion protein. In some embodiments, a modified immune cell (e.g., a stem cell, macrophage, monocyte, or dendritic cell) comprising a fusion protein of the present disclosure maintains a pro-inflammatory phenotype longer than an immune cell induced by pre-treatment with a soluble cytokine.

[0200] In some embodiments, a modified immune cell (e.g., a stem cell, macrophage, monocyte, or dendritic cell) comprising a fusion protein of the present disclosure maintains an anti-inflammatory phenotype over time. In some embodiments, a modified immune cell (e.g., a stem cell, macrophage, monocyte, or dendritic cell) comprising a fusion protein of the present disclosure maintains an anti-inflammatory phenotype at least 4 hours, 2 days, 4 days, 7 days, 14 days, and/or 28 days after an immune cell is modified with a nucleic acid encoding the fusion protein. In some embodiments, a modified immune cell (e.g., a stem cell, macrophage, monocyte, or dendritic cell) comprising a fusion protein of the present disclosure maintains an anti-inflammatory phenotype longer than an immune cell induced by pre-treatment with a soluble cytokine.

[0201] In some embodiments, a modified immune cell (e.g., a stem cell, macrophage, monocyte, or dendritic cell) comprising a fusion protein of the present disclosure maintains a pro-inflammatory phenotype and/or otherwise resists subversion when challenged by anti-inflammatory cytokines. In some embodiments, the sensitivity of a modified immune cell to environmental cytokines is measured by generating a dose-response curve of pro-inflammatory markers by treating modified immune cells comprising pro-inflammatory fusion proteins with increasing concentrations of anti-inflammatory cytokines. In some embodiments, the sensitivity of a modified immune cell to environmental cytokines is measured by generating a dose-response curve of pro-inflammatory markers by treating modified immune cells comprising pro-inflammatory fusion proteins with increasing concentrations of pro-inflammatory cytokines (e.g., quantifying the effect of soluble IFN-β on modified immune cells comprising an IFN-β fusion protein).

[0202] In some embodiments, a modified immune cell (e.g., a stem cell, macrophage, monocyte, or dendritic cell) comprising a fusion protein of the present disclosure maintains an anti-inflammatory phenotype and/or otherwise resists subversion when challenged by pro-inflammatory cytokines. In some embodiments, the sensitivity of a modified immune cell to environmental cytokines is measured by generating a dose-response curve of anti-inflammatory markers by treating modified immune cells comprising anti-inflammatory fusion proteins with increasing concentrations of pro-inflammatory cytokines. In some embodiments, the sensitivity of a modified immune cell to environmental cytokines is measured by generating a dose-response curve of anti-inflammatory markers by treating modified immune cells comprising anti-inflammatory fusion proteins with increasing concentrations of anti-inflammatory cytokines (e.g., quantifying the effect of soluble IL-10 on modified immune cells comprising an IL-10 fusion protein).

[0203] In some embodiments, a modified immune cell (e.g., a stem cell, macrophage, monocyte, or dendritic cell) comprising a fusion protein of the present disclosure has minimal effects on neighboring cells. In some embodiments, the effect of a modified immune cell (e.g., a stem cell, macrophage, monocyte, or dendritic cell) comprising a fusion protein of the present disclosure on an unmodified cell (e.g., an immune cell that doesn't comprise a fusion protein of the present disclosure) can be tested by co-culturing modified immune cells with unmodified immune cells and using flow cytometry to analyze the expression of pro-inflammatory and anti-inflammatory markers in the unmodified cells. In some embodiments, modified immune cells and unmodified immune cells can be co-cultured in a culture dish where the modified immune cells and unmodified immune cells contact each other. In some embodiments, modified immune cells and unmodified immune cells can be co-cultured in a culture dish where the modified immune cells and unmodified immune cells are separated by a transwell assay membrane. In some embodiments, a positive control for testing the effect of modified immune cells on unmodified immune cells comprises modified immune cells that express soluble cytokine that can diffuse to stimulate neighboring cells, instead of a fusion protein of the present disclosure.

[0204] In some embodiments, a modified immune cell (e.g., a stem cell, macrophage, monocyte, or dendritic cell) comprising a fusion protein of the present disclosure has minimal cytotoxic effects on neighboring cells. In some embodiments, modifying an immune cell to

comprise a fusion protein of the present disclosure is not cytotoxic to the modified immune cell. In some embodiments, RNAseq data from modified immune cells are examined to determine if upregulation of genes indicative of cytotoxic effects is present.

[0205] In some embodiments, expression of a fusion protein of the present disclosure in a modified immune cell (e.g., a stem cell, macrophage, monocyte, or dendritic cell) also comprising a CAR does not decrease a targeted effector function (e.g., phagocytosis, targeted cellular cytotoxicity, antigen presentation, or cytokine secretion) of the modified immune cell relative to a modified immune cell comprising the CAR but not comprising the fusion protein. In some embodiments, expression of a fusion protein of the present disclosure in a modified immune cell (e.g., a stem cell, macrophage, monocyte, or dendritic cell) also comprising a CAR increases a targeted effector function (e.g., phagocytosis, targeted cellular cytotoxicity, antigen presentation, or cytokine secretion) of the modified immune cell relative to a modified immune cell comprising the CAR but not comprising the fusion protein.

Cytokines

[0206] The present disclosure provides fusion proteins comprising cytokines. In some embodiments, a cytokine is or comprises a pro-inflammatory (M1) cytokine. In some embodiments, a pro-inflammatory cytokine is or comprises a Type I Inteferon (IFN-α1, IFN-α2, IFN-α4, IFN-α5, IFN-α6, IFN-α7, IFN-α8, IFN-α10, IFN-α13, IFN-α14, IFN-α16, IFN-α17, IFN-α21, IFN-β, IFN-ω, IFN-ε, or IFN-κ), Type II Interferon (IFN-γ), Type III Interferon (IFN-λ1, IFN-λ2, IFN-λ3, or IFN-λ4), TNF-α, IL-1β, IL-6, IL-12, IL-17, IL-23, or GM-CSF. In some embodiments, a cytokine is or comprises an anti-inflammatory (M2) cytokine. In some embodiments, an anti-inflammatory cytokine is or comprises IL-4, IL-10, IL-13, IL-18, M-CSF, or TGF-β. In some embodiments, a cytokine is or comprises a Type I Inteferon (IFN-α1, IFN-α2, IFN-α4, IFN-α5, IFN-α6, IFN-α7, IFN-α8, IFN-α10, IFN-α13, IFN-α14, IFN-α16, IFN-α17, IFN-α21, IFN-β, IFN-ω, IFN-ε, or IFN-κ), Type II Interferon (IFN-γ), Type III Interferon (IFN-λ1, IFN-λ2, IFN-λ3, or IFN-λ4), TNF-α, IL-1β, IL-6, IL-12, IL-17, IL-23, GM-CSF, IL-4, IL-10, IL-13, IL-18, M-CSF, or TGF-β . In some embodiments, a cytokine is selected from **Table 1**.

[0207] In some embodiments, a fusion protein of the present invention comprises a cytokine comprising the same linear amino acid sequence as an endogenous cytokine (e.g., sequences in **Table 2a** and **Table 2b**). In some embodiments, a fusion protein of the present invention comprises a cytokine comprising an engineered amino acid sequence (e.g., sequences in **Table 6**). In some embodiments, an engineered cytokine amino acid sequence is derived from an endogenous cytokine sequence.

[0208] In some embodiments, an engineered cytokine is or comprises a circular permutation. A circular permutation is a version of a protein wherein sections of amino acids are rearranged such that a region of amino acids in the middle of an endogenous protein is instead at the N-terminal or C-terminal end, but with the resulting protein still having an overall three-dimensional shape similar to the endogenous protein. In some embodiments, a fusion protein comprising a circular permutation of a cytokine will have increased binding between the cytokine and the cytokine receptor relative to a fusion protein comprising a cytokine comprising the same linear amino acid sequence as an endogenous cytokine. In some embodiments, a fusion protein comprising a circular permutation of a cytokine will have increased signaling relative to a fusion protein comprising a cytokine comprising the same linear amino acid sequence as an endogenous cytokine. In some embodiments, a fusion protein comprising a circular permutation of a cytokine comprises a shorter linker relative to a fusion protein comprising a cytokine comprising the same linear amino acid sequence as an endogenous cytokine. In some embodiments, a fusion protein of the present invention comprises a circular permutation of IL-1β, IL-4, IL-10, or IL-13.

[0209] In some embodiments, an engineered cytokine is or comprises a single-chain cytokine. As used herein, a single-chain cytokine comprises two or more copies of a cytokine fused together. In some embodiments, the two or more copies of a cytokine in a single-chain cytokine are separated by a linker. In some embodiments, a single-chain cytokine allows a fusion protein of the present disclosure to mimic an endogenous cytokine that acts as a multimer when binding to the cytokine receptor. In some embodiments, a fusion protein of the present invention comprises a single-chain cytokine comprising two or more copies of IFN-γ, TNF-α, IL-12, or IL-10.

[0210] In some embodiments, an engineered cytokine is or comprises a monomeric cytokine. As used herein, a monomeric cytokine has been engineered so that it does not need to multimerize (e.g., dimerize or trimerize) in order to bind to its corresponding cytokine receptor. In some embodiments, a fusion protein of the present invention comprises a monomeric cytokine comprising an engineered version of IFN-γ, TNF-α, IL-12, or IL-10.

[0211] In some embodiments, a fusion protein of the present disclosure comprises an amino acid sequence at least 80% identical to a sequence selected from **Table 2a**, **Table 2b**, or **Table 6**. In some embodiments, a fusion protein of the present disclosure comprises an amino acid sequence at least 85% identical to a sequence selected from **Table 2a**, **Table 2b**, or **Table 6**. In some embodiments, a fusion protein of the present disclosure comprises an amino acid sequence at least 90% identical to a sequence selected from **Table 2a**, **Table 2b**, or **Table 6**. In some embodiments, a fusion protein of the present disclosure comprises an amino acid sequence at least 95% identical to a sequence selected from **Table 2a**, **Table 2b**, or **Table 6**. In some embodiments, a fusion protein of the present disclosure comprises an amino acid sequence at least 96% identical to a sequence selected from **Table 2a**, **Table 2b**, or **Table 6**. In some embodiments, a fusion protein of the present disclosure comprises an amino acid sequence at least 97% identical to a sequence selected from **Table 2a**, **Table 2b**, or **Table 6**. In some embodiments, a fusion protein of the present disclosure comprises an amino acid sequence at least 98% identical to a sequence selected from **Table 2a**, **Table 2b**, or **Table 6**. In some embodiments, a fusion protein of the present disclosure comprises an amino acid sequence at least 99% identical to a sequence selected from **Table 2a**, **Table 2b**, or **Table 6**. In some embodiments, a fusion protein of the present disclosure comprises an amino acid sequence identical to a sequence selected from **Table 2a**, **Table 2b**, or **Table 6**.

[0212] In some embodiments, a fusion protein of the present disclosure is encoded by one or more nucleic acids comprise a sequence at least 80% identical to a sequence selected from **Table 4a**, **Table 4b**, or **Table** 7. In some embodiments, a fusion protein of the present disclosure is encoded by one or more nucleic acids comprising a sequence at least 85% identical to a sequence selected from **Table 4a**, **Table 4b**, or **Table** 7. In some embodiments, a fusion protein of the present disclosure is encoded by one or more nucleic acids comprising a sequence at least 90% identical to a sequence selected from **Table 4a**, **Table 4b**, or **Table** 7. In some

embodiments, a fusion protein of the present disclosure is encoded by one or more nucleic acids comprising a sequence at least 95% identical to a sequence selected from **Table 4a**, **Table 4b**, or **Table 7**. In some embodiments, a fusion protein of the present disclosure is encoded by one or more nucleic acids comprising a sequence at least 96% identical to a sequence selected from **Table 4a**, **Table 4b**, or **Table 7**. In some embodiments, a fusion protein of the present disclosure is encoded by one or more nucleic acids comprising a sequence at least 97% identical to a sequence selected from **Table 4a**, **Table 4b**, or **Table 7**. In some embodiments, a fusion protein of the present disclosure is encoded by one or more nucleic acids comprising a sequence at least 98% identical to a sequence selected from **Table 4a**, **Table 4b**, or **Table 7**. In some embodiments, a fusion protein of the present disclosure is encoded by one or more nucleic acids comprising a sequence at least 99% identical to a sequence selected from **Table 4a**, **Table 4b**, or **Table 7**. In some embodiments, a fusion protein of the present disclosure is encoded by one or more nucleic acids comprising a sequence identical to a sequence selected from **Table 4a**, **Table 4b**, or **Table 7**.

Linkers

[0213] In some embodiments, a fusion protein of the present disclosure comprises a linker. In some embodiments, a fusion protein of the present disclosure comprises a linker between the cytokine and cytokine receptor. In some embodiments, the linker is a flexible linker. In some embodiments, a flexible linker comprises predominantly small amino acids, either non-polar (e.g., serine or threonine) or polar (e.g., glycine). In some embodiments, a flexible linker comprises amino acid substitutions (e.g., lysine, glutamic acid, glutamine, aspartic acid, and/or asparagine) relative to a known linker in order to improve solubility of the linker. In some embodiments, the flexibility of a linker is determined using circular dichroism spectroscopy to test if a linker is folded into a helix (i.e., a rigid structure) or a non-structured (i.e., flexible) coil. In some embodiments, the linker is a cleavable linker. In some embodiments, a linker comprises 5-50 amino acids. In some embodiments, a linker comprises 19-26 amino acids. In some embodiments, a linker comprises 26 amino acids. In some embodiments, a linker is at least 90 angstroms in length. In some embodiments, a linker

comprises amino acids selected from glycine (G), serine (S), threonine (T), lysine (K), proline (P), glutamic acid (E), glutamine (Q), aspartic acid (D), asparagine (N), or alanine (A).

[0214] In some embodiments, a linker is or comprises a linker selected from a group consisting of: a $(G4S)_n$ linker (wherein n = 1-5) **(SEQ ID NO: 170)**, a Whitlow linker, and Linker 26.

[0215] In some embodiments, a fusion protein of the present disclosure comprises an amino acid sequence at least 80% identical to a linker sequence selected from **Table 8**. In some embodiments, a fusion protein of the present disclosure comprises an amino acid sequence at least 85% identical to a linker sequence selected from **Table 8**. In some embodiments, a fusion protein of the present disclosure comprises an amino acid sequence at least 90% identical to a linker sequence selected from **Table 8**. In some embodiments, a fusion protein of the present disclosure comprises an amino acid sequence at least 95% identical to a linker sequence selected from **Table 8**. In some embodiments, a fusion protein of the present disclosure comprises an amino acid sequence at least 96% identical to a linker sequence selected from **Table 8**. In some embodiments, a fusion protein of the present disclosure comprises an amino acid sequence at least 97% identical to a linker sequence selected from **Table 8**. In some embodiments, a fusion protein of the present disclosure comprises an amino acid sequence at least 98% identical to a linker sequence selected from **Table 8**. In some embodiments, a fusion protein of the present disclosure comprises an amino acid sequence at least 99% identical to a linker sequence selected from **Table 8**. In some embodiments, a fusion protein of the present disclosure comprises an amino acid sequence identical to a linker sequence selected from **Table 8**.

[0216] In some embodiments, a fusion protein of the present disclosure is encoded by one or more nucleic acids comprising a sequence at least 80% identical to a linker sequence selected from **Table 8**. In some embodiments, a fusion protein of the present disclosure is encoded by one or more nucleic acids comprising a sequence at least 85% identical to a linker sequence selected from **Table 8**. In some embodiments, a fusion protein of the present disclosure is encoded by one or more nucleic acids comprising a sequence at least 90% identical to a linker sequence selected from **Table 8**. In some embodiments, a fusion protein of the present disclosure is encoded by one or more nucleic acids comprising a sequence at least 95% identical to a linker sequence selected from **Table 8**. In some embodiments, a fusion protein of

the present disclosure is encoded by one or more nucleic acids comprising a sequence at least 96% identical to a linker sequence selected from **Table 8**. In some embodiments, a fusion protein of the present disclosure is encoded by one or more nucleic acids comprising a sequence at least 97% identical to a linker sequence selected from **Table 8**. In some embodiments, a fusion protein of the present disclosure is encoded by one or more nucleic acids comprising a sequence at least 98% identical to a linker sequence selected from **Table 8**. In some embodiments, a fusion protein of the present disclosure is encoded by one or more nucleic acids comprising a sequence at least 99% identical to a linker sequence selected from **Table 8**. In some embodiments, a fusion protein of the present disclosure is encoded by one or more nucleic acids comprising a sequence identical to a linker sequence selected from **Table 8**.

Cytokine Receptors

[0217] The present disclosure provides fusion proteins comprising cytokine receptors. In some embodiments, a cytokine receptor is or comprises a pro-inflammatory (M1) cytokine receptor. In some embodiments, a pro-inflammatory cytokine receptor is or comprises IFNAR1, IFNAR2, IFNGR1, IFNGR2, IFNLR1, TNFR1, TNFR2, IL-1R1, IL-1R3, IL-6Rα, gp130, IL-12Rβ1, IL-12Rβ2, IL-17RA, IL-17RB, IL-17RC, IL-23R, CSF2-Rα, or CSF2-Rβ. In some embodiments, a cytokine receptor is or comprises an anti-inflammatory (M2) cytokine receptor. In some embodiments, an anti-inflammatory cytokine receptor is or comprises IL-4Rα, IL-4Rα1, IL-2Rγc, IL-10R1, IL-10R2, IL-13Rα1, IL-18Rα, IL-18Rβ, CSF1-R, TGF-βR1, or TGF-βR2. In some embodiments, a cytokine receptor is or comprises IFNAR1, IFNAR2, IFNGR1, IFNGR2, IFNLR1, TNFR1, TNFR2, IL-1R1, IL-1R3, IL-6Rα, gp130, IL-12Rβ1, IL-12Rβ2, IL-17RA, IL-17RB, IL-17RC, IL-23R, CSF2-Rα, CSF2-Rβ, IL-4Rα, IL-4Rα1, IL-2Rγc, IL-10R1, IL-10R2, IL-13Rα1, IL-18Rα, IL-18Rβ, CSF1-R, TGF-βR1, or TGF-βR2.

[0218] In some embodiments, a fusion protein of the present invention comprises a cytokine receptor comprising the same linear amino acid sequence as an endogenous cytokine (e.g., sequences in **Table 3a** and **Table 3b**). In some embodiments, a fusion protein of the present invention comprises a cytokine receptor comprising an engineered amino acid sequence. In some embodiments, an engineered cytokine amino acid sequence is derived from an endogenous cytokine sequence.

[0219] Many cytokines, including IFN-β and IL-10, signal through heterodimeric receptor complexes. In some embodiments, a fusion protein of the present disclosure comprises a cytokine and either cytokine receptor subunit (see **Table 1**). In some embodiments, a cytokine of the present disclosure will bind its tethered receptor subunit (receptor subunit included with the cytokine in the fusion protein) and then recruit an endogenously expressed second receptor subunit. For example, a fusion protein comprising IFN-β and IFNAR-1 would recruit endogenous IFNAR-2. Alternatively, a fusion protein comprising IFN-β and IFNAR-2 would recruit endogenous IFNAR-1. In some embodiments, a fusion protein of the present disclosure comprises a cytokine and both receptor subunits (e.g., a cytokine selected from **Table 1** and both Receptor 1 and Receptor 2 from the same row in **Table 1**). In some embodiments, a fusion protein of the present disclosure comprising a cytokine and both receptor subunits further comprises a cleavable linker between the receptor subunits.

[0220] In some embodiments, a fusion protein of the present disclosure comprises an amino acid sequence at least 80% identical to a sequence selected from **Table 3a** or **Table 3b**. In some embodiments, a fusion protein of the present disclosure comprises an amino acid sequence at least 85% identical to a sequence selected from **Table 3a** or **Table 3b**. In some embodiments, a fusion protein of the present disclosure comprises an amino acid sequence at least 90% identical to a sequence selected from **Table 3a** or **Table 3b**. In some embodiments, a fusion protein of the present disclosure comprises an amino acid sequence at least 95% identical to a sequence selected from **Table 3a** or **Table 3b**. In some embodiments, a fusion protein of the present disclosure comprises an amino acid sequence at least 96% identical to a sequence selected from **Table 3a** or **Table 3b**. In some embodiments, a fusion protein of the present disclosure comprises an amino acid sequence at least 97% identical to a sequence selected from **Table 3a** or **Table 3b**. In some embodiments, a fusion protein of the present disclosure comprises an amino acid sequence at least 98% identical to a sequence selected from **Table 3a** or **Table 3b**. In some embodiments, a fusion protein of the present disclosure comprises an amino acid sequence at least 99% identical to a sequence selected from **Table 3a** or **Table 3b**. In some embodiments, a fusion protein of the present disclosure comprises an amino acid sequence identical to a sequence selected from **Table 3a** or **Table 3b**.

[0221] In some embodiments, a fusion protein of the present disclosure is encoded by one or more nucleic acids comprise a sequence at least 80% identical to a sequence selected from **Table 5a** or **Table 5b**. In some embodiments, a fusion protein of the present disclosure is encoded by one or more nucleic acids comprising a sequence at least 85% identical to a sequence selected from **Table 5a** or **Table 5b**. In some embodiments, a fusion protein of the present disclosure is encoded by one or more nucleic acids comprising a sequence at least 90% identical to a sequence selected from **Table 5a** or **Table 5b**. In some embodiments, a fusion protein of the present disclosure is encoded by one or more nucleic acids comprising a sequence at least 95% identical to a sequence selected from **Table 5a** or **Table 5b**. In some embodiments, a fusion protein of the present disclosure is encoded by one or more nucleic acids comprising a sequence at least 96% identical to a sequence selected from **Table 5a** or **Table 5b**. In some embodiments, a fusion protein of the present disclosure is encoded by one or more nucleic acids comprising a sequence at least 97% identical to a sequence selected from **Table 5a** or **Table 5b**. In some embodiments, a fusion protein of the present disclosure is encoded by one or more nucleic acids comprising a sequence at least 98% identical to a sequence selected from **Table 5a** or **Table 5b**. In some embodiments, a fusion protein of the present disclosure is encoded by one or more nucleic acids comprising a sequence at least 99% identical to a sequence selected from **Table 5a** or **Table 5b**. In some embodiments, a fusion protein of the present disclosure is encoded by one or more nucleic acids comprising a sequence identical to a sequence selected from **Table 5a** or **Table 5b**.

Signal Peptides

[0222] In some embodiments, a fusion protein of the present disclosure comprises a signal peptide. In some embodiments, a fusion protein of the present disclosure comprises a signal peptide at the N-terminus. In some embodiments, a nucleic acid encoding a signal peptide comprises a nucleic acid encoding a signal peptide. In some embodiments, a signal peptide is or comprises a human signal peptide. In some embodiments, a signal peptide of the present disclosure is from a membrane-expressed or secreted protein. In some embodiments, a signal peptide of the present disclosure is from a membrane-expressed or secreted cytokine. In some embodiments, a signal peptide of the present disclosure is or comprises any signal peptide that

leads to cell membrane localization of an engineered protein. In some embodiments, a signal peptide comprises a CD8 signal peptide.

[0223] In some embodiments, a fusion protein of the present disclosure comprises an amino acid sequence at least 80% identical to a signal peptide sequence selected from **Table 8**. In some embodiments, a fusion protein of the present disclosure comprises an amino acid sequence at least 85% identical to a signal peptide sequence selected from **Table 8**. In some embodiments, a fusion protein of the present disclosure comprises an amino acid sequence at least 90% identical to a signal peptide sequence selected from **Table 8**. In some embodiments, a fusion protein of the present disclosure comprises an amino acid sequence at least 95% identical to a signal peptide sequence selected from **Table 8**. In some embodiments, a fusion protein of the present disclosure comprises an amino acid sequence at least 96% identical to a signal peptide sequence selected from **Table 8**. In some embodiments, a fusion protein of the present disclosure comprises an amino acid sequence at least 97% identical to a signal peptide sequence selected from **Table 8**. In some embodiments, a fusion protein of the present disclosure comprises an amino acid sequence at least 98% identical to a signal peptide sequence selected from **Table 8**. In some embodiments, a fusion protein of the present disclosure comprises an amino acid sequence at least 99% identical to a signal peptide sequence selected from **Table 8**. In some embodiments, a fusion protein of the present disclosure comprises an amino acid sequence identical to a signal peptide sequence selected from **Table 8**.

[0224] In some embodiments, a fusion protein of the present disclosure is encoded by one or more nucleic acids comprising a sequence at least 80% identical to a signal peptide sequence selected from **Table 8**. In some embodiments, a fusion protein of the present disclosure is encoded by one or more nucleic acids comprising a sequence at least 85% identical to a signal peptide sequence selected from **Table 8**. In some embodiments, a fusion protein of the present disclosure is encoded by one or more nucleic acids comprising a sequence at least 90% identical to a signal peptide sequence selected from **Table 8**. In some embodiments, a fusion protein of the present disclosure is encoded by one or more nucleic acids comprising a sequence at least 95% identical to a signal peptide sequence selected from **Table 8**. In some embodiments, a fusion protein of the present disclosure is encoded by one or more nucleic acids comprising a sequence at least 96% identical to a signal peptide sequence selected from **Table 8**.

In some embodiments, a fusion protein of the present disclosure is encoded by one or more nucleic acids comprising a sequence at least 97% identical to a signal peptide sequence selected from **Table 8**. In some embodiments, a fusion protein of the present disclosure is encoded by one or more nucleic acids comprising a sequence at least 98% identical to a signal peptide sequence selected from **Table 8**. In some embodiments, a fusion protein of the present disclosure is encoded by one or more nucleic acids comprising a sequence at least 99% identical to a signal peptide sequence selected from **Table 8**. In some embodiments, a fusion protein of the present disclosure is encoded by one or more nucleic acids comprising a sequence identical to a signal peptide sequence selected from **Table 8**.

Chimeric Antigen Receptors (CAR)

[0225] The term "chimeric antigen receptor" or "CAR," as used herein, refers to an artificial cell surface receptor that is engineered to be expressed on an immune effector cell and specifically targets a cell and/or binds an antigen. CARs may be used, for example, as a therapy with adoptive cell transfer. For example, in some embodiments, immune cells (e.g., stem cells, macrophages, monocytes, and/or dendritic cells are removed from a patient (e.g., from blood, tumor or ascites fluid) and modified so that they express a receptor specific to a particular form of antigen. In some embodiments, such modified immune cells are then reintroduced to the same or a different subject as a therapeutics. In some embodiments, CARs have been expressed with specificity to an antigen, for example, a tumor associated antigen. In some embodiments, a CAR comprises an extracellular domain, a transmembrane domain and an intracellular domain.

[0226] In some embodiments, a modified immune cell, for example, a modified stem cell, macrophage, monocyte, or dendritic cell, is generated by expressing a CAR therein. In some embodiments, an immune cell comprises a CAR comprising an extracellular domain, a transmembrane domain, and an intracellular domain, wherein the immune cell comprises a stem cell, macrophage, monocyte, or dendritic cell.

[0227] In some embodiments, a CAR may further comprise one or more of: one or more extracellular leader domains, one or more extracellular hinge domains and one or more intracellular co-stimulatory domains.

[0228] In some embodiments, a CAR comprises a spacer domain or hinge between an extracellular domain and a transmembrane domain. In some embodiments, a CAR comprises a spacer domain or hinge between an intracellular domain and a transmembrane domain. As used herein, the term "spacer domain" or "hinge" refers to any oligo- or polypeptide that functions to link a transmembrane domain to either an extracellular domain or to an intracellular domain in a polypeptide chain. In some embodiments, a spacer domain or hinge may comprise up to 300 amino acids, preferably 10 to 100 amino acids and most preferably 25 to 50 amino acids. In some embodiments, a short oligo- or polypeptide linker, preferably between 2 and 10 amino acids in length, may form a linkage between a transmembrane domain and an intracellular domain of a CAR. An example of a linker includes a glycine-serine doublet.

[0229] In some embodiments, an immune cell (e.g., a stem cell, macrophage, monocyte, or dendritic cell) comprising a CAR may comprise one or more control systems including, but not limited to: a safety switch (e.g., an on switch, and off switch, a suicide switch), a logic gate, for example an AND gate (e.g., two or more CARs, each of which lacks one or more signaling domains such that activation of both/all CARs is required for full immune cell (e.g., stem cell, macrophage, monocyte, or dendritic cell) activation or function), an OR gate (e.g., two or more CARs, each with an intracellular domain such as CD3ζ and a co-stimulatory domain), and/or a NOT gate (e.g., two or more CARs, one of which includes an inhibitory domain that antagonizes the function of the other CAR[s]).

[0230] The present disclosure also provides immune cells (e.g., stem cells, macrophages, monocytes, or dendritic cells) comprising a nucleic acid sequence (e.g., an isolated nucleic acid sequence) encoding a CAR, wherein the nucleic acid sequence comprises a nucleic acid sequence encoding an extracellular domain, a nucleic acid sequence encoding a transmembrane domain and a nucleic acid sequence encoding an intracellular domain, wherein the cell is a stem cell, macrophage, monocyte or dendritic cell that expresses the CAR.

[0231] In some embodiments, a CAR comprises an extracellular domain that is operably linked to another domain of the CAR, such as a transmembrane domain or an intracellular domain, for expression in an immune cell. In some embodiments, a nucleic acid encoding an extracellular domain is operably linked to a nucleic acid encoding a transmembrane domain and

the nucleic acid encoding the transmembrane domain is operably linked to a nucleic acid encoding an intracellular domain.

[0232] In some embodiments, an effector activity of an immune cell comprising a CAR is directed against a target cell comprising an antigen that specifically binds an antigen binding domain of the CAR. In some embodiments, a targeted effector activity directed against a target cell is or comprises phagocytosis, targeted cellular cytotoxicity, antigen presentation, or cytokine secretion.

[0233] In some embodiments, a CAR described herein comprises at least one domain (e.g., an extracellular domain, a transmembrane domain, and/or an intracellular domain) that inhibits anti-phagocytic signaling in an immune cell described herein (e.g., a stem cell, macrophage, monocyte, or dendritic cell). In some embodiments, a CAR described herein improves effector activity of an immune cell described herein (e.g., a stem cell, macrophage, monocyte, or dendritic cell), e.g., by enhancing inhibition of CD47 and/or SIRPα activity. In some embodiments, a CAR described herein binds CD47, e.g., and serves as a dominant negative receptor, inhibiting SIRPα activity (e.g., a CD47 sink). In some embodiments, a CAR described herein that binds SIRPα, e.g., comprises an activating receptor (e.g., comprises a CD3z intracellular domain). In some embodiments, a CAR described herein inhibits at least one interaction of CD47 and SIRPα. In some embodiments, a CAR is or comprises a phagocytic logic gate.

[0234] In some embodiments, an immune cell described herein (e.g., comprising or expressing an exogenous cytokine, fusion protein and/or a CAR described herein) comprises or expresses at least one variant or fragment of: SIRPα (e.g., a dominant negative SIRPα or a high-affinity engineered variant of SIRPα (e.g., CV1)), 5F9 scFv, B6H12 scFv (e.g., a humanized B6H12 scFv), PD1 (e.g., a dominant negative PD1 or HAC-I), anti-PD1 scFv (e.g., E27 or durvalumab), Siglec-10, Siglec-9, Siglec-11, and/or SHP-1. In some embodiments, a variant or fragment comprises a mutated intracellular domain. In some embodiments, a variant or fragment does not comprise or express at least one intracellular domain (e.g., an immune cell comprises or expresses an anti-CD47 scFv, CD8 hinge domain, and CD8 transmembrane). In some embodiments, an immune cell described herein (e.g., comprising or expressing an exogenous

cytokine, fusion protein and/or a CAR described herein) comprises a dominant negative receptor, e.g., blocking an inhibitory checkpoint.

[0235] In some embodiments, a CAR described herein further comprises a cleavage peptide (e.g., a P2A, F2A, E2A and/or T2A peptide) and at least one second CAR comprising at least one inhibitory domain of anti-phagocytic signaling. In some embodiments, at least one second CAR comprises a SIRPα (e.g., a high-affinity engineered variant of SIRPα (e.g., CV1)), 5F9 scFv, B6H12 scFv (e.g., a humanized B6H12 scFv), or a CD47 binding extracellular domain or a fragment thereof. In some embodiments, at least one second CAR comprises a SIRPα transmembrane domain or a fragment thereof. In certain embodiments, a second CAR further comprises a hinge domain (e.g., a CD8 hinge domain). In certain embodiments, at least one second CAR comprises: (i) a leader sequence (e.g., a CD8 leader); ii) an extracellular domain (e.g., a SIRPα, CV1, 5F9 scFv, or B6H12 scFv (e.g., a humanized B6H12 scFv) extracellular domain); and ii) a transmembrane domain (e.g., a SIRPα transmembrane domain). In some embodiments, a CAR described herein further comprises a cleavage peptide (e.g., a P2A peptide) and at least one marker protein (e.g., CD20 or a fragment thereof, CD19 or a fragment thereof, NGFR or a fragment thereof, a synthetic peptide, and/or a fluorescent protein).

[0236] In some embodiments, an immune cell described herein (e.g., comprising or expressing an exogenous cytokine, fusion protein and/or a CAR described herein) comprises or expresses one or more phosphatase dead domains (e.g. a phosphatase dead Shp1, phosphatase dead 72-5ptase (INPP5E), phosphatase dead Shp2, and/or phosphatase dead SHIP-1 domain) and/or a constitutively active kinase domain (e.g., a constitutively active LYN domain). In some embodiments, a CAR described herein further comprises a cleavage peptide (e.g., a P2A, F2A, E2A and/or T2A peptide) and one or more phosphatase dead domains (e.g. a phosphatase dead Shp1, phosphatase dead 72-5ptase (INPP5E), phosphatase dead Shp2, and/or phosphatase dead SHIP-1 domain) and/or a constitutively active kinase domain (e.g., a constitutively active LYN domain).

Extracellular Domains

[0237] The present disclosure provides chimeric antigen receptors (CAR) comprising extracellular domains. In some embodiments, an extracellular domain comprises an Fc receptor

(FcR) extracellular domain. In some embodiments, an extracellular domain comprises a toll-like receptor (TLR) extracellular domain. In some embodiments, an extracellular domain comprises a leader domain. In some embodiments, an extracellular domain comprises an antigen binding domain. In some embodiments, an extracellular domain comprises a hinge domain. In some embodiments, an extracellular domain comprises one or more of an FcR extracellular domain, a TLR extracellular domain, a leader domain, an antigen binding domain and a hinge domain. In some embodiments, an extracellular domain may be a domain that is endogenous to a particular immune cell type (e.g., a modified immune cell as provided herein). In some embodiments, an extracellular domain may be a domain that is not endogenous to a particular immune cell type (e.g., a modified immune cell as provided herein).

FcR Extracellular Domains

[0238] In some embodiments, an FcR extracellular domain comprises a full-length FcR extracellular domain. In some embodiments, an FcR extracellular domain comprises a portion of a full-length FcR extracellular domain. In some embodiments, an FcR extracellular domain (or portion thereof) is or comprises a human FcR extracellular domain. In some embodiments, an FcR extracellular domain may be a domain that is endogenous to a particular immune cell type (e.g., a modified immune cell as provided herein). In some embodiments, an FcR extracellular domain may be a domain that is not endogenous to a particular immune cell type (e.g., a modified immune cell as provided herein). In some embodiments, an FcR extracellular domain comprises a CD64 (FcγRI), CD32a (FcγRIIa), CD32b (FcγRIIb), CD32c, CD16a (FcγRIIIa), CD16b (FcγRIIIb), FcεRI, FcεRII, or FcαRI (CD89) domain.

TLR Extracellular Domains

[0239] In some embodiments, a TLR extracellular domain comprises a full-length TLR extracellular domain. In some embodiments, a TLR extracellular domain comprises a portion of a full-length TLR extracellular domain. In some embodiments, a TLR extracellular domain (or portion thereof) is or comprises a human TLR extracellular domain. In some embodiments, a TLR extracellular domain may be a domain that is endogenous to a particular immune cell type (e.g., a modified immune cell as provided herein). In some embodiments, a TLR extracellular domain may be a domain that is not endogenous to a particular immune cell type (e.g., a

modified immune cell as provided herein). In some embodiments, a TLR extracellular domain comprises a TLR1, TLR2, TLR3, TLR4, TLR5, TLR6, TLR7, TLR8, or TLR9 domain.

Leader Domains

[0240] In some embodiments, a CAR comprises one or more extracellular leader domains. In some embodiments, a nucleic acid encoding a CAR comprises a nucleic acid sequence encoding an extracellular leader domain, but the extracellular leader domain is cleaved from the CAR before the CAR is expressed in an immune cell. In some embodiments, an extracellular leader domain is or comprises a human extracellular leader domain. In some embodiments, an extracellular leader domain may be a domain that is endogenous to a particular immune cell type (e.g., a modified immune cell as provided herein). In some embodiments, an extracellular leader domain may be a domain that is not endogenous to a particular immune cell type (e.g., a modified immune cell as provided herein). In some embodiments, an extracellular leader domain comprises a CD8 extracellular leader domain. In some embodiments, an extracellular leader domain comprises a leader domain from a stimulatory or co-stimulatory domain (e.g., a TLR1, TLR2, TLR3, TLR4, TLR5, TLR6, TLR7, TLR8, TLR9, ALK, AXL, DDR2, EGFR, EphA1, INSR, cMET, MUSK, PDGFR, PTK7, RET, ROR1, ROS1, RYK, TIE2, TRK, VEGFR, CD40, CD19, CD20, 41BB, CD28, OX40, GITR, TREM-1, TREM-2, DAP12, MR, ICOS, MyD88 domain).

Antigen Binding Domains

[0241] In some embodiments, a CAR comprises an antigen binding domain that binds to an antigen, for example, on a target cell. In some embodiments, a CAR comprises an antigen binding domain that binds to an antigen associated with viral infection, bacterial infection, parasitic infection, autoimmune disease, and/or cancer cells. In some embodiments, an antigen binding domain recognizes an antigen that acts as a cell surface marker on a target cell associated with a particular disease state.

[0242] In some embodiments, an antigen binding domain binds to a tumor antigen, such as an antigen that is specific for a tumor or cancer of interest. In some embodiments a tumor antigen comprises one or more antigenic cancer epitopes. In some embodiments, a tumor antigen comprises CD19; CD123; CD22; CD30; CD171; CS-1 (also referred to as CD2 subset 1, CRACC, SLAMF7, CD319, and 19A24); C-type lectin-like molecule-1 (CLL-1 or CLECL1);

CD33; epidermal growth factor receptor variant III (EGFRvIII); ganglioside G2 (GD2); ganglioside GD3 (aNeu5Ac(2-8)aNeu5Ac(2-3)bDGalp(1-4)bDGlcp(1-1)Cer); TNF receptor family member B cell maturation (BCMA); Tn antigen ((Tn Ag) or (GalNAcα-Ser/Thr)); prostate-specific membrane antigen (PSMA); Receptor tyrosine kinase-like orphan receptor 1 (ROR1); Fms-Like Tyrosine Kinase 3 (FLT3); Tumor-associated glycoprotein 72 (TAG72); CD38; CD44v6; Carcinoembryonic antigen (CEA); Epithelial cell adhesion molecule (EPCAM); B7H3 (CD276); KIT (CD117); Interleukin-13 receptor subunit alpha-2 (IL-13Ra2 or CD213A2); Mesothelin; Interleukin 11 receptor alpha (IL-11Ra); prostate stem cell antigen (PSCA); Protease Serine 21 (Testisin or PRSS21); vascular endothelial growth factor receptor 2 (VEGFR2); Lewis(Y) antigen; CD24; Platelet-derived growth factor receptor beta (PDGFR-beta); Stage-specific embryonic antigen-4 (SSEA-4); CD20; Folate receptor alpha; Receptor tyrosine-protein kinase ERBB2 (Her2/neu); Mucin 1, cell surface associated (MUC1); epidermal growth factor receptor (EGFR); neural cell adhesion molecule (NCAM); Prostase; prostatic acid phosphatase (PAP); elongation factor 2 mutated (ELF2M); Ephrin B2; fibroblast activation protein alpha (FAP); insulin-like growth factor 1 receptor (IGF-I receptor), carbonic anhydrase IX (CAIX); Proteasome (Prosome, Macropain) Subunit, Beta Type, 9 (LMP2); glycoprotein 100 (gp100); oncogene fusion protein consisting of breakpoint cluster region (BCR) and Abelson murine leukemia viral oncogene homolog 1 (Abl) (bcr-abl); tyrosinase; ephrin type-A receptor 2 (EphA2); Fucosyl GM1; sialyl Lewis adhesion molecule (sLe); ganglioside GM3 (aNeu5Ac(2-3)bDGalp(1-4)bDGlcp(1-1)Cer); transglutaminase 5 (TGS5); high molecular weight-melanoma-associated antigen (HMWMAA); o-acetyl-GD2 ganglioside (OAcGD2); Folate receptor beta; tumor endothelial marker 1 (TEM1/CD248); tumor endothelial marker 7-related (TEM7R); claudin 6 (CLDN6); thyroid stimulating hormone receptor (TSHR); G protein-coupled receptor class C group 5, member D (GPRC5D); chromosome X open reading frame 61 (CXORF61); CD97; CD179a; anaplastic lymphoma kinase (ALK); Polysialic acid; placenta-specific 1 (PLAC1); hexasaccharide portion of globoH glycoceramide (GloboH); mammary gland differentiation antigen (NY-BR-1); uroplakin 2 (UPK2); Hepatitis A virus cellular receptor 1 (HAVCR1); adrenoceptor beta 3 (ADRB3); pannexin 3 (PANX3); G protein-coupled receptor 20 (GPR20); lymphocyte antigen 6 complex, locus K 9 (LY6K); Olfactory receptor 51E2 (OR51E2); TCR Gamma Alternate Reading Frame Protein (TARP); Wilms tumor protein (WT1); Cancer/testis antigen 1 (NY-ESO-1); Cancer/testis antigen 2 (LAGE-1a); Melanoma-

associated antigen 1 (MAGE-A1); ETS translocation-variant gene 6, located on chromosome 12p (ETV6-AML); sperm protein 17 (SPA17); X Antigen Family, Member 1A (XAGE1); angiopoietin-binding cell surface receptor 2 (Tie 2); melanoma cancer testis antigen-1 (MAD-CT-1); melanoma cancer testis antigen-2 (MAD-CT-2); Fos-related antigen 1; tumor protein p53 (p53); p53 mutant; prostein; surviving; telomerase; prostate carcinoma tumor antigen-1 (PCTA-1 or Galectin 8), melanoma antigen recognized by T cells 1 (MelanA or MART1); Rat sarcoma (Ras) mutant; human Telomerase reverse transcriptase (hTERT); sarcoma translocation breakpoints; melanoma inhibitor of apoptosis (ML-IAP); ERG (transmembrane protease, serine 2 (TMPRSS2) ETS fusion gene); N-Acetyl glucosaminyl-transferase V (NA17); paired box protein Pax-3 (PAX3); Androgen receptor; Cyclin B1; v-myc avian myelocytomatosis viral oncogene neuroblastoma derived homolog (MYCN); Ras Homolog Family Member C (RhoC); Tyrosinase-related protein 2 (TRP-2); Cytochrome P450 1B1 (CYP1B1); CCCTC-Binding Factor (Zinc Finger Protein)-Like (BORIS or Brother of the Regulator of Imprinted Sites), Squamous Cell Carcinoma Antigen Recognized By T Cells 3 (SART3); Paired box protein Pax-5 (PAX5); proacrosin binding protein sp32 (OY-TES1); lymphocyte-specific protein tyrosine kinase (LCK); A kinase anchor protein 4 (AKAP-4); synovial sarcoma, X breakpoint 2 (SSX2); Receptor for Advanced Glycation Endproducts (RAGE-1); renal ubiquitous 1 (RU1); renal ubiquitous 2 (RU2); legumain; human papilloma virus E6 (HPV E6); human papilloma virus E7 (HPV E7); intestinal carboxyl esterase; heat shock protein 70-2 mutated (mut hsp70-2); CD79a; CD79b; CD72; Leukocyte-associated immunoglobulin-like receptor 1 (LAIR1); Fc fragment of IgA receptor (FCAR or CD89); Leukocyte immunoglobulin-like receptor subfamily A member 2 (LILRA2); CD300 molecule-like family member f (CD300LF); C-type lectin domain family 12 member A (CLEC12A); bone marrow stromal cell antigen 2 (BST2); EGF-like module-containing mucin-like hormone receptor-like 2 (EMR2); lymphocyte antigen 75 (LY75); Glypican-3 (GPC3); Fc receptor-like 5 (FCRL5); or immunoglobulin lambda-like polypeptide 1 (IGLL1). In certain embodiments, a tumor antigen comprises ERBB2 (Her2/neu). In certain embodiments, a tumor antigen comprises PSMA. In certain embodiments, a tumor antigen comprises Mesothelin.

[0243] In some embodiments, an antigen binding domain binds to a misfolded protein antigen or a protein of a protein aggregate, such as a protein that is specific for a disease/disorder of interest. In some embodiments, the disease/disorder is a neurodegenerative disease/disorder,

an inflammatory disease/disorder, a cardiovascular disease/disorder, a fibrotic disease/disorder, or amyloidosis (e.g., mediated by protein aggregates of immunoglobulin light chains or of transthyretin). In some embodiments, the neurodegenerative disease/disorder is selected from the group consisting of tauopathy, asynucleopathy, presenile dementia, senile dementia, Alzheimer's disease (mediated by protein aggregates ofbeta-amyloid), Parkinsonism linked to chromosome 17 (FTDP-17), progressive supranuclear palsy (PSP), Pick' s disease, primary progressive aphasia, frontotemporal dementia, corticobasal dementia, Parkinson's disease, Parkinson's disease with dementia, dementia with Lewy bodies, Down syndrome, multiple system atrophy, amyotrophic lateral sclerosis (ALS), Hallervorden-Spatz syndrome, polyglutamine disease, trinucleotide repeat disease, Familial British dementia, Fatal Familial Insomnia, Gerstmann-Straussler-Scheinker Syndrome, Hereditary cerebral hemorrhage with amyloidosis (Icelandic) (HCHW A-I), Sporadic Fatal Insomnia (sFI), Variably Protease-Sensitive Prionopathy (VPSPr), Familial Danish dementia, and prion disease (such as Creutzfeldt-Jakob disease, CJD and Variant Creutzfeldt-Jakob Disease (vCJD)).

[0244] In some embodiments, an antigen binding domain comprises any domain that binds to an antigen. In some embodiments, an antigen binding domain is or comprises a monoclonal antibody, a polyclonal antibody, a synthetic antibody, a human antibody, a humanized antibody, a non-human antibody, or any fragment thereof, for example an scFv. In some embodiments, an antigen binding domain is or comprises an aptamer, a darpin, a centyrin, a naturally occurring or synthetic receptor, an affibody, or other engineered protein recognition molecule. In some embodiments, an antigen binding domain is or comprises a mammalian antibody or a fragment thereof. In some embodiments, an antigen binding domain is derived, in whole or in part, from the same species in which the CAR will ultimately be used. For example, for use in humans, an antigen binding domain of a CAR comprises a human antibody, a humanized antibody, or a fragment thereof (e.g. a scFv). In some embodiments, an antigen binding domain may be a domain that is endogenous to a particular immune cell type (e.g., a modified immune cell as provided herein). In some embodiments, an antigen binding domain may be a domain that is not endogenous to a particular immune cell type (e.g., a modified immune cell as provided herein).

[0245] In some embodiments, a CAR comprises one or more antigen binding domains. In some embodiments, a CAR comprises two or more antigen binding domains. In some embodiments, a CAR is a bispecific CAR. In some embodiments, an immune cell comprises two or more different CARs comprising one or more antigen binding domains. In some embodiments, an immune cell comprising a bispecific CAR and/or comprising two or more different CARs comprising one or more antigen binding domains can reduce off-target and/or on-target off-tissue effects by requiring that two antigens are present. In some embodiments, an immune cell comprises a bispecific CAR and/or comprises two or more different CARs comprising one or more antigen binding domains, wherein the CARs provide distinct signals that in isolation are insufficient to mediate activation of the modified cell, but are synergistic together, stimulating activation of the modified cell. In some embodiments, such a construct may be referred to as an 'AND' logic gate.

[0246] In some embodiments, an immune cell comprising a bispecific CAR and/or comprising two or more different CARs comprising one or more antigen binding domains can reduce off-target and/or on-target off-tissue effects by requiring that one antigen is present and a second, normal protein antigen is absent before the cell's activity is stimulated. In some embodiments, such a construct may be referred to as a 'NOT' logic gate. In contrast to AND gates, NOT gated CAR-modified cells are activated by binding to a single antigen. However, the binding of a second receptor to the second antigen functions to override the activating signal being perpetuated through the CAR. Typically, such an inhibitory receptor would be targeted against an antigen that is abundantly expressed in a normal tissue but is absent in tumor tissue.

Hinge Domains

[0247] In some embodiments, a CAR comprises one or more extracellular hinge domains. In some embodiments, an extracellular hinge domain is or comprises a human extracellular hinge domain. In some embodiments, an extracellular hinge domain may be a domain that is endogenous to a particular immune cell type (e.g., a modified immune cell as provided herein). In some embodiments, an extracellular hinge domain may be a domain that is not endogenous to a particular immune cell type (e.g., a modified immune cell as provided herein). In some embodiments, one or more extracellular hinge domains comprise a CD8a extracellular hinge domain or an IgG4 or a CD28 extracellular hinge domain. In some

embodiments, an extracellular hinge domain optimizes the physicochemical parameters of a CAR, e.g., optimal size relative to tumor antigen (e.g., allowing for exclusion of inhibitory molecules), optimal flexibility, optimal protein folding, optimal protein stability, optimal binding, optimal homodimerization, and/or lack of homodimerization.

Transmembrane Domains

[0248] In some embodiments, a CAR comprises a transmembrane domain, for example, that connects an extracellular domain to an intracellular domain. In some embodiments, a transmembrane domain is naturally associated with one or more other domain(s) of a CAR. In some embodiments, a transmembrane domain can be modified to avoid binding to transmembrane domains of other surface membrane proteins, in order to minimize interactions with other members of a receptor complex. In some embodiments, a transmembrane domain may be derived either from a naturally-occurring or from a synthetic source. In some embodiments a transmembrane domain is derived from a naturally-occurring membrane-bound or transmembrane protein. In some embodiments, a transmembrane domain is or comprises a human transmembrane domain. In some embodiments, a transmembrane domain may be a domain that is endogenous to a particular immune cell type (e.g., a modified immune cell as provided herein). In some embodiments, a transmembrane domain may be a domain that is not endogenous to a particular immune cell type (e.g., a modified immune cell as provided herein). In some embodiments, a transmembrane domain comprises a CD8a, CD64, CD32a, CD32c, CD16a, TRL1, TLR2, TLR3, TRL4, TLR5, TLR6, TLR7, TLR8, TLR9, ALK, AXL, DDR2, EGFR, EphA1, INSR, cMET, MUSK, PDGFR, PTK7, RET, ROR1, ROS1, RYK, TIE2, TRK, VEGFR, CD40, CD19, CD20, 41BB, CD28, OX40, GITR, TREM-1, TREM-2, DAP12, MR, ICOS, MyD88, CD3-zeta, FcR γ, V/I/LxYxxL/V, SIRPα, CD45, Siglec-10, PD1, SHP-1, SHP-2, KIR-2DL, KIR-3DL, NKG2A, CD170, CD33, BTLA, CD32b, SIRPβ, CD22, PIR-B, LILRB1, CD36, or Syk transmembrane domain.

FcR Transmembrane Domains

[0249] In some embodiments, an FcR transmembrane domain comprises a full-length FcR transmembrane domain. In some embodiments, an FcR transmembrane domain comprises a portion of a full-length FcR transmembrane domain. In some embodiments, an FcR

transmembrane domain is or comprises a human FcR transmembrane domain, or portion thereof. In some embodiments, an FcR transmembrane domain may be a domain that is endogenous to a particular immune cell type (e.g., a modified immune cell as provided herein). In some embodiments, an FcR transmembrane domain may be a domain that is not endogenous to a particular immune cell type (e.g., a modified immune cell as provided herein). In some embodiments, an FcR transmembrane domain comprises a CD64 (FcγRI), CD32a (FcγRIIa), CD32b (FcγRIIb), CD32c, CD16a (FcγRIIIa), CD16b (FcγRIIIb), FcεRI, FcεRII, or FcαRI (CD89) domain.

TLR Transmembrane Domains

[0250] In some embodiments, a TLR transmembrane domain comprises a full-length TLR transmembrane domain. In some embodiments, a TLR transmembrane domain comprises a portion of a full-length TLR transmembrane domain. In some embodiments, a TLR transmembrane domain is or comprises a human TLR transmembrane domain, or portion thereof. In some embodiments, a TLR transmembrane domain may be a domain that is endogenous to a particular immune cell type (e.g., a modified immune cell as provided herein). In some embodiments, a TLR transmembrane domain may be a domain that is not endogenous to a particular immune cell type (e.g., a modified immune cell as provided herein). In some embodiments, a TLR transmembrane domain comprises a TLR1, TLR2, TLR3, TLR4, TLR5, TLR6, TLR7, TLR8, or TLR9 domain.

Intracellular Domains

[0251] In some embodiments, a CAR comprises one or more intracellular domains. In some embodiments, an intracellular domain is or comprises a human intracellular domain, or portion thereof. In some embodiments, an intracellular domain may be a domain that is endogenous to a particular immune cell type (e.g., a modified immune cell as provided herein). In some embodiments, an intracellular domain may be a domain that is not endogenous to a particular immune cell type (e.g., a modified immune cell as provided herein). In some embodiments, an intracellular domain and/or other cytoplasmic domain of a CAR is responsible for activation of the cell in which the CAR is expressed (e.g., an immune cell). In some

embodiments, an intracellular domain of a CAR is responsible for signal activation and/or transduction in an immune cell comprising said CAR.

[0252] In some embodiments, an intracellular domain of a CAR includes at least one domain responsible for signal activation and/or transduction. In some embodiments, an intracellular domain is or comprises at least one of a co-stimulatory molecule and a signaling domain. In some embodiments, an intracellular domain of a CAR comprises dual signaling domains. In some embodiments, an intracellular domain of a CAR comprises more than two signaling domains.

[0253] In some embodiments, an intracellular domain comprises a cytoplasmic portion of a surface receptor. In some embodiments, an intracellular domain comprises a co-stimulatory molecule. In some embodiments, an intracellular domain comprises a molecule that acts to initiate signal transduction in an immune cell.

[0254] In some embodiments, an intracellular domain of a CAR includes any portion of one or more co-stimulatory molecules, such as at least one signaling domain from CD3, Fc epsilon RI gamma chain, any derivative or variant thereof, any synthetic sequence thereof that has the same functional capability, and any combination thereof.

FcR Intracellular Domains

[0255] In some embodiments, an FcR intracellular domain comprises a full-length FcR intracellular domain. In some embodiments, an FcR intracellular domain comprises a portion of a full-length FcR intracellular domain. In some embodiments, an FcR intracellular domain is or comprises a human FcR intracellular domain, or portion thereof. In some embodiments, an FcR intracellular domain may be a domain that is endogenous to a particular immune cell type (e.g., a modified immune cell as provided herein). In some embodiments, an FcR intracellular domain may be a domain that is not endogenous to a particular immune cell type (e.g., a modified immune cell as provided herein). In some embodiments, an FcR intracellular domain comprises a CD64 (FcγRI), CD32a (FcγRIIa), CD32b (FcγRIIb), CD32c, CD16a (FcγRIIIa), CD16b (FcγRIIIb), FcεRI, FcεRII, or FcαRI (CD89) domain.

TLR Intracellular Domains

[0256] In some embodiments, a TLR intracellular domain comprises a full-length TLR intracellular domain. In some embodiments, a TLR intracellular domain comprises a portion of a full-length TLR intracellular domain. In some embodiments, a TLR intracellular domain is or comprises a human TLR intracellular domain, or portion thereof. In some embodiments, a TLR intracellular domain may be a domain that is endogenous to a particular immune cell type (e.g., a modified immune cell as provided herein). In some embodiments, a TLR intracellular domain may be a domain that is not endogenous to a particular immune cell type (e.g., a modified immune cell as provided herein). In some embodiments, a TLR intracellular domain comprises a TLR1, TLR2, TLR3, TLR4, TLR5, TLR6, TLR7, TLR8, or TLR9 domain.

Signaling Domains

[0257] In some embodiments, a CAR comprises one or more intracellular signaling domains. In some embodiments, an intracellular signaling domain is or comprises a human intracellular signaling domain, or portion thereof. In some embodiments, a signaling domain may be a domain that is endogenous to a particular immune cell type (e.g., a modified immune cell as provided herein). In some embodiments, a signaling domain may be a domain that is not endogenous to a particular immune cell type (e.g., a modified immune cell as provided herein).

[0258] In some embodiments, one or more intracellular signaling domains comprise a CD3-zeta, FcR γ, CD64, CD32a, CD32c, CD16a, TLR1, TLR2, TLR3, TLR4, TLR5, TLR6, TLR7, TLR8, TLR9, ALK, AXL, DDR2, EGFR, EphA1, INSR, cMET, MUSK, PDGFR, PTK7, RET, ROR1, ROS1, RYK, TIE2, TRK, VEGFR, CD40, CD19, CD20, 41BB, CD28, OX40, GITR, TREM-1, TREM-2, DAP12, MR, ICOS, MyD88, V/I/LxYxxL/V, SIRPα, CD45, Siglec-10, PD1, SHP-1, SHP-2, KIR-2DL, KIR-3DL, NKG2A, CD170, CD33, BTLA, CD32b, SIRPβ, CD22, PIR-B, LILRB1,Syk, 41BB ligand (41BBL; TNFSF9), CD27, OX40L, CD32b, CD11b, ITGAM, SLAMF7, CD206, CD163, CD209, Dectin-2, or one or more cytokine receptor signaling domains (e.g., an IL1R, an IL2R, an IL3R, an IL4R, an IL5R, an IL6R, an IL7R, an IL8R, an IL9R, an IL10R, an IL11R, an IL12R, an IL13R, an IL14R, an IL15R, an IL17R, an IFNaR, an IFNgR, an TNFR, an CSF1R, an CSF2R, Dap10, CD36, Dectin-1, or ICOSL intracellular signaling domain)

[0259] In some embodiments, an intracellular domain of a CAR comprises dual signaling domains, such as 41BB, CD28, ICOS, TLR1, TLR2, TLR3, TLR4, TLR5, TLR6, TLR7, TLR8,

TLR9, TLR10, TLR11, CD116 receptor beta chain, CSF1-R, LRP1/CD91, SR-A1, SR-A2, MARCO, SR-CL1, SR-CL2, SR-C, SR-E, CR1, CR3, CR4, dectin 1, DEC-205, DC-SIGN, CD14, CD36, LOX-1, CD11b, together with any of the signaling domains listed in the above paragraph in any combination.

Co-stimulatory Domains

[0260] As used herein, a "co-stimulatory molecule" or "co-stimulatory domain" refers to a molecule in an immune cell that is used to heighten or dampen an initial stimulus. For example, pathogen-associated pattern recognition receptors, such as TLR or the CD47/SIRPα axis, are molecules on immune cells that, respectively, heighten or dampen an initial stimulus. In some embodiments, a co-stimulatory domain comprises TCR, CD3 zeta, CD3 gamma, CD3 delta, CD3 epsilon, CD86, common FcR gamma, FcR beta (Fc Epsilon R1b), CD79a, CD79b, Fcgamma RIIa, DAP10, DAP12, T cell receptor (TCR), CD27, CD28, 4-1BB (CD137), OX40, CD30, CD40, PD-1, ICOS, lymphocyte function-associated antigen-1 (LFA-1), CD2, CD7, LIGHT, NKG2C, B7-H3, a ligand that specifically binds with CD83, CDS, ICAM-1, GITR, BAFFR, HVEM (LIGHTR), SLAMF7, NKp80 (KLRF1), CD127, CD160, CD19, CD4, CD8alpha, CD8beta, IL2R beta, IL2R gamma, IL7R alpha, ITGA4, VLA1, CD49a, ITGA4, IA4, CD49D, ITGA6, VLA-6, CD49f, ITGAD, CD11d, ITGAE, CD103, ITGAL, CD11a, LFA-1, ITGAM, CD11b, ITGAX, CD11c, ITGB1, CD29, ITGB2, CD18, LFA-1, ITGB7, TNFR2, TRANCE/RANKL, DNAM1 (CD226), SLAMF4 (CD244, 2B4), CD84, CD96 (Tactile), CEACAM1, CRTAM, Ly9 (CD229), CD160 (BY55), PSGL1, CD100 (SEMA4D), CD69, SLAMF6 (NTB-A, Ly108), SLAM (SLAMF1, CD150, IPO-3), BLAME (SLAMF8), SELPLG (CD162), LTBR, LAT, GADS, SLP-76, PAG/Cbp, NKp44, NKp30, NKp46, NKG2D, other co-stimulatory molecules described herein, any derivative, variant, or fragment thereof, any synthetic sequence of a co-stimulatory molecule that has the same functional capability, and any combinations thereof.

[0261] In some embodiments, a co-stimulatory domain may be a domain that is endogenous to a particular immune cell type (e.g., a modified immune cell as provided herein). In some embodiments, a co-stimulatory domain may be a domain that is not endogenous to a particular immune cell type (e.g., a modified immune cell as provided herein).

[0262] As used herein, a "co-stimulatory signal" refers to a signal, which in combination with a primary signal, such as activation of a CAR on an immune cell, leads to activation of the immune cell.

Cleavage Peptides

[0263] As used herein, a cleavage peptide refers to a peptide that can induce the cleaving of a recombinant protein in a cell. In some embodiments, a cleavage peptide is a 2A peptide. In some embodiments, a cleavage peptide is or comprises a P2A, F2A, E2A or T2A peptide. In some embodiments, a nucleic acid as described herein comprises one or more nucleic acid sequences encoding one or more cleavage peptides. In some embodiments, a nucleic acid comprising a nucleic acid sequence encoding a cleavage peptide also comprises one or more nucleic acid sequences encoding one or more intracellular domains and one or more nucleic acid sequences comprising one or more peptide agents, wherein translation of the nucleic acid results in a protein comprising one or more intracellular domains separated from one or more peptide agents by a cleavage peptide. In some embodiments, a first promoter is operably linked to one or more nucleic acids encoding a CAR and a second promoter is operably linked to one or more nucleic acids encoding a peptide agent. In some embodiments, a nucleic acid sequence comprising a CAR, and optionally one or more peptide agents, further comprises an internal ribosome entry site (IRES) sequence. An IRES sequence may be any viral, chromosomal or artificially designed sequence that initiates cap-independent ribosome binding to mRNA facilitates the initiation of translation.

Peptide Agents

[0264] As used herein, a peptide agent refers to a peptide co-expressed with a CAR in an immune cell. In some embodiments, a peptide agent is co-expressed with a CAR to ensure stoichiometric balance and optimal signaling of a CAR. In some embodiments, a peptide agent forms a homodimer with an identical peptide agent. In some embodiments, a peptide agent forms a heterodimer with a different peptide agent. In some embodiments, a nucleic acid as described herein comprises one or more nucleic acid sequences encoding one or more peptide agents. In some embodiments, a peptide agent is or comprises an FcR gamma chain.

[0265] In some embodiments, a peptide agent comprises any peptide, protein, receptor, secreted antibody or a fragment thereof (e.g., an scFv, Fab, Fab', F(ab')2, Fc, or nanobody). In

some embodiments, a peptide agent comprises one or more cytokines (e.g., one or more of IL-1, IL-2, IL-6, IL-8, TNF-a, IFNa, IFNb, IFN-y, GMCSF, or MCSF), CD40-L, dominant negative SIRPα, dominant negative PD1, dominant negative CD45, dominant negative SIGLEC 10, or dominant negative LILRB.

Fc Receptors (FcR)

[0266] In some embodiments, a CAR comprises one or more antigen binding domains and an FcR extracellular domain, and/or the transmembrane domain of the CAR comprises an FcR transmembrane domain, and/or the intracellular domain of the CAR comprises an FcR intracellular domain. In some embodiments, a CAR comprises, from N-terminus to C-terminus, one or more extracellular binding domains, an FcR extracellular domain, an FcR transmembrane domain, and an FcR intracellular domain. In some embodiments, one or more of the FcR extracellular domain, the FcR transmembrane domain and the FcR intracellular domain is or comprises a human FcR domain. In some embodiments, an FcR extracellular domain, an FcR transmembrane domain and an FcR intracellular domain together comprise a full-length FcR. In some embodiments, an FcR extracellular domain, an FcR transmembrane domain and an FcR intracellular domain together comprise a portion of a full-length FcR. In some embodiments, an FcR extracellular domain comprises a portion of a full-length FcR extracellular domain. In some embodiments, an FcR transmembrane domain comprises a portion of a full-length FcR transmembrane domain. In some embodiments, an FcR intracellular domain comprises a portion of a full-length FcR intracellular domain.

Toll-Like Antigen Receptors (TLR)

[0267] In some embodiments, a CAR comprises one or more antigen binding domains and a toll-like receptor (TLR) extracellular domain and/or the transmembrane domain of the CAR comprises a TLR transmembrane domain and/or the intracellular domain of the CAR comprises a TLR intracellular domain. In some embodiments, a CAR comprises, from N-terminus to C-terminus, one or more extracellular binding domains, a TLR extracellular domain, a TLR transmembrane domain, and a TLR intracellular domain. In some embodiments, one or more of the TLR extracellular domain, the TLR transmembrane domain and the TLR

intracellular domain is or comprises a human TLR domain. In some embodiments, a TLR extracellular domain, a TLR transmembrane domain and a TLR intracellular domain together comprise a full-length TLR. In some embodiments, a TLR extracellular domain, a TLR transmembrane domain and a TLR intracellular domain together comprise portion of a full-length TLR. In some embodiments, a TLR extracellular domain comprises a portion of a full-length TLR extracellular domain. In some embodiments, a TLR transmembrane domain comprises a portion of a full-length TLR transmembrane domain. In some embodiments, a TLR intracellular domain comprises a portion of a full-length TLR intracellular domain.

Nucleic Acid Constructs

[0268] The present disclosure provides, among other things, nucleic acid molecules encoding at least one exogenous cytokine described herein or a fragment thereof. The present disclosure provides, among other things, nucleic acid molecules encoding at least one fusion protein described herein or a fragment thereof. In some embodiments, the present disclosure provides nucleic acid molecules encoding at least one CAR described herein or a fragment thereof. An immune cell (e.g., stem cell, macrophage, monocyte, or dendritic cell) can comprise a nucleic acid molecule (e.g., an exogenous nucleic acid molecule) encoding at least one protein (e.g., an exogenous cytokine of the present disclosure, a fusion protein of the present disclosure or a CAR of the present disclosure) described herein. In some embodiments, a nucleic acid molecule encoding at least one fusion protein comprises a cytokine and a cytokine receptor.

[0269] Unless otherwise specified, a "nucleotide sequence encoding an amino acid sequence" includes all nucleotide sequences that are degenerate versions of each other and that encode the same amino acid sequence. The phrase "nucleotide sequence that encodes a protein or an RNA" may also include introns to the extent that the nucleotide sequence encoding the protein may in some version contain an intron(s). The term "encoding" refers to the inherent property of specific sequences of nucleotides in a polynucleotide, such as a gene, a cDNA, or an mRNA, to serve as templates for synthesis of other polymers and macromolecules in biological processes having either a defined sequence of nucleotides (e.g., rRNA, tRNA and mRNA) or a defined sequence of amino acids and the biological properties resulting therefrom. Thus, a gene, cDNA, or RNA, encodes a protein if transcription and translation of mRNA corresponding to

that gene produces the protein in a cell or other biological system. Both the coding strand, the nucleotide sequence of which is identical to the mRNA sequence and is usually provided in sequence listings, and the non-coding strand, used as the template for transcription of a gene or cDNA, can be referred to as encoding the protein or other product of that gene or cDNA.

[0270] The term "operably linked" or "transcriptional control" refers to functional linkage between a regulatory sequence and a heterologous nucleic acid sequence resulting in expression of the heterologous nucleic acid sequence. For example, a first nucleic acid sequence is operably linked with a second nucleic acid sequence when the first nucleic acid sequence is placed in a functional relationship with the second nucleic acid sequence. For instance, a promoter is operably linked to a coding sequence if the promoter affects the transcription or expression of the coding sequence. Operably linked DNA sequences can be contiguous with each other and, e.g., where necessary to join two protein coding regions, are in the same reading frame.

[0271] Nucleic acid molecules encoding at least one protein (e.g., an exogenous cytokine of the present disclosure, a fusion protein of the present disclosure or a CAR of the present disclosure) described herein or a fragment thereof can be a DNA molecule, an RNA molecule, or a combination thereof. In some embodiments, a nucleic acid molecule comprises or is a messenger RNA (mRNA) transcript encoding at least one protein (e.g., an exogenous cytokine of the present disclosure, a fusion protein of the present disclosure or a CAR of the present disclosure) described herein or a fragment thereof. In some embodiments, a nucleic acid molecule comprises or is a DNA construct encoding at least one protein (e.g., an exogenous cytokine of the present disclosure, a fusion protein of the present disclosure or a CAR of the present disclosure) described herein or a fragment thereof.

[0272] In some embodiments, all or a fragment of a protein (e.g., an exogenous cytokine of the present disclosure, a fusion protein of the present disclosure or a CAR of the present disclosure) described herein is encoded by a codon optimized nucleic acid molecule, e.g., for expression in a cell (e.g., a mammalian cell). A variety of codon optimization methods are known in the art, e.g., as disclosed in US Patent Nos. 5,786,464 and 6,114,148, each of which is hereby incorporated by reference in its entirety.

[0273] Expression of nucleic acids as described herein may be achieved by operably linking a nucleic acid encoding a protein (e.g., an exogenous cytokine of the present disclosure, a fusion protein of the present disclosure or a CAR of the present disclosure) or fragment thereof to a promoter in an expression vector. Exemplary promoters (e.g., constitutive promoters) include, but are not limited to, an elongation factor-1α promoter (EF-1α) promoter, immediate early cytomegalovirus (CMV) promoter, ubiquitin C promoter, phosphoglycerokinase (PGK) promoter, simian virus 40 (SV40) early promoter, mouse mammary tumor virus (MMTV) promoter, human immunodeficiency virus (HIV) long terminal repeat (LTR) promoter, Moloney murine leukemia virus (MoMuLV) promoter, an avian leukemia virus promoter, an Epstein-Barr virus immediate early promoter, a Rous sarcoma virus promoter, an actin promoter, a myosin promoter, a hemoglobin promoter, or a creatine kinase promoter. Examples of inducible promoters include, but are not limited to a metallothionine promoter, a glucocorticoid promoter, a progesterone promoter, and a tetracycline promoter. A vector can also comprise additional promoter elements, e.g., enhancers, to regulate the frequency of transcriptional initiation.

[0274] In some embodiments, a vector comprising a nucleic acid molecule encoding a protein (e.g., an exogenous cytokine of the present disclosure, a fusion protein of the present disclosure or a CAR of the present disclosure) or fragment thereof comprises or is a viral vector. Viral vector technology is well known in the art and is described (e.g., in Sambrook et al., 2012, MOLECULAR CLONING: A LABORATORY MANUAL, volumes 1-4, Cold Spring Harbor Press, NY). Examples of viral vectors include, but are not limited to, adenoviral vectors, adeno-associated viral vectors, or retroviral vectors (e.g., a lentiviral vector or a gammaretroviral vector). In some embodiments, a vector comprises a lentiviral vector (e.g., as described in US Patent No. 9,149,519 or International Publication No. WO 2017/044487, each of which is hereby incorporated by reference in its entirety).

[0275] In some embodiments, a viral vector comprises an adenoviral vector. Adenoviruses are a large family of viruses containing double stranded DNA. They replicate within the nucleus of a host cell, using the host's cell machinery to synthesize viral RNA, DNA and proteins. Adenoviruses are known in the art to affect both replicating and non-replicating cells, to accommodate large transgenes, and to code for proteins without integrating into the host

cell genome. In some embodiments, an adenoviral vector comprises an Ad2 vector or an Ad5 vector (e.g., Ad5f35 adenoviral vector, e.g., a helper-dependent Ad5F35 adenoviral vector).

[0276] In some embodiments, a viral vector is an adeno-associated virus (AAV) vector. AAV systems are generally well known in the art (see, e.g., Kelleher and Vos, Biotechniques, 17(6):1110-17 (1994); Cotten et al., P.N.A.S. U.S.A., 89(13):6094-98 (1992); Curiel, Nat Immun, 13(2-3):141-64 (1994); Muzyczka, Curr Top Microbiol Immunol, 158:97-129 (1992); and Asokan A, et al., Mol. Ther., 20(4):699-708 (2012)). Methods for generating and using recombinant AAV (rAAV) vectors are described, for example, in U.S. Pat. Nos. 5,139,941 and 4,797,368.

[0277] Several AAV serotypes have been characterized, including AAV1, AAV2, AAV3 (e.g., AAV3B), AAV4, AAV5, AAV6, AAV7, AAV8, AAV9, AAV10, and AAV11, as well as variants thereof. Generally, any AAV serotype may be used to deliver a protein (e.g., an exogenous cytokine of the present disclosure, a fusion protein of the present disclosure or a CAR of the present disclosure) or fragment thereofdescribed herein. In some embodiments, an AAV serotype has a tropism for a particular tissue.

[0278] In some embodiments, CRISPR/Cas9 system has recently been shown to facilitate high levels of precise genome editing using adeno associated viral (AAV) vectors to serve as donor template DNA during homologous recombination (HR).

[0279] In some embodiments, a vector comprises a gammaretroviral vector (e.g., as described in Tobias Maetzig et al., "Gammaretroviral Vectors: Biology, Technology and Application" Viruses. 2011 Jun; 3(6): 677–713, which is hereby incorporated by reference in its entirety). Exemplary gammaretroviral vectors include Murine Leukemia Virus (MLV), Spleen-Focus Forming Virus (SFFV), and Myeloproliferative Sarcoma Virus (MPSV), and vectors derived therefrom.

[0280] In some embodiments, a vector comprises two or more nucleic acid sequences encoding proteins, e.g., at least one exogenous cytokine described herein and a CAR described herein. In some embodiments, a vector comprises two or more nucleic acid sequences encoding proteins, e.g., at least one fusion protein described herein, and a CAR described herein. In some embodiments, two or more nucleic acid sequences encoding an exogenous cytokine and a CAR are encoded by a single nucleic molecule, e.g., in same frame and as a single polypeptide chain.

In some embodiments, two or more nucleic acid sequences encoding a fusion protein and a CAR are encoded by a single nucleic molecule, e.g., in same frame and as a single polypeptide chain. In some embodiments, two or more proteins (e.g., an exogenous cytokine and a CAR) are separated by one or more cleavage peptide sites (e.g., an auto-cleavage site or a substrate for an intracellular protease). In some embodiments, two or more proteins (e.g., a fusion protein and a CAR) are separated by one or more cleavage peptide sites (e.g., an auto-cleavage site or a substrate for an intracellular protease). In certain embodiments, a cleavage peptide comprises a porcine teschovirus-l (P2A) peptide, Thosea asigna virus (T2A) peptide, equine rhinitis A virus (E2A) peptide, foot-and-mouth disease virus (F2A) peptide, or a variant thereof.

[0281] In some embodiments, a vector comprises at least one nucleic acid sequence encoding a protein, e.g., at least one exogenous cytokine described herein, at least one fusion protein described herein or at least one CAR described herein, and at least one nucleic acid encoding at least one gene co-expressed with a second protein, e.g., a cytokine described herein (e.g., TNF, IL-12, IFN, GM-CSF, G-CSF, M-CSF, and/or IL-1) or a stimulatory ligand described herein (e.g., CD7, B7-1 (CD80), B7-2 (CD86), PD-L1, PD-L2, 4-1BBL, OX40L, ICOS-L, ICAM, CD30L, CD40, CD40L, CD70, CD83, HLA-G, MICA, MICB, HVEM, lymphotoxin beta receptor, 3/TR6, ILT3, ILT4, HVEM, an agonist or antibody that binds Toll ligand receptor, and/or a B7-H3 ligand).

Pharmaceutical Compositions

[0282] The present disclosure, among other things, provides pharmaceutical compositions comprising immune cells as described herein (e.g., stem cells, macrophages, monocytes, or dendritic cells) in combination with one or more pharmaceutically or physiologically acceptable carriers, diluents, or excipients.

[0283] When "a therapeutically effective amount, "an immunologically effective amount," "an anti-immune response effective amount," or "an immune response-inhibiting effective amount" is indicated, a precise amount of a pharmaceutical composition comprising immune cells as described herein (e.g., stem cells, macrophages, monocytes, or dendritic cells) can be determined by a physician with consideration of individual differences in age, weight, immune response, and condition of the patient (subject).

[0284] Pharmaceutical compositions comprising immune cells as described herein (e.g., stem cells, macrophages, monocytes, or dendritic cells) may comprise buffers, such as neutral buffered saline or phosphate buffered saline (PBS); carbohydrates, such as glucose, mannose, sucrose, dextrans, or mannitol; proteins, polypeptides, or amino acids (e.g., glycine); antioxidants; chelating agents, such as EDTA or glutathione; adjuvants (e.g., aluminum hydroxide); serum and preservatives, such as cryoprotectant. In some embodiments, a pharmaceutical composition is substantially free of contaminants, e.g., there are no detectable levels of a contaminant (e.g., an endotoxin).

[0285] Pharmaceutical compositions described herein may be administered in a manner appropriate to the disease, disorder, or condition to be treated or prevented. Quantity and frequency of administration will be determined by such factors as condition of a patient, and type and severity of a patient's disease, disorder, or condition, although appropriate dosages may be determined by clinical trials.

[0286] Pharmaceutical compositions described herein may be in a variety of forms. These include, for example, liquid, semi-solid and solid dosage forms, such as liquid solutions (e.g., injectable and infusible solutions), dispersions or suspensions, liposomes, and suppositories. Preferred compositions may be injectable or infusible solutions. Pharmaceutical compositions described herein can be formulated for administration intravenously, subcutaneously, intradermally, intratumorally, intranodally, intramedullary, intramuscularly, transarterially, or intraperitoneally.

[0287] In some embodiments, a pharmaceutical composition described herein is formulated for parenteral (e.g., intravenous, subcutaneous, intraperitoneal, or intramuscular) administration. In some embodiments, a pharmaceutical composition described herein is formulated for intravenous infusion or injection. In some embodiments, a pharmaceutical composition described herein is formulated for intramuscular or subcutaneous injection. Pharmaceutical compositions described herein can be formulated for administered by using infusion techniques that are commonly known in immunotherapy (See, e.g., Rosenberg et al., New Eng. J. of Med. 319:1676, 1988, which is hereby incorporated by reference in its entirety).

[0288] As used herein, the terms "parenteral administration" and "administered parenterally" refer to modes of administration other than enteral and topical administration,

usually by injection or infusion, and include, without limitation, intravenous, intramuscular, intraarterial, intrathecal, intracapsular, intraorbital, intracardiac, intradermal, intraperitoneal, transtracheal, subcutaneous, subcuticular, intraarticular, subcapsular, subarachnoid, intraspinal, epidural, intratumoral, and intrasternal injection and infusion.

[0289] Pharmaceutical compositions comprising immune cells as described herein may be administered at a dosage of about 104 to about 109 cells/kg body weight (e.g., about 105 to about 106 cells/kg body weight), including all integer values within those ranges. In some embodiments, a dose of immune cells as described herein (e.g., stem cells, macrophages, monocytes, or dendritic cells) comprises at least about 1 x 106, about 1.1 x 106, about 2 x 106, about 3.6 x 106, about 5 x 106, about 1 x 107, about 1.8 x 107, about 2 x 107, about 5 x 107, about 1 x 108, about 2 x 108, about 5 x 108, about 1 x 109, about 2 x 109, or about 5 x 109 cells. Pharmaceutical compositions described herein may also be administered multiple times at a certain dosage. An optimal dosage and treatment regime for a particular patient can readily be determined by one skilled in the art by monitoring a patient for signs of a disease, disorder, or condition and adjusting treatment accordingly.

[0290] It may be desired to administer pharmaceutical compositions comprising immune cells (e.g., stem cells, macrophages, monocytes, or dendritic cells) as described herein to a subject and then subsequently redraw blood (or have apheresis performed), activate collected immune cells, and reinfuse a subject with activated immune cells. This process can be performed multiple times, e.g., every few weeks. Immune cells (e.g., stem cells, macrophages, monocytes, or dendritic cells) can be activated from blood draws of from about 10 cc to about 400 cc. In some embodiments, immune cells (e.g., macrophages, monocytes, or dendritic cells) are activated from blood draws of about 20 cc, about 30 cc, about 40 cc, about 50 cc, about 60 cc, about 70 cc, about 80 cc, about 90 cc, or about 100 cc. Without being bound by theory, methods comprising multiple blood draw and reinfusions as described herein may select for certain immune cell populations. In some embodiments, pharmaceutical compositions comprising immune cells as described herein (e.g., stem cells, macrophages, monocytes, or dendritic cells) are administered in combination with (e.g., before, simultaneously, or following) a second therapy. For example, a second therapy can include, but is not limited to antiviral therapy (e.g., cidofovir, interleukin-2, Cytarabine (ARA-C), or natalizumab), chimeric antigen

receptor-T cell (CAR-T) therapy, T-cell receptor (TCR)-T cell therapy, chemotherapy, radiation, an immunosuppressive agent (e.g., cyclosporin, azathioprine, methotrexate, mycophenolate, FK506 antibody, or glucocorticoids), an antagonist (e.g., one or more of a PD-1 antagonist, a PD-L1 antagonist, CTLA4 antagonist, CD47 antagonist, SIRPα antagonist, CD40 agonists, CSF1/CSF1R antagonist, or a STING agonist), or an immunoablative agent (e.g., an anti-CD52 antibody (e.g., alemtuzumab), an anti-CD3 antibody, cytoxin, fludaribine, cyclosporin, FK506, rapamycin, mycophenolic acid, a steroid, FR901228, or irradiation).

[0291] In some embodiments, pharmaceutical compositions comprising immune cells as described herein (e.g., stem cells, macrophages, monocytes, or dendritic cells) are administered in combination with (e.g., before, simultaneously, or following) bone marrow transplantation or lymphocyte ablative therapy using a chemotherapy agent (e.g., fludarabine, external-beam radiation therapy (XRT), cyclophosphamide, or Rituxan). In certain embodiments, subjects undergo standard treatment with high dose chemotherapy followed by peripheral blood stem cell transplantation. In certain embodiments, following transplant, subjects receive an infusion of a pharmaceutical composition comprising immune cells as described herein. Pharmaceutical compositions described herein may be administered before or following surgery.

[0292] A dosage of any aforementioned therapy to be administered to a subject will vary with a disease, disorder, or condition being treated and based on a specific subject. Scaling of dosages for human administration can be performed according to art-accepted practices. For example, a dose of alemtuzumab will generally be about 1 mg to about 100 mg for an adult, usually administered daily for a period of between about 1 day to about 30 days, e.g., a daily dose of about 1 mg to about 10 mg per day (e.g., as described in U.S. Patent No. 6,120,766, which is hereby incorporated by reference in its entirety).

Methods of Treatment

[0293] The present disclosure, among other things, provides methods of treating a disease or disorder (e.g., a disease or a disorder described herein) in a subject comprising delivering a pharmaceutical composition comprising immune cells as described herein (e.g., stem cells, macrophages, monocytes, or dendritic cells). In some embodiments, a therapeutically effective amount of a pharmaceutical composition described herein is administered to a subject

having a disease or disorder. Pharmaceutical compositions as described herein can be for use in the manufacture of a medicament for treating a disease or disorder in a subject or stimulating an immune response in a subject.

[0294] A subject to be treated with methods described herein can be a mammal, e.g., a primate, e.g., a human (e.g., a patient having, or at risk of having, a disease or disorder described herein). In some embodiments, immune cells (e.g., stem cells, macrophages, monocytes, or dendritic cells) may be autologous, allogeneic, or xenogeneic with respect to a subject. Pharmaceutical compositions as described herein can be administered to a subject in accordance with a dosage regimen described herein, alone or in combination with one or more therapeutic agents, procedures, or modalities.

[0295] Pharmaceutical composition comprising immune cells as described herein (e.g., stem cells, macrophages, monocytes, or dendritic cells) can be used to treat or prevent a disease associated with a tumor or cancer, a neurodegenerative disease or disorder, an inflammatory disease or disorder, a cardiovascular disease or disorder, a fibrotic disease or disorder, a disease associated with amyloidosis, and a combination of thereof.

[0296] A method of treating (e.g., one or more of reducing, inhibiting, or delaying progression of) a cancer or a tumor in a subject with a pharmaceutical composition comprising immune cells as described herein (e.g., stem cells, macrophages, monocytes, or dendritic cells) is provided. A subject can have an adult or pediatric form of cancer. A cancer may be at an early, intermediate, or late stage, or a metastatic cancer. A cancer can include, but is not limited to, a solid tumor, a hematological cancer (e.g., leukemia, lymphoma, or myeloma, e.g., multiple myeloma), or a metastatic lesion. Examples of solid tumors include malignancies, e.g., sarcomas and carcinomas, e.g., adenocarcinomas of the various organ systems, such as those affecting the lung, breast, ovarian, lymphoid, gastrointestinal (e.g., colon), anal, genitals and genitourinary tract (e.g., renal, urothelial, bladder cells, prostate), pharynx, CNS (e.g., brain, neural or glial cells), head and neck, skin (e.g., melanoma, e.g., a cutaneous melanoma), pancreas, and bones (e.g., a chordoma).

[0297] In some embodiments, a cancer is chosen from a lung cancer (e.g., a non-small cell lung cancer (NSCLC) (e.g., a non-small cell lung cancer (NSCLC) with squamous and/or non-squamous histology, or a NSCLC adenocarcinoma), or a small cell lung cancer (SCLC)), a

skin cancer (e.g., a Merkel cell carcinoma or a melanoma (e.g., an advanced melanoma)), an ovarian cancer, a mesothelioma, a bladder cancer, a soft tissue sarcoma (e.g., a hemangiopericytoma (HPC)), a bone cancer (a bone sarcoma), a kidney cancer (e.g., a renal cancer (e.g., a renal cell carcinoma)), a liver cancer (e.g., a hepatocellular carcinoma), a cholangiocarcinoma, a sarcoma, a myelodysplastic syndrome (MDS), a prostate cancer, a breast cancer (e.g., a breast cancer that does not express one, two or all of estrogen receptor, progesterone receptor, or Her2/neu, e.g., a triple negative breast cancer), a colorectal cancer (e.g., a relapsed colorectal cancer or a metastatic colorectal cancer, e.g., a microsatellite unstable colorectal cancer, a microsatellite stable colorectal cancer, a mismatch repair proficient colorectal cancer, or a mismatch repair deficient colorectal cancer), a nasopharyngeal cancer, a duodenal cancer, an endometrial cancer, a pancreatic cancer, a head and neck cancer (e.g., head and neck squamous cell carcinoma (HNSCC)), an anal cancer, a gastro-esophageal cancer, a thyroid cancer (e.g., anaplastic thyroid carcinoma), a cervical cancer (e.g., a squamous cell carcinoma of the cervix), a neuroendocrine tumor (NET) (e.g., an atypical pulmonary carcinoid tumor), a lymphoproliferative disease (e.g., a post-transplant lymphoproliferative disease), a lymphoma (e.g., T-cell lymphoma, B-cell lymphoma, or a non-Hodgkin lymphoma), a myeloma (e.g., a multiple myeloma), or a leukemia (e.g., a myeloid leukemia or a lymphoid leukemia).

[0298] In some embodiments, a cancer is a brain tumor, e.g., a glioblastoma, a gliosarcoma, or a recurrent brain tumor. In some embodiments, a cancer is a pancreatic cancer, e.g., an advanced pancreatic cancer. In some embodiments, a cancer is a skin cancer, e.g., a melanoma (e.g., a stage II-IV melanoma, an HLA-A2 positive melanoma, an unresectable melanoma, or a metastatic melanoma), or a Merkel cell carcinoma. In some embodiments, a cancer is a renal cancer, e.g., a renal cell carcinoma (RCC) (e.g., a metastatic renal cell carcinoma). In some embodiments, a cancer is a breast cancer, e.g., a metastatic breast carcinoma or a stage IV breast carcinoma, e.g., a triple negative breast cancer (TNBC). In some embodiments, a cancer is a virus-associated cancer. In some embodiments, a cancer is an anal canal cancer (e.g., a squamous cell carcinoma of the anal canal). In some embodiments, a cancer is a cervical cancer (e.g., a squamous cell carcinoma of the cervix). In some embodiments, a cancer is a gastric cancer (e.g., an Epstein Barr Virus (EBV) positive gastric cancer, or a gastric or gastro-esophageal junction carcinoma). In some embodiments, a cancer is a head and neck cancer (e.g., an HPV positive and negative squamous cell cancer of the head and neck

(SCCHN)). In some embodiments, a cancer is a nasopharyngeal cancer (NPC). In some embodiments, a cancer is a colorectal cancer, e.g., a relapsed colorectal cancer, a metastatic colorectal cancer, e.g., a microsatellite unstable colorectal cancer, a microsatellite stable colorectal cancer, a mismatch repair proficient colorectal cancer, or a mismatch repair deficient colorectal cancer.

[0299] In some embodiments, a cancer is a hematological cancer. In some embodiments, a cancer is a leukemia, e.g., acute myeloid leukemia, chronic myeloid leukemia, acute lymphoblastic leukemia, chronic lymphocytic leukemia, chronic leukemia, or acute leukemia. In some embodiments, a cancer is a lymphoma, e.g., Hodgkin lymphoma (HL), non-Hodgkin's lymphoma, lymphocytic lymphoma, or diffuse large B cell lymphoma (DLBCL) (e.g., a relapsed or refractory HL or DLBCL). In some embodiments, a cancer is a myeloma, e.g., multiple myeloma.

[0300] Pharmaceutical composition comprising immune cells as described herein (e.g., stem cells, macrophages, monocytes, or dendritic cells) can be used to enhance or modulate an immune response in a subject. In one embodiment, a pharmaceutical composition described herein enhances, stimulates, or increases an immune response in a subject (e.g., a subject having, or at risk of, a disease or disorder described herein). In certain embodiments, a subject is, or is at risk of being, immunocompromised. For example, a subject is undergoing or has undergone a chemotherapeutic treatment and/or radiation therapy.

[0301] In some embodiments, a subject has, or is at risk of, developing an inflammatory disorder (e.g., a chronic or acute inflammatory disorder). In some embodiments, a subject has, or is at risk, of developing an autoimmune disease or disorder. Exemplary autoimmune diseases that can be treated with methods described herein include, but are not limited to, Alzheimer's disease, asthma (e.g., bronchial asthma), an allergy (e.g., an atopic allergy), Acquired Immunodeficiency Syndrome (AIDS), atherosclerosis, Behcet's disease, celiac, cardiomyopathy, Crohn's disease, cirrhosis, diabetes, diabetic retinopathy, eczema, fibromyalgia, fibromyositis, glomerulonephritis, graft vs. host disease (GVHD), Guillain-Barre syndrome, hemolytic anemia, multiple sclerosis, myasthenia gravis, osteoarthritis, polychondritis, psoriasis, rheumatoid arthritis, sepsis, stroke, vasculitis, ventilator-induced lung injury, transplant rejection, Raynaud's

phenomena, Reiter's syndrome, rheumatic fever, sarcoidosis, scleroderma, Sjogren's syndrome, ulcerative colitis, uveitis, vitiligo, or Wegener's granulomatosis.

[0302] Administration of pharmaceutical compositions described herein may be carried out in any convenient manner (e.g., injection, ingestion, transfusion, inhalation, implantation, or transplantation). In some embodiments, a pharmaceutical compositions described herein is administered by injection or infusion. Pharmaceutical compositions described herein may be administered to a patient transarterially, subcutaneously, intravenously, intradermally, intratumorally, intranodally, intramedullary, intramuscularly, or intraperitoneally. In some embodiments, a pharmaceutical composition described herein is administered parenterally (e.g., intravenously, subcutaneously, intraperitoneally, or intramuscularly). In some embodiments, a pharmaceutical composition described herein is administered by intravenous infusion or injection. In some embodiments, a pharmaceutical composition described herein is administered by intramuscular or subcutaneous injection. Pharmaceutical compositions described herein may be injected directly into a site of inflammation, a local disease site, a lymph node, an organ, a tumor, or site of infection in a subject.

[0303] All publications, patent applications, patents, and other references mentioned herein, including GenBank Accession Numbers, are incorporated by reference in their entirety. In addition, the materials, methods, and examples are illustrative only and not intended to be limiting. 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 belongs. Although methods and materials similar or equivalent to those described herein can be used in the practice or testing of the present invention, suitable methods and materials are described herein.

[0304] The disclosure is further illustrated by the following examples. An example is provided for illustrative purposes only. It is not to be construed as limiting the scope or content of the disclosure in any way.

EXAMPLES

[0305] The following examples are provided so as to describe to the skilled artisan how to make and use methods and compositions described herein, and are not intended to limit the scope of the present disclosure.

Example 1: Trafficking of Fusion Proteins to Cell Surface of HEK293T Cells

[0306] On Day 0, HEK293T cells were transiently transfected with plasmid DNA using Lipofectamine 3000. On Day 2, the HEK293T cells were evaluated for expression and trafficking of fusion proteins expressed from exemplary constructs of the present disclosure (see **Figure 5A** and **Figure 5B**). Immunostaining for a FLAG-tag at the N-terminus of a fusion protein indicates proper folding and trafficking of the fusion protein to the cell surface, while Western blots were performed to detect full-length fusion protein mass.

[0307] As shown in **Figure 6A**, transfection of HEK293T cells with constructs encoding fusion proteins did not affect the viability of the cells relative to nontransfected cells. As shown in **Figure 6B**, HEK cells were able to express 3 separate fusion proteins (IFN-β and IFNAR1, IL-4 and IL2Rγc and IL-4 and IL13Rα) at the cell surface, as indicated by immunostaining for the FLAG tag. Additionally, as shown in **Figure** 7, there was a correlation between detection of a FLAG tag by an antibody and mCherry expression in the IFNβ-IFNAR1 and IL4-IL13Rα groups. Western blot analyses further confirmed expression of the fusion proteins (see **Figure 8**). By using antibodies that targeted the cytokines (which are small molecular masses), the larger molecular mass that results from direct fusion with the cytokine receptor was detected. Fusion to the cytokine receptor was particularly evident in the case of IFNβ. IFNAR1 is heavily glycosylated, increasing its mass almost 2-fold beyond the predicted mass based off amino acid confirmation, and resulted in a smeared band in the Western blot. By targeting the cytokine IFNβ, the Western blot captured the glycosylated nature of IFNAR1, demonstrating the fusion of these two proteins.

Example 2: Expression of Fusion Proteins in Primary Macrophages

[0308] On Day 0, macrophages were transduced with VPX-Lentivirus comprising a fusion protein (MOI 10). On Day 2, the macrophage media with replaced with fresh media. On

Day 4, flow cytometry (FCM) was performed to analyze surface expression of fusion proteins encoded by exemplary constructs of the present disclosure, with immunostaining for a FLAG-tag at the N-terminus of the fusion protein (see **Figure 9**).

[0309] As shown in **Figure 10A**, transfection of macrophages with constructs encoding fusion proteins reduced viability of the cells relative to nontransfected macrophages. As shown in **Figure 10A** and **Figure 10B**, IL4-based fusion proteins were successfully expressed at the surface of macrophages, while IFN-β-based fusion proteins were not detected at the surface of macrophages. These results, compared to those in Example 1, indicate that macrophages may be more sensitive than HEK293T cells to the design of each fusion protein. Additionally, these results could indicate that surface expression is not necessary for signaling, for example, a functional signaling cascade could occur from the endoplasmic reticulum. Total protein expression can be determined using western blot, while flow cytometry plus cell permeabilization can be used to determine intracellular expression. It is also possible that the IFN-β-based fusion protein was expressed at the cell surface, but was not detectable in the system's signal-to-noise ratio. Finally, the results shown in **Figure 11A** and **Figure 11B** illustrate viability, P2A-mCherry expression, and surface expression of fusion proteins in macrophages transduced with VPX-Lentivirus comprising a fusion protein.

Example 3: Effect of Pro-Inflammatory Fusion Protein on Pro-Inflammatory and Anti-Inflammatory Markers

[0310] On Day 0, macrophages were transduced with VPX-Lentivirus comprising a fusion protein (MOI 10). On Day 3, the macrophage media with replaced with fresh media. On Day 4, flow cytometry (FCM) was performed to analyze pro-inflammatory (i.e., M1) (CD80 and CD86) and anti-inflammatory (i.e. M2) (CD163 and CD206) markers.

[0311] As shown in **Figure 12A** and **Figure 12B**, transduction with a pro-inflammatory fusion protein (IFNβ-IFNAR1) successfully induced a pro-inflammatory macrophage phenotype, with an upregulation in pro-inflammatory markers and a downregulation in anti-inflammatory markers. Transduction with lentivirus alone induces a pro-inflammatory phenotype, so it important to note that the IFNβ-IFNAR1 fusion protein polarized macrophages beyond the effect of lentivirus alone (represented by the mCherry control).

[0312] Although IFNβ-IFNAR1 was not detected at the macrophage surface (see Example 2), results from this M1/M2 panel indicate that surface expression may not be required for fusion protein function.

Example 4: Effect of Cytokine and CAR Co-Expression on Macrophage Viability and CAR Expression

[0313] Macrophages were derived from peripheral blood CD14+ monocytes, which were differentiated using 10 ng/mL GM-CSF for 7 days. Primary human monocyte-derived macrophages were electroporated with 50 μM mRNA (comprising chemical modifications) encoding an anti-HER2 CAR (CAR1) with or without 50 μM mRNA encoding a cytokine. Using flow cytometry, the percent of live cells was quantified after 24 hours (**Figure 13**). Additionally, the percent of CAR+ cells was evaluated using flow cytometry. As shown in **Figure 14**, over 50% of macrophages transfected with CAR, with or without co-transfection with cytokine mRNA, expressed the CAR on their surface within 24 hours.

Example 5: Effect of Cytokine and CAR Co-Expression on Cytokine Expression

[0314] 2 x 10^6 human macrophages were transfected with 50 μM CAR mRNA or with 50 μM CAR mRNA and 50 μM mRNA encoding IFN-γ, IL-10, CCL19, or CXCL12 (see **Figures 15**, **16**, **17** and **18**). Supernatants were collected 24 hours post-electroporation and cytokine levels were evaluated using an MSD instrument. As shown in **Figure 15**, macrophages transfected with CAR mRNA and IFN-γ mRNA (CAR1+IFNg group) secreted high levels of IFN-γ, while transfection with CAR mRNA and mRNA encoding IL-10, CCL19 or CXCL12 did not lead to IFN-γ secretion. Similarly, as shown in **Figure 16**, macrophages co-transfected with CAR and IL-10 mRNAs secreted high levels of IL-10, while macrophages transfected with CAR mRNA and mRNA encoding IFN-γ, CCL19 or CXCL12 did not lead to IL-10 secretion. Also, as shown in **Figure 17**, macrophages transfected with CAR mRNA and CCL19 mRNA secreted high levels of CCL19, while transfection with CAR mRNA and mRNA encoding IFN-γ, IL-10, or CXCL12 did not lead to CCL19 secretion. Finally, as shown in **Figure 18**, macrophages transfected with CAR mRNA and CXCL12 mRNA secreted higher levels of CXCL12 than

transfection with CAR mRNA and mRNA encoding IFN-γ, IL-10, or CCL19. CCL19 and CXCL12 are both chemoattractant chemokines that lead to the recruitment of T cells and other immune cells.

Example 6: Effect of Cytokine and CAR Co-Expression on Macrophage Phenotype

[0315] To evaluate the ability of transfected macrophages to self-polarize to pro-inflammatory (M1) or anti-inflammatory (M2) phenotypes, macrophage phenotype was evaluated using flow cytometry 24 hours post-electroporation. As shown in **Figure 19**, macrophages electroporated with CAR mRNA and IFN-γ mRNA (CAR1+IFNg group) demonstrated the highest level of surface expression of human M1 macrophage markers CD80 and CD86. These data demonstrate that co-transfecting a macrophage with CAR mRNA and IFN-γ mRNA allows for polarization to an M1 phenotype. As shown in **Figure 20**, macrophages electroporated with CAR mRNA and IL-10 mRNA (CAR+IL10 group) demonstrated the highest level of surface expression of human M2 macrophage markers CD163 and CD206. These data demonstrate that co-transfecting a macrophage with CAR mRNA and IL-10 mRNA allows for polarization to an M2 phenotype.

EXEMPLARY SEQUENCES

Table 2a – Amino Acid Sequences of Endogenous Proteins (Pro-Inflammatory Cytokines)

Name	Uniprot	Amino Acid Sequence	Notes
IFN-α2	P01563	CDLPQTHSLGSRRTLMLLAQMRKISLFSCLKDRHDFGFP QEEFGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDET LLDKFYTELYQQLNDLEACVIQGVGVTETPLMKEDSILA VRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNLQ ESLRSKE **(SEQ ID NO: 1)**	Signal peptide removed
IFN-β	P01574	MSYNLLGFLQRSSNFQCQKLLWQLNGRLEYCLKDRMNF DIPEEIKQLQQFQKEDAALTIYEMLQNIFAIFRQDSSSTGW NETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMS SLHLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFIN RLTGYLRN **(SEQ ID NO: 2)**	Signal peptide removed
IFN-γ	P01579	QDPYVKEAENLKKYFNAGHSDVADNGTLFLGILKNWKE ESDRKIMQSQIVSFYFKLFKNFKDDQSIQKSVETIKEDMN VKFFNSNKKKRDDFEKLTNYSVTDLNVQRKAIHELIQVM AELSPAAKTGKRKRSQMLFRG **(SEQ ID NO: 3)**	Signal peptide removed,

			propeptide removed
TNF-α	P01375	VRSSSRTPSDKPVAHVVANPQAEGQLQWLNRRANALLA NGVELRDNQLVVPSEGLYLIYSQVLFKGQGCPSTHVLLTH TISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIY LGGVFQLEKGDRLSAEINRPDYLDFAESGQVYFGIIAL **(SEQ ID NO: 4)**	Soluble form (TMD removed) - Wang et al 1985
IL-1β	P01584	APVRSLNCTLRDSQQKSLVMSGPYELKALHLQGQDMEQ QVVFSMSFVQGEESNDKIPVALGLKEKNLYLSCVLKDDK PTLQLESVDPKNYPKKKMEKRFVFNKIEINNKLEFESAQF PNWYISTSQAENMPVFLGGTKGGQDITDFTMQFVSS **(SEQ ID NO: 5)**	Propeptide removed for mature form
IL-6	P05231	VPPGEDSKDVAAPHRQPLTSSERIDKQIRYILDGISALRKE TCNKSNMCESSKEALAENNLNLPKMAEKDGCFQSGFNE ETCLVKIITGLLEFEVYLEYLQNRFESSEEQARAVQMSTK VLIQFLQKKAKNLDAITTPDPTTNASLLTKLQAQNQWLQ DMTTHLILRSFKEFLQSSLRALRQM **(SEQ ID NO: 6)**	Signal peptide removed
IL-12 subunit p35	p29459	RNLPVATPDPGMFPCLHHSQNLLRAVSNMLQKARQTLEF YPCTSEEIDHEDITKDKTSTVEACLPLELTKNESCLNSRET SFITNGSCLASRKTSFMMALCLSSIYEDLKMYQVEFKTM NAKLLMDPKRQIFLDQNMLAVIDELMQALNFNSETVPQK SSLEEPDFYKTKIKLCILLHAFRIRAVTIDRVMSYLNAS **(SEQ ID NO: 7)**	Signal peptide removed
IL-12 subunit p40	P29460	IWELKKDVYVVELDWYPDAPGEMVVLTCDTPEEDGITW TLDQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGEVLSH SLLLLHKKEDGIWSTDILKDQKEPKNKTFLRCEAKNYSG RFTCWWLTTISTDLTFSVKSSRGSSDPQGVTCGAATLSAE RVRGDNKEYEYSVECQEDSACPAAEESLPIEVMVDAVHK LKYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRQVEVSWE YPDTWSTPHSYFSLTFCVQVQGKSKREKKDRVFTDKTSA TVICRKNASISVRAQDRYYSSSWSEWASVPCS **(SEQ ID NO: 8)**	Signal peptide removed

Table 2b – Amino Acid Sequences of Endogenous Proteins (Anti-Inflammatory Cytokines)

Name	Uniprot	Amino Acid Sequence	Notes
IL-4	P05112	HKCDITLQEIIKTLNSLTEQKTLCTELTVTDIFAASKNTTE KETFCRAATVLRQFYSHHEKDTRCLGATAQQFHRHKQLI RFLKRLDRNLWGLAGLNSCPVKEANQSTLENFLERLKTI MREKYSKCSS **(SEQ ID NO: 9)**	Signal peptide removed
IL-10	P22301	SPGQGTQSENSCTHFPGNLPNMLRDLRDAFSRVKTFFQM KDQLDNLLLKESLLEDFKGYLGCQALSEMIQFYLEEVMP QAENQDPDIKAHVNSLGENLKTLRLRLRRCHRFLPCENK SKAVEQVKNAFNKLQEKGIYKAMSEFDIFINYIEAYMTM KIRN **(SEQ ID NO: 10)**	Signal peptide removed

IL-13	P35225	LTCLGGFASPGPVPPSTALRELIEELVNITQNQKAPLCNGS MVWSINLTAGMYCAALESLINVSGCSAIEKTQRMLSGFC PHKVSAGQFSSLHVRDTKIEVAQFVKDLLLHLKKLFREG RFN **(SEQ ID NO: 11)**	Signal peptide removed
IL-18	Q14116	YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCR DNAPRTIFIISMYKDSQPRGMAVTISVKCEKISTLSCENKII SFKEMNPPDNIKDTKSDIIFFQRSVPGHDNKMQFESSSYE GYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED **(SEQ ID NO: 12)**	Signal peptide removed

Table 3a – Amino Acid Sequences of Endogenous Proteins (Pro-Inflammatory Cytokine Receptors)

Name	Uniprot	Amino Acid Sequence	Notes
IFNAR 1	P17181	KNLKSPQKVEVDIIDDNFILRWNRSDESVGNVTFSFDYQK TGMDNWIKLSGCQNITSTKCNFSSLKLNVYEEIKLRIRAE KENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHISP GTKDSVMWALDGLSFTYSLVIWKNSSGVEERIENIYSRH KIYKLSPETTYCLKVKAALLTSWKIGVYSPVHCIKTTVEN ELPPPENIEVSVQNQNYVLKWDYTYANMTFQVQWLHAF LKRNPGNHLYKWKQIPDCENVKTTQCVFPQNVFQKGIYL LRVQASDGNNTSFWSEEIKFDTEIQAFLLPPVFNIRSLSDS FHIYIGAPKQSGNTPVIQDYPLIYEIIFWENTSNAERKIIEK KTDVTVPNLKPLTVYCVKARAHTMDEKLNKSSVFSDAV CEKTKPGNTSKIWLIVGICIALFALPFVIYAAKVFLRCINY VFFPSLKPSSSIDEYFSEQPLKNLLLSTSEEQIEKCFIIENIST IATVEETNQTDEDHKKYSSQTSQDSGNYSNEDESESKTSE ELQQDFV **(SEQ ID NO: 13)**	Signal peptide removed
IFNAR 2	P48551	ISYDSPDYTDESCTFKISLRNFRSILSWELKNHSIVPTHYTL LYTIMSKPEDLKVVKNCANTTRSFCDLTDEWRSTHEAYV TVLEGFSGNTTLFSCSHNFWLAIDMSFEPPEFEIVGFTNHI NVMVKFPSIVEEELQFDLSLVIEEQSEGIVKKHKPEIKGN MSGNFTYIIDKLIPNTNYCVSVYLEHSDEQAVIKSPLKCTL LPPGQESESAESAKIGGIITVFLIALVLTSTIVTLKWIGYICL RNSLPKVLNFHNFLAWPFPNLPPLEAMDMVEVIYINRKK KVWDYNYDDESDSDTEAAPRTSGGGYTMHGLTVRPLGQ ASATSTESQLIDPESEEEPDLPEVDVELPTMPKDSPQQLEL LSGPCERRKSPLQDPFPEEDYSSTEGSGGRITFNVDLNSVF LRVLDDEDSDDLEAPLMLSSHLEEMVDPEDPDNVQSNHL LASGEGTQPTFPSPSSEGLWSEDAPSDQSDTSESDVDLGD GYIMR **(SEQ ID NO: 14)**	Signal peptide removed
IFNGR 1	P15260	EMGTADLGPSSVPTPTNVTIESYNMNPIVYWEYQIMPQVP VFTVEVKNYGVKNSEWIDACINISHHYCNISDHVGDPSNS LWVRVKARVGQKESAYAKSEEFAVCRDGKIGPPKLDIRKE	Signal peptide removed

		EKQIMIDIFHPSVFVNGDEQEVDYDPETTCYIRVYNVYVR MNGSEIQYKILTQKEDDCDEIQCQLAIPVSSLNSQYCVSAE GVLHVWGVTTEKSKEVCITIFNSSIKGSLWIPVVAALLLFL VLSLVFICFYIKKINPLKEKSIILPKSLISVVRSATLETKPESK YVSLITSYQPFSLEKEVVCEEPLSPATVPGMHTEDNPGKV EHTEELSSITEVVTTEENIPDVVPGSHLTPIERESSSPLSSNQ SEPGSIALNSYHSRNCSESDHSRNGFDTDSSCLESHSSLSD SEFPPNNKGEIKTEGQELITVIKAPTSFGYDKPHVLVDLLV DDSGKESLIGYRPTEDSKEFS **(SEQ ID NO: 15)**	
IFNGR 2	P38484	APPDPLSQLPAPQHPKIRLYNAEQVLSWEPVALSNSTRPV VYQVQFKYTDSKWFTADIMSIGVNCTQITATECDFTAASP SAGFPMDFNVTLRLRAELGALHSAWVTMPWFQHYRNVT VGPPENIEVTPGEGSLIIRFSSPFDIADTSTAFFCYYVHYWE KGGIQQVKGPFRSNSISLDNLKPSRVYCLQVQAQLLWNK SNIFRVGHLSNISCYETMADASTELQQVILISVGTFSLLSVL AGACFFLVLKYRGLIKYWFHTPPSIPLQIEEYLKDPTQPILE ALDKDSSPKDDVWDSVSIISFPEKEQEDVLQTL **(SEQ ID NO: 16)**	Signal peptide removed
TNFR1	P19438	LVPHLGDREKRDSVCPQGKYIHPQNNSICCTKCHKGTYL YNDCPGPGQDTDCRECESGSFTASENHLRHCLSCSKCRK EMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFN CSLCLNGTVHLSCQEKQNTVCTCHAGFFLRENECVSCSN CKKSLECTKLCLPQIENVKGTEDSGTTVLLPLVIFFGLCLL SLLFIGLMYRYQRWKSKLYSIVCGKSTPEKEGELEGTTTK PLAPNPSFSPTPGFTPTLGFSPVPSSTFTSSSTYTPGDCPNF AAPRREVAPPYQGADPILATALASDPIPNPLQKWEDSAHK PQSLDTDDPATLYAVVENVPPLRWKEFVRRLGLSDHEIDR LELQNGRCLREAQYSMLATWRRRTPRREATLELLGRVLR DMDLLGCLEDIEEALCGPAALPPAPSLLR **(SEQ ID NO: 17)**	Signal peptide removed. Membrane bound form
TNFR2	P20333	LPAQVAFTPYAPEPGSTCRLREYYDQTAQMCCSKCSPGQ HAKVFCTKTSDTVCDSCEDSTYTQLWNWVPECLSCGSR CSSDQVETQACTREQNRICTCRPGWYCALSKQEGCRLCA PLRKCRPGFGVARPGTETSDVVCKPCAPGTFSNTTSSTDI CRPHQICNVVAIPGNASMDAVCTSTSPTRSMAPGAVHLPQ PVSTRSQHTQPTPEPSTAPSTSFLLPMGPSPPAEGSTGDFA LPVGLIVGVTALGLLIIGVVNCVIMTQVKKKPLCLQREAK VPHLPADKARGTQGPEQQHLLITAPSSSSSSLESSASALDR RAPTRNQPQAPGVEASGAGEARASTGSSDSSPGGHGTQV NVTCIVNVCSSSDHSSQCSSQASSTMGDTDSSPSESPKDE QVPFSKEECAFRSQLETPETLLGSTEEKPLPLGVPDAGMK PS **(SEQ ID NO: 18)**	Signal peptide removed. Membrane bound form
IL-1R1	P14778	LEADKCKEREEKIILVSSANEIDVRPCPLNPNEHKGTITW YKDDSKTPVSTEQASRIHQHKEKLWFVPAKVEDSGHYYC VVRNSSYCLRIKISAKFVENEPNLCYNAQAIFKQKLPVAG DGGLVCPYMEFFKNENNELPKLQWYKDCKPLLLDNIHFS	Signal peptide removed.

		GVKDRLIVMNVAEKHRGNYTCHASYTYLGKQYPITRVIE FITLEENKPTRPVIVSPANETMEVDLGSQIQLICNVTGQLS DIAYWKWNGSVIDEDDPVLGEDYYSVENPANKRRSTLIT VLNISEIESRFYKHPFTCFAKNTHGIDAAYIQLIYPVTNFQ KHMIGICVTLTVIIVCSVFIYKIFKIDIVLWYRDSCYDFLPI KASDGKTYDAYILYPKTVGEGSTSDCDIFVFKVLPEVLEK QCGYKLFIYGRDDYVGEDIVEVINENVKKSRRLIIILVRET SGFSWLGGSSEEQIAMYNALVQDGIKVVLLELEKIQDYE KMPESIKFIKQKHGAIRWSGDFTQGPQSAKTRFWKNVRY HMPVQRRSPSSKHQLLSPATKEKLQREAHVPLG **(SEQ ID NO: 19)**	Membrane bound form
IL-1R3	Q9NPH3	SERCDDWGLDTMRQIQVFEDEPARIKCPLFEHFLKFNYST AHSAGLTLIWYWTRQDRDLEEPINFRLPENRISKEKDVL WFRPTLLNDTGNYTCMLRNTTYCSKVAFPLEVVQKDSCF NSPMKLPVHKLYIEYGIQRITCPNVDGYFPSSVKPTITWY MGCYKIQNFNNVIPEGMNLSFLIALISNNGNYTCVVTYPE NGRTFHLTRTLTVKVVGSPKNAVPPVIHSPNDHVVYEKEP GEELLIPCTVYFSFLMDSRNEVWWTIDGKKPDDITIDVTI NESISHSRTEDETRTQILSIKKVTSEDLKRSYVCHARSAKG EVAKAAKVKQKVPAPRYTVELACGFGATVLLVVILIVVY HVYWLEMVLFYRAHFGTDETILDGKEYDIYVSYARNAE EEEFVLLTLRGVLENEFGYKLCIFDRDSLPGGIVTDETLSF IQKSRRLLVVLSPNYVLQGTQALLELKAGLENMASRGNI NVILVQYKAVKETKVKELKRAKTVLTVIKWKGEKSKYP QGRFWKQLQVAMPVKKSPRRSSSDEQGLSYSSLKNV **(SEQ ID NO: 20)**	Signal peptide removed
IL-6Rα	P08887	LAPRRCPAQEVARGVLTSLPGDSVTLTCPGVEPEDNATVH WVLRKPAAGSHPSRWAGMGRRLLLRSVQLHDSGNYSCY RAGRPAGTVHLLVDVPPEEPQLSCFRKSPLSNVVCEWGP RSTPSLTTKAVLLVRKFQNSPAEDFQEPCQYSQESQKFSC QLAVPEGDSSFYIVSMCVASSVGSKFSKTQTFQGCGILQP DPPANITVTAVARNPRWLSVTWQDPHSWNSSFYRLRFEL RYRAERSKTFTTWMVKDLQHHCVIHDAWSGLRHVVQL RAQEEFGQGEWSEWSPEAMGTPWTESRSPPAENEVSTP MQALTTNKDDDNILFRDSANATSLPVQDSSSVPLPTFLVA GGSLAFGTLLCIAIVLRFKKTWKLRALKEGKTSMHPPYS LGQLVPERPRPTPVLVPLISPPVSPSSLGSDNTSSHNRPDA RDPRSPYDISNTDYFFPR **(SEQ ID NO: 21)**	Signal peptide removed. Membrane bound form
gp130	P40189	ELLDPCGYISPESPVVQLHSNFTAVCVLKEKCMDYFHVN ANYIVWKTNHFTIPKEQYTIINRTASSVTFTDIASLNIQLTC NILTFGQLEQNVYGITIISGLPPEKPKNLSCIVNEGKKMRC EWDGGRETHLETNFTLKSEWATHKFADCKAKRDTPTSCT VDYSTVYFVNIEVWVEAENALGKVTSDHINFDPVYKVK PNPPHNLSVINSEELSSILKLTWTNPSIKSVIILKYNIQYRT KDASTWSQIPPEDTASTRSSFTVQDLKPFTEYVFRIRCMK EDGKGYWSDWSEEASGITYEDRPSKAPSFWYKIDPSHTQ	Signal peptide removed

		GYRTVQLVWKTLPPFEANGKILDYEVTLTRWKSHLQNYT VNATKLTVNLTNDRYLATLTVRNLVGKSDAAVLTIPACDF QATHPVMDLKAFPKDNMLWVEWTTPRESVKKYILEWC VLSDKAPCITDWQQEDGTVHRTYLRGNLAESKCYLITVT PVYADGPGSPESIKAYLKQAPPSKGPTVRTKKVGKNEAVL EWDQLPVDVQNGFIRNYTIFYRTIIGNETAVNVDSSHTEY TLSSLTSDTLYMVRMAAYTDEGGKDGPEFTFTTPKFAQG EIEAIVVPVCLAFLLTTLLGVLFCFNKRDLIKKHIWPNVPD PSKSHIAQWSPHTPPRHNFNSKDQMYSDGNFTDVSVVEI EANDKKPFPEDLKSLDLFKKEKINTEGHSSGIGGSSCMSS SRPSISSSDENESSQNTSSTVQYSTVVHSGYRHQVPSVQV FSRSESTQPLLDSEERPEDLQLVDHVDGGDGILPRQQYFK QNCSQHESSPDISHFERSKQVSSVNEEDFVRLKQQISDHIS QSCGSGQMKMFQEVSAADAFGPGTEGQVERFETVGMEA ATDEGMPKSYLPQTVRQGGYMPQ **(SEQ ID NO: 22)**	
IL-12-Rβ1	P42701	CRTSECCFQDPPYPDADSGSASGPRDLRCYRISSDRYECS WQYEGPTAGVSHFLRCCLSSGRCCYFAAGSATRLQFSDQ AGVSVLYTVTLWVESWARNQTEKSPEVTLQLYNSVKYEP PLGDIKVSKLAGQLRMEWETPDNQVGAEVQFRHRTPSSP WKLGDCGPQDDDTESCLCPLEMNVAQEFQLRRRQLGSQ GSSWSKWSSPVCVPPENPPQPQVRFSVEQLGQDGRRRLT LKEQPTQLELPEGCQGLAPGTEVTYRLQLHMLSCPCKAK ATRTLHLGKMPYLSGAAYNVAVISSNQFGPGLNQTWHIPA DTHTEPVALNISVGTNGTTMYWPARAQSMTYCIEWQPV GQDGGLATCSLTAPQDPDPAGMATYSWSRESGAMGQEK CYYITIFASAHPEKLTLWSTVLSTYHFGGNASAAGTPHHV SVKNHSLDSVSVDWAPSLLSTCPGVLKEYVVRCRDEDSK QVSEHPVQPTETQVTLSGLRAGVAYTVQVRADTAWLRG VWSQPQRFSIEVQVSDWLIFFASLGSFLSILLVGVLGYLGL NRAARHLCPPLPTPCASSAIEFPGGKETWQWINPVDFQEE ASLQEALVVEMSWDKGERTEPLEKTELPEGAPELALDTE LSLEDGDRCKAKM **(SEQ ID NO: 23)**	Signal peptide removed
IL-12-Rβ2	Q99665	KIDACKRGDVTVKPSHVILLGSTVNITCSLKPRQGCFHYS RRNKLILYKFDRRINFHHGHSLNSQVTGLPLGTTLFVCKL ACINSDEIQICGAEIFVGVAPEQPQNLSCIQKGEQGTVACT WERGRDTHLYTEYTLQLSGPKNLTWQKQCKDIYCDYLD FGINLTPESPESNFTAKVTAVNSLGSSSSLPSTFTFLDIVRPL PPWDIRIKFQKASVSRCTLYWRDEGLVLLNRLRYRPSNSR LWNMVNVTKAKGRHDLLDLKPFTEYEFQISSKLHLYKGS WSDWSESLRAQTPEEEPTGMLDVWYMKRHIDYSRQQIS LFWKNLSVSEARGKILHYQVTLQELTGGKAMTQNITGHT SWTTVIPRTGNWAVAVSAANSKGSSLPTRINIMNLCEAGL LAPRQVSANSEGMDNILVTWQPPRKDPSAVQEYVVEWR ELHPGGDTQVPLNWLRSRPYNVSALISENIKSYICYEIRV YALSGDQGGCSSILGNSKHKAPLSGPHINAITEEKGSILIS WNSIPVQEQMGCLLHYRIYWKERDSNSQPQLCEIPYRVS	Signal peptide removed

		QNSHPINSLQPRVTYVLWMTALTAAGESSHGNEREFCLQ GKANWMAFVAPSICIAIIMVGIFSTHYFQQKVFVLLAALR PQWCSREIPDPANSTCAKKYPIAEEKTQLPLDRLLIDWPT PEDPEPLVISEVLHQVTPVFRHPPCSNWPQREKGIQGHQA SEKDMMHSASSPPPPRALQAESRQLVDLYKVLESRGSDP KPENPACPWTVLPAGDLPTHDGYLPSNIDDLPSHEAPLAD SLEELEPQHISLSVFPSSSLHPLTFSCGDKLTLDQLKMRCD SLML **(SEQ ID NO: 24)**	

Table 3b – Amino Acid Sequences of Endogenous Proteins (Anti-Inflammatory Cytokine Receptors)

Name	Uniprot	Amino Acid Sequence	Notes
IL-4Rα	P24394	MKVLQEPTCVSDYMSISTCEWKMNGPTNCSTELRLLYQL VFLLSEAHTCIPENNGGAGCVCHLLMDDVVSADNYTLD LWAGQQLLWKGSFKPSEHVKPRAPGNLTVHTNVSDTLLL TWSNPYPPDNYLYNHLTYAVNIWSENDPADFRIYNVTYL EPSLRIAASTLKSGISYRARVRAWAQCYNTTWSEWSPSTK WHNSYREPFEQHLLLGVSVSCIVILAVCLLCYVSITKIKKE WWDQIPNPARSRLVAIIIQDAQGSQWEKRSRGQEPAKCPH WKNCLTKLLPCFLEHNMKRDEDPHKAAKEMPFQGSGKS AWCPVEISKTVLWPESISVVRCVELFEAPVECEEEEEVEE EKGSFCASPESSRDDFQEGREGIVARLTESLFLDLLGEENG GFCQQDMGESCLLPPSGSTSAHMPWDEFPSAGPKEAPPW GKEQPLHLEPSPPASPTQSPDNLTCTETPLVIAGNPAYRSFS NSLSQSPCPRELGPDPLLARHLEEVEPEMPCVPQLSEPTT VPQPEPETWEQILRRNVLQHGAAAAPVSAPTSGYQEFVH AVEQGGTQASAVVGLGPPGEAGYKAFSSLLASSAVSPEK CGFGASSGEEGYKPFQDLIPGCPGDPAPVPVPLFTFGLDR EPPRSPQSSHLPSSSPEHLGLEPGEKVEDMPKPPLPQEQAT DPLVDSLGSGIVYSALTCHLCGHLKQCHGQEDGGQTPVM ASPCCGCCCGDRSSPPTTPLRAPDPSPGGVPLEASLCPASL APSGISEKSKSSSSFHPAPGNAQSSSQTPKIVNFVSVGPTY MRVS **(SEQ ID NO: 25)**	Signal peptide removed. Membrane bound form
IL-2Rγc	P31785	LNTTILTPNGNEDTTADFFLTTMPTDSLSVSTLPLPEVQCF VFNVEYMNCTWNSSSEPQPTNLTLHYWYKNSDNDKVQ KCSHYLFSEEITSGCQLQKKEIHLYQTFVVQLQDPREPRR QATQMLKLQNLVIPWAPENLTLHKLSESQLELNWNNRFL NHCLEHLVQYRTDWDHSWTEQSVDYRHKFSLPSVDGQK RYTFRVRSRFNPLCGSAQHWSEWSHPIHWGSNTSKENPF LFALEAVVISVGSMGLIISLLCVYFWLERTMPRIPTLKNLE DLVTEYHGNFSAWSGVSKGLAESLQPDYSERLCLVSEIPP KGGALGEGPGASPCNQHSPYWAPPCYTLKPET **(SEQ ID NO: 26)**	Signal peptide removed

IL-13Rα1	P78552	GGGGAAPTETQPPVTNLSVSVENLCTVIWTWNPPEGASS NCSLWYFSHFGDKQDKKIAPETRRSIEVPLNERICLQVGS QCSTNESEKPSILVEKCISPPEGDPESAVTELQCIWHNLSY MKCSWLPGRNTSPDTNYTLYYWHRSLEKIHQCENIFREG QYFGCSFDLTKVKDSSFEQHSVQIMVKDNAGKIKPSFNIV PLTSRVKPDPPHIKNLSFHNDDLYVQWENPQNFISRCLFY EVEVNNSQTETHNVFYVQEAKCENPEFERNVENTSCFM VPGVLPDTLNTVRIRVKTNKLCYEDDKLWSNWSQEMSIG KKRNSTLYITMLLIVPVIVAGAIIVLLLYLKRLKIIIFPPIPDP GKIFKEMFGDQNDDTLHWKKYDIYEKQTKEETDSVVLIE NLKKASQ **(SEQ ID NO: 27)**	Signal peptide removed
IL-10R1	Q13651	HGTELPSPPSVWFEAEFFHHILHWTPIPNQSESTCYEVALL RYGIESWNSISNCSQTLSYDLTAVTLDLYHSNGYRARVRA VDGSRHSNWTVTNTRFSVDEVTLTVGSVNLEIHNGFILG KIQLPRPKMAPANDTYESIFSHFREYEIAIRKVPGNFTFTH KKVKHENFSLLTSGEVGEFCVQVKPSVASRSNKGMWSK EECISLTRQYFTVTNVIIFFAFVLLLSGALAYCLALQLYVR RRKKLPSVLLFKKPSPFIFISQRPSPETQDTIHPLDEEAFLK VSPELKNLDLHGSTDSGFGSTKPSLQTEEPQFLLPDPHPQ ADRTLGNREPPVLGDSCSSGSSNSTDSGICLQEPSLSPSTG PTWEQQVGSNSRGQDDSGIDLVQNSEGRAGDTQGGSAL GHHSPPEPEVPGEEDPAAVAFQGYLRQTRCAEEKATKTG CLEEESPLTDGLGPKFGRCLVDEAGLHPPALAKGYLKQD PLEMTLASSGAPTGQWNQPTEEWSLLALSSCSDLGISDW SFAHDLAPLGCVAAPGGLLGSFNSDLVTLPLISSLQSSE **(SEQ ID NO: 28)**	Signal peptide removed
IL-10R2	Q08334	MVPPPENVRMNSVNFKNILQWESPAFAKGNLTFTAQYLS YRIFQDKCMNTTLTECDFSSLSKYGDHTLRVRAEFADEHS DWVNITFCPVDDTIIGPPGMQVEVLADSLHMRFLAPKIEN EYETWTMKNVYNSWTYNVQYWKNGTDEKFQITPQYDF EVLRNLEPWTTYCVQVRGFLPDRNKAGEWSEPVCEQTT HDETVPSWMVAVILMASVFMVCLALLGCFALLWCVYKK TKYAFSPRNSLPQHLKEFLGHPHHNTLLFFSFPLSDENDV FDKLSVIAEDSESGKQNPGDSCSLGTPPGQGPQS **(SEQ ID NO: 29)**	Signal peptide removed
IL-18Rα	Q13478	AESCTSRPHITVVEGEPFYLKHCSCSLAHEIETTTKSWYK SSGSQEHVELNPRSSSRIALHDCVLEFWPVELNDTGSYFF QMKNYTQKWKLNVIRRNKHSCFTERQVTSKIVEVKKFF QITCENSYYQTLVNSTSLYKNCKKLLLENNKNPTIKKNAE FEDQGYYSCVHFLHHNGKLFNITKTFNITIVEDRSNIVPVL LGPKLNHVAVELGKNVRLNCSALLNEEDVIYWMFGEEN GSDPNIHEEKEMRIMTPEGKWHASKVLRIENIGESNLNVL YNCTVASTGGTDTKSFILVRKADMADIPGHVFTRGMIIAV LILVAVVCLVTVCVIYRVDLVLFYRHLTRRDETLTDGKTY DAFVSYLKECRPENGEEHTFAVEILPRVLEKHFGYKLCIFE RDVVPGGAVVDEIHSLIEKSRRLIIVLSKSYMSNEVRYELE	Signal peptide removed

		SGLHEALVERKIKIILIEFTPVTDFTFLPQSLKLLKSHRVLK WKADKSLSYNSRFWKNLLYLMPAKTVKPGRDEPEVLPV LSES **(SEQ ID NO: 30)**	
IL-18Rβ	O95256	FNISGCSTKKLLWTYSTRSEEEFVLFCDLPEPQKSHFCHR NRLSPKQVPEHLPFMGSNDLSDVQWYQQPSNGDPLEDIR KSYPHIIQDKCTLHFLTPGVNNSGSYICRPKMIKSPYDVAC CVKMILEVKPQTNASCEYSASHKQDLLLGSTGSISCPSLS CQSDAQSPAVTWYKNGKLLSVERSNRIVVDEVYDYHQG TYVCDYTQSDTVSSWTVRAVVQVRTIVGDTKLKPDILDP VEDTLEVELGKPLTISCKARFGFERVFNPVIKWYIKDSDL EWEVSVPEAKSIKSTLKDEIIERNIILEKVTQRDLRRKFVC FVQNSIGNTTQSVQLKEKRGVVLLYILLGTIGTLVAVLAA SALLYRHWIEIVLLYRTYQSKDQTLGDKKDFDAFVSYAK WSSFPSEATSSLSEEHLALSLFPDVLENKYGYSLCLLERD VAPGGVYAEDIVSIIKRSRRGIFILSPNYVNGPSIFELQAAV NLALDDQTLKLILIKFCYFQEPESLPHLVKKALRVLPTVT WRGLKSVPPNSRFWAKMRYHMPVKNSQGFTWNQLRITS RIFQWKGLSRTETTGRSSQPKEW **(SEQ ID NO: 31)**	Signal peptide removed

Table 4a – Codon Optimized DNA Sequences of Endogenous Proteins (Pro-Inflammatory Cytokines)

Name	Uniprot	Codon Optimized Sequence	Notes
IFN-α2	P01563	Tgcgaccttccacagacccattccctcggctctcgaagaactctgatgttgctggcccaga tgcggaagatttctcttttctcatgtctgaaagacaggcacgactttggttttccccaggagg agttcggaaaccagttccagaaagcggaaaccattcctgtgctgcacgaaatgatccaac aaattttcaacctgttttcaactaaagatagctccgctgcatgggacgagacactcctcgata agttttatacagagctttaccagcagttaaatgatctggaagcttgtgtcatccaaggggtcg gcgtaaccgagacgcccctgatgaaggaggatagcatactggcagtgcggaagtacttc cagaggatcaccctctatctaaaggaaaaaaagtacagtccgtgcgcctgggaagtggtt agagccgaaatcatgcgtagcttttccttatctacaaatttgcaggagtcgttgcgcagtaaa gag **(SEQ ID NO: 32)**	Signal peptide removed
IFN-β	P01574	Atgagttataatttactcggatttctacagcggtctagcaacttccaatgtcagaagctgctg tggcaactcaacggcaggctggagtactgcctcaaagatagaatgaactttgatattcccg aagaaatcaagcagcttcagcagttccagaaagaggacgccgcactaaccatatacgag atgctgcagaacattttcgctatattcagacaggactcgtcctctactggatggaatgagac catcgtcgagaatttgctggccaatgtgtatcatcaaattaccacctcaagacggtgcttga agaaaagttggaaaaagaggacttcactagaggcaaactgatgtcatcccttcacctcaaa cgctactatgggaggatcctgcactacttaaaggcgaaggagtatagccattgcgcttgga caatcgttcgcgtagagattctgcggaatttttactttatcaatcgtttgacaggttacctgcga aac **(SEQ ID NO: 33)**	Signal peptide removed
IFN-γ	P01579	Caggatccctacgtgaaggaagcagaaaatctcaaaaagtatttcaatgcgggccatagc gatgtggccgataacggcaccctgtttctggggattcttaagaattggaaagaggagtctg ataggaagattatgcagtcccagatcgtgagcttctatttcaagctgttcaaaaacttcaaag acgaccagtcgatccaaaaatctgttgagacaataaaagaggacatgaatgtgaagttttt	Signal peptide removed,

		aattcaaacaaaaagaagcgcgacgattttgagaaattaacgaactactccgtcaccgactgaacgtacaacgaaaggctattcacgaactaatccaggtcatggctgaactgagtcctgccgccaagactggtaagcgtaaacggagtcagatgctctttagagga **(SEQ ID NO: 34)**	propeptide removed
TNF-α	P01375	Gtgcgatcttcaagccggacaccctcagacaagccagtggcacacgtggtagcgaaccacaagctgaggggcagctccagtggctcaatcggcgtgccaacgccctgttagccaatggggtcgagcttagggacaaccaacttgtggtaccctcggaaggattatacttgatttacagtcaggtgctgttcaaaggacagggctgcccttccacacatgttctgctcactcacacgatctcccgcattgcagtgtcttatcagaccaaggtcaacttgctaagcgctatcaaaagtccatgtcagagagagaccccggagggtgctgaggctaagccttggtacgaacctatttatctgggcggagtctttcaactggaaaaaggtgatagactgagcgcagagatcaataggcccgattactggacttcgccgaatccggccaggtttattttgggataatcgccctc **(SEQ ID NO: 35)**	Soluble form (TMD removed) - Wang et al 1985
IL-1β	P01584	Gcgcctgtcagaagcctcaactgcacgctgagggactcacagcaaaagagcctggtcatgagtggcccctacgagctgaaagcactccaccttcaggggcaggacatggaacaacaggtggttttctccatgtctttcgtacagggagaggagtctaacgataagatccccgtggctttggcttaaaagagaaaaacctgtatctgagctgtgtgctaaaggacgataagcccacacttcagctcgagtccgttgatccaaaaaattatccaaagaagaaaatggaaaagcggtttgtgtttaacaagattgagattaataacaaattggaattcgaatcagcccagttccctaattggtacatcagtacctctcaagccgaaaatatgccggtgtttctgggagggaccaagggtggccaggatataacagacttcactatgcagtttgtctcgtcc **(SEQ ID NO: 36)**	Propeptide removed for mature form
IL-6	P05231	Gtgccgcccggggaagatagcaaggatgtggctgctcctcacaggcagccactgacaagcagcgagagaatcgacaagcaaataaggtatattcttgatggaatcagcgcgctgcgaaaggagacatgtaacaagtcgaatatgtgcgagtcttccaaagaagcacttgctgaaaataatctgaacctcccaaaaatggccgagaaagacggctgctttcagtccggttttaacgaggagacttgtttagtaaagattataacgggcttgttggaattcgaagtctacctagaatacctccaaaatagattcgagagtagtgaggaacaggcccgcgctgttcagatgtcaacaaaagtgttgatccaattcctgcagaaaaaagccaagaacttagatgcaatcaccacacctgaccccactaccaatgcctctctgctcaccaagctgcaagcccagaaccagtggctgcaggacatgactaccccatctaattctgcggtcttttaaggagttcctccagtcatccctgcgtgcacttcggcagatg **(SEQ ID NO: 37)**	Signal peptide removed
IL-12 subunit p35	p29459	Cgaaatctgccagtggctacccccgacccgggcatgtttccctgcctccatcatagccagaatctgctcagagcggtcagcaacatgctacagaaggcccgccagaccttagagttttaccccttgcacctctgaggaaatcgatcacgaagacatcaccaaagataagactagcaccgttgaagcctgtctcccattggaacttacaaaaaatgaatcttgtctgaattccagagagacatctttatcactaatggaagttgcctcgccagtcggaaaacttccttcatgatggccctgtgtctgagttcaatctacgaggatcttaagatgtatcaagtggaattcaaaacgatgaacgcaaaactgttgatggatcctaagaggcagatatttttggatcagaacatgttagctgtgatcgacgagctgatgcaagcactcaacttcaactcagagacagtcccccagaagtcctccctggaggagcctgacttctacaagacgaaaattaagctatgcattctgcttcacgcattcaggatacgggccgtaacaattgaccgtgtgatgagctatctgaacgcttcg **(SEQ ID NO: 38)**	Signal peptide removed
IL-12 subunit p40	P29460	Atctgggagctcaaaaaggatgtttatgtggtcgaacttgactggtacccggacgcaccaggggagatggtggtgttgacctgcgacacccccgaagaggacgggattacatggactttggaccagtccagtgaagtcctgggctcgggaaagaccctgactatccaggtgaaggagttcggagatgctggacaatatacatgccacaagggcggggaagttttgagccattccctcctgctgctgcataaaaaagaggatggtatttggagcactgatattctgaaagaccagaaggaa	Signal peptide removed

		cccaagaacaaaactttctgcggtgtgaggccaagaattacagtggaagattcacctgttg gtggttaaccacaatctctaccgatcttacctttccgtcaaatcaagtcgcggcagcagcg atccacagggcgtgacgtgcggcgctgccacactaagcgcggagagagtgcggggtg acaacaaggaatacgagtactccgttgagtgtcaagaagactctgcatgccctgccgcag aggaatcattaccgatcgaagtaatggtggatgctgttcacaaactgaagtatgaaaactac acttcttcatttttcataagggacattatcaagcctgatcctccaaagaacctccaacttaaac cactcaagaatagccgtcaggtagaggtgtcctgggagtaccccgatacctggtcaacgc ccactcatatttctccctgacgttctgtgtgcaggtgcaggggaaatccaagagggagaa gaaagacagggtctttacagataagacatctgccactgtcatctgcagaaaaaatgcctcta tatccgtgcgagcccaggaccgctactattctagtagctggagcgagtgggctagtgtacc ttgttcg **(SEQ ID NO: 39)**	

Table 4b – Codon Optimized DNA Sequences of Endogenous Proteins (Anti-Inflammatory Cytokines)

Name	Uniprot	Codon Optimized Sequence	Notes
IL-4	P05112	Cacaagtgtgatattacactccaagaaataatcaagaccctgaacagcctaaccgagcag aaaactctctgtacggaattgaccgttaccgatatcttcgcagctagtaagaatacaactga aaaagagacgttttgtcgtgccgccacagtcctgaggcagttttattcacatcacgagaaag acacccggtgccttggggcaactgcccaacagtttcatcgccacaaacagctgatcagatt cttgaagcggctggacaggaatctctggggattagctggcctgaattcttgccccgtgaag gaggcgaaccagagcactctggagaacttcctggaacgacttaagacaattatgagaga gaagtactccaaatgctcctct **(SEQ ID NO: 40)**	Signal peptide removed
IL-10	P22301	Tcacccggacagggtactcaatctgaaaatagttgcacccattttccaggaaatctgccta acatgctgagggacttacgcgatgcattttcgcgtgtaaaaacattctttcagatgaaagatc aactggataacctgttgctaaaagagagcctgcttgaggatttcaagggctatctgggctgt caggcgctctccgaaatgattcaattctacctcgaagaggtgatgccccaggccgagaac caggacccagacatcaaggcccacgtgaattctctgggggagaatctgaaaacgctcag attgcgactcagacggtgccacaggtttttaccttgtgaaaacaagagcaaagccgttgag caggtcaagaacgcttttaataagcttcaggaaaaagggatctataaggcaatgtccgagtt cgacatattcattaattacattgaggcttacatgaccatgaagatccggaac **(SEQ ID NO: 41)**	Signal peptide removed
IL-13	P35225	Ttaacatgtctgggcgggttcgcctcacctggaccagttccccccttcaaccgctctcagag aactgattgaggagctcgtcaatatcacccagaaccaaaaagccccactctgcaatggaa gtatggtgtggtctattaacttgactgccggcatgtactgtgccgcactggagtctttgatca acgtgtccgggtgcagtgcaatcgaaaagacgcagcggatgctgagcggcttttgcccc cacaaggtgagcgctggtcagttttccagccttcacgtgcgagatacaaagatagaagtag cgcagttcgtcaaggacctgctgctgcatcttaaaaaactatttcgcgagggtaggttcaat **(SEQ ID NO: 42)**	Signal peptide removed
IL-18	Q14116	Tattttggcaaactcgaaagtaagctgagcgtgattcggaatcttaacgatcaggtgttattc atcgatcaaggcaacagaccactctttgaagatatgacagattcagactgtagggataatg cccctaggaccatctttattataagcatgtataaggactctcagccccgcggtatggcagta acgattagcgttaagtgcgagaagatttctacactttcatgcgaaaacaaaatcatctccttc aaagagatgaaccctcccgataatatcaaagataccaagtcggacataattttctttcagag atccgtcccaggacacgacaataagatgcaattcgaatccagcagttacgagggatacttt	Signal peptide removed

		ctggcttgtgagaaggaacgtgacttgttcaaactgatcctgaagaaagaggacgagcta ggggaccgatctatcatgttcactgtgcagaacgaggac **(SEQ ID NO: 43)**	

Table 5a – Codon Optimized DNA Sequences of Endogenous Proteins (Pro-Inflammatory Cytokine Receptors)

Name	Uniprot	Codon Optimized Sequence	Notes
IFNAR1	P17181	aagaacctgaaatccccacagaaagtcgaggtggacatcatcgatgacaatttcatcttaag atggaaccgtagcgatgagtccgtcggaaatgtcacattttcttttgattatcagaagaccgg gatggacaactggattaagctgtccggttgccagaacataaccagtaccaagtgtaacttca gcagcctcaaactcaatgtatatgaggaaatcaagctgaggatccgggccgagaaggaaa acacaagctcctggtatgaagttgattcatttactccatttcgaaaagcgcaaataggacccc cggaagttcacctcgaggctgaagataaagcaattgtaatacacatatcgcctggcaccaa ggactctgtgatgtgggctttagatgggctgtcattcacgtacagcctggtgatctggaagaa cagttctggggtggaggagagaatagaaaacatttatagtcgccacaaaatctacaaattgt cacccgaaacaacctattgcctgaaggtcaaggcggcactattgacgtcctggaagatcgg cgtgtactcaccagtgcattgtataaagacaacagtggaaaacgagcttcccccgccggag aatattgaggtttccgtgcagaatcagaattatgtgttgaagtgggactacacatatgccaata tgaccttccaggttcaatggcttcatgcatttctgaaaagaaaccctggtaaccacctttacaa atggaagcagattcctgactgcgagaatgtcaagaccacacagtgcgtgtttcctcaaaacg ttttccagaaaggcatctatctgctacgggtccaggcttccgatggcaataatacctcattttg gagcgaggaaattaaattcgacactgaaatccaagccttcctactccctcccgtatttaacat caggagtctgtctgatagcttccatatttacatcggtgctcccaagcagtctggaaacactcc cgtgatccaggattacccccctcatctacgagatcattttctgggaaaacacctctaacgccga acggaagattatagagaagaaaactgacgtcactgtgcctaacctgaaaccattaactgtct attgcgtcaaagctagggcccacaccatggatgaaaaactgaacaagtctagcgtgttcag cgacgcagtttgtgagaaaacgaagccaggaaatacttctaagatttggcttatcgtgggca tttgtatcgctctgttcgcactgccctttgtaatctacgccgccaaggtttttctccgctgtattaa ttatgtgtttttcccatccctgaagccatcatcgtcgattgacgagtacttctctgagcaacctct taaaaacctgttgttgtccaccagtgaagagcagattgagaaatgcttcattatcgaaaatattt caacaatcgccacagtggaggagacgaatcagaccgacgaggaccataagaagtacag cagtcagacatctcaggattccgggaattacagcaatgaagatgaaagtgaatccaaaact agcgaggagctccaacaggactttgtg **(SEQ ID NO: 44)**	Signal peptide removed
IFNAR2	P48551	atcagctacgactcccccgattacaccgacgagtcctgtacctttaaaatctccctacgtaact tcaggtccattctctcctgggaactgaaaaaccatagcattgtgccgactcactatacactgct gtataccataatgtctaaacccgaggatctgaaggtggtgaagaactgtgcgaacaccaca agatccttctgcgacctgacagatgagtggcgatctacccatgaagcctacgtcacggtcct cgagggcttcagcggtaataccacacttttcagctgctcacataacttttggttggccatcgat atgtcctttgaaccacccgagttcgagattgtcggtttcacaaaccacatcaatgtcatggtga aatttccttctattgtcgaggaagaactccagtttgatttgagcctcgtgattgaggagcagtc agagggaatcgtgaagaagcataagcccgaaataaagggaaatatgagtgggaacttcac ttacataatcgacaagctcatccccaacacgaattattgtgtgtcagtgtatctcgagcactcg	Signal peptide removed

		gatgagcaagccgtgatcaagtctccacttaagtgcactctcctgccgccaggccaggagt cagagagcgctgaatcggctaagataggcgggatcattaccgtcttcctcatcgcactggtg ttgacttctactattgttaccctgaagtggatcggatacatctgcttgcgcaactctctgccaaa agttctaaactttcacaattttctggcctggcccttccccaatcttcctcctctggaggccatgg acatggttgaggttatctatataaatcggaaaaaaaaagtctgggactacaattacgatgacg aaagtgactcagacacggaggccgcaccaaggacctctggagggggctatactatgcac ggccttaccgtgagacctttaggacaggcatctgctacaagcactgaaagccagctgattg acccagagagcgaggaagagcctgatctaccagaagtggatgtagagctgccgacaatg cctaaggactccccccaacagctcgaactgttgagcggcccttgtgaaaggcgcaaaagt cccttgcaagatccgttccctgaagaagactatagcagtaccgaaggatccggcggtcgga ttacattcaacgtggatttaaatagtgtatttttacgggttctggacgatgaggacagtgatgat ctggaggcgccccttatgctgtcctcccatctggaggagatggtagaccccgaagatccag ataacgtgcagtctaatcaccttctggcttccggggaaggtactcagccaacctttcctagtc cttcttcagagggcttatggtcagaagacgcaccaagcgatcagtcagacacaagtgagag cgacgtagacctcggggacgggtacattatgaga **(SEQ ID NO: 45)**	
IFNGR1	P15260	gaaatggggactgccgacttgggacctagcagtgtccccactcccaccaacgtgaccatc gagtcttataatatgaatcctattgtttattgggaatatcagatcatgcctcaggttccagtgttc actgttgaagtgaaaaattacggagtgaagaactcagagtggatagacgcttgcataaacat atctcaccattactgcaatatttccgaccacgtgggcgaccccagcaacagtttgtgggtca gagtgaaagctcgcgtgggccagaaggagagtgcttatgccaaaagcgaagaattcgcc gtttgtagagatggcaagatcgggcccccccaaattagacattcgcaaagaagaaaaacaa attatgatcgatatcttccatccctctgtcttcgtcaacggcgacgaacaggaggtagattatg atccagagacaacgtgttacatcagggtatacaacgtttacgtgaggatgaatgggtcaga gatccagtataagatcctcactcaaaaggaggacgactgtgacgaaattcagtgtcaactc gccatcccagtgtcttcgctgaatagccagtactgcgtgtctgccgagggtgtgcttcacgtt tggggagtcacaactgaaaagtccaaagaagtttgtattaccatttttaacagctctatcaag ggctccctgtggataccagtggtggcggcactgctgctgttccttgtactcagcctggtcttc atctgcttctatattaagaagatcaaccctctgaaggagaagagcatcatactacccaagtcg cttatctcagtcgtgcggtccgccaccctagaaactaagcccgaatcaaaatatgtatccctg atcacaagctaccagccattttcattagagaaagaagtcgtgtgcgaggagcctctgtcccc agcaactgtgccaggtatgcatacggaggacaatccgggtaaagtagagcacaccgagg agctgtccagcattacagaggtcgtcaccacagaggagaacatacccgatgtggtgcctg gaagtcatctcacacctattgagcgtgaatctagcagtcccttgtcttctaatcagagtgaacc ggggagtattgcattaaactcctaccactcccggaattgcagcgaaagcgaccactcgaga aatgggtttgataccgatagttcttgtctggaatcccactcatcactgagcgattctgagtttcc gccaaacaacaagggcgaaattaaaacggagggacaagagctcatcaccgtcatcaagg ctccaaccagttttggttacgacaagcctcatgttttggtggatctgcttgtggatgactcagg caaggagtccctcattggataccgacctacagaggattccaaagagtttagc **(SEQ ID NO: 46)**	Signal peptide removed
IFNGR2	P38484	Gccccccctgatcctctctcacagctacccgccccacagcatcccaagataagactgtaca atgccgagcaggtgcttagctgggagcccgtggcactatcaaacagtacgagacccgtgg tgtaccaggtacagttcaagtacacagacagcaagtggtttaccgctgacattatgagcatt ggagtcaattgcactcagatcaccgcaaccgagtgtgactttacagcagcttcaccctccgc cggattccctatggacttcaacgtcactctgcggcttcgtgcagaactgggcgctcttcattc cgcctgggtgacaatgccttggttccagcactatcggaacgtcaccgtagggccccctgaa aatatcgaagtaacccctggagaaggttcgctgataataaggttcagctctccgtttgacatt	Signal peptide removed

		gctgatacatccactgcgttcttctgctactatgtgcactactgggagaagggcgggattcaa caagtgaaagggccattcaggagcaacagtatcagtctcgacaacctgaaaccttctcgcg tctattgcctccaagtgcaggctcaactgctgtggaacaaaagtaatattttccgagttggcc acctgtctaatatctcctgttatgagaccatggccgacgcatctacggagttgcagcaggtc atcctcatttctgtgggcacattttccctgctgtcggttctggccggtgcctgttttttctcgtttt gaaataccgcggcttgatcaaatactggtttcataccccaccatcaataccattacagatcga agagtatcttaaagatccaactcagccaattttagaggcgctcgataaggactctagcccga aggacgatgtgtgggattccgtgtccatcatcagctttcccgaaaaggagcaggaagatgtt ctgcaaactttg **(SEQ ID NO: 47)**	
TNFR1	P19438	ttggtaccccatcttggcgaccgagagaaacgggatagtgtctgtccccaagggaaatatat acacccacagaataactctatctgctgcactaagtgccataaaggaacgtacctttataacga ctgcccaggccccggccaagatactgactgcagagagtgcgagtctgggagcttcaccgc ctccgagaatcacttgagacattgcctgagttgtagcaagtgcaggaaggagatggggca ggttgagatctcatcatgtaccgttgatcgggacaccgtctgtggatgccgcaaaaatcagt atcggcattattggtccgaaaacctatttcagtgttttaactgttctttgtgcctgaacggaaca gtccacctgagttgccaggaaaaacagaatacagtttgcacttgccacgctggctttttctcc gcgagaacgaatgtgtgtcctgttccaattgtaagaagtctctagaatgtacaaagctgtgtct gccccaaatcgagaacgtgaaaggaactgaggacagtggtacaaccgtgttgctgcctct ggtgatcttcttcgggctctgcctcctcagtctgcttttcattgggctaatgtaccggtaccagc gttggaaatctaagttatactcaattgtctgtgggaagtccacccctgagaaggaaggagaa ctggaaggtactaccaccaaaccactggctccaaacccctccttctctcctacacccggcttt actcctaccctgggcttctcaccggtgcccagctcaacgttcaccagctcgagcacatacac ccctggcgattgtcccaacttcgcagcaccaaggcgtgaagtggccccaccctaccaggg tgctgatccaatacttgccaccgcattagccagcgatccgattcctaatcctttacagaagtg ggaggattcggcccacaaaccccagagcctggacactgacgaccccgccacgctgtatg ctgtggtcgagaatgtaccgcctctcagatggaaggaatttgtgaggcgactgggcctgtcc gatcacgagatcgacagactggagttgcaaaatggtcgatgcctccgggaggcccagtac agcatgctggctacatggaggaggcgcacacctcgcagggaggcgactcttgaattgctg ggacgcgtgctcagagatatggacttactcggatgtcttgaagacattgaagaggcgctctg cggcccagcagccctgcctccggcaccatccctgctcaga **(SEQ ID NO: 48)**	Signal peptide removed. Membrane bound form
TNFR2	P20333	ctgcctgcccaggtcgcttttacaccatatgcacctgagcctggttccacgtgtaggcttagg gagtactacgatcaaaccgctcagatgtgttgctccaagtgtagtccaggccagcacgcaa aagtcttttgtacaaagacgtcagataccgtgtgcgacagctgcgaagatagcacctatacc cagctgtggaattgggttcccgaatgtttgtcttgtggctcccgctgctctagtgaccaggtg gaaacacaggcctgcactcgggaacagaaccgtatttgtacctgcaggcccggttggtact gcgcactgtccaaacaagaggggtgtagactgtgtgccccttgcgcaagtgtcgtccagg cttcggtgtggcaagacctggaacagagacttcagacgtcgtttgtaagccctgcgcccctg gcacattctccaataccacctcatctaccgacatatgcagaccccaccaaatatgcaacgtg gtggctatccctgggaacgcctccatggacgctgtttgcacttccacttctcccactcggtcta tggctcccggtgccgtgcatttaccccaacccgtgagcactcggagccaacacacacagc caacacccgagccaagtaccgccccgagtaccagcttcctactccccatgggcccatctcc accggctgagggatctaccggggattttgctctgcctgtcgggctaatcgtcggggtgacg gcgctcggattgctcattatcggagtggtaaactgcgtgattatgactcaggtgaaaaagaa gcctttatgcctccagagagaagcgaaagttccccacctgcctgcagacaaggccagggg tacacagggcccggaacagcaacatctgctgatcaccgccccctcttcaagctccagcag cctggaatccagtgccagtgcacttgatcggcgcgcaccaacgcgaaaccagccccagg	Signal peptide removed. Membrane bound form

		ccccctggggtagaggcatcaggcgctggagaagcgcgcgctagcacaggcagttccgat tccagccctggagggcatggaacacaggtaaatgtcacctgcatcgttaatgtgtgctcgtc ctcggaccacagctctcaatgttcaagccaggcctcaagcactatgggcgacactgatagc tctccctccgagtcaccgaaggacgagcaggtcccatttagtaaagaggagtgtgccttcc gaagtcagctggagacaccagaaaccctgcttgggtctactgaagagaaaccactccctct tggcgtgccagatgcgggaatgaagccgtcg **(SEQ ID NO: 49)**	
IL-1R1	P14778	ctcgaggccgataagtgcaaagaaagagaggaaaaaatcattctggtttctagcgccaacg aaatcgatgtccgcccctgtccactgaatcctaacgagcataaggggactataacatggtat aaggacgacagcaagacccctgtgtctacagaacaagcaagcaggatacaccagcacaa agaaaagctttggtttgtaccagcaaaggtcgaggacagcgggcattattattgcgtggtac gaaacagttcttactgcctcagaatcaagatttccgctaagtttgtcgagaacgaacctaactt atgttacaacgcacaggctatttttaaacagaagctcccagttgctggggatggcggcctgg tgtgtccctacatggagtttttttaaaaatgagaataatgagctacctaaactgcaatggtacaa ggactgcaaacccctttttgctcgacaatattcacttcagcggagtgaaagatcggctgattgt gatgaacgtggctgagaaacaccgcgggaactatacatgccacgcctcttatacgtacctg ggcaagcagtacccgatcactagagtgattgaatttataacactggaagagaacaagccaa ctcgtcctgtcatagtatcccccgcaaacgaaaccatggaggtggacttgggttctcagatc cagctgatttgcaatgttaccgggcaattgagtgatatcgcctattggaagtggaatggttctg tcattgacgaagacgatccagtgttaggagaggactattatagcgtagaaaatcctgcgaac aagaggcggtcgactctgataactgtcctgaacatcagtgagatcgagagccgattttataa acatccattcacatgtttcgccaaaaatacacacgggatcgacgccgcctacattcagctgat ctaccccgtaaccaatttccagaagcacatgatcgggatatgcgtgacgctaaccgtgatca ttgtttgctcagtgttcatttacaagatcttcaagatcgacatcgtcctttggtatagggatagct gttacgactttctgcccattaaggcatcggatggcaaaacctacgacgcttacatcttgtacc caaagaccgtgggagaaggctcaacctccgactgtgacattttcgtctttaaggtgctccctg aggtcctcgagaaacagtgtggctataaactgttcatctatggccgggatgactacgtgggc gaggatatagttgaagtcataaatgaaaatgttaagaaatcacggaggctgatcatcattcta gtgcgggagacctcaggtttttcctggctcggcggctcctcagaggagcagattgcgatgt acaacgctctggtgcaagatggaatcaaggtggttctgttggagctcgaaaagatccagga ttacgagaaaatgcccgagagcattaagttcatcaaacaaaaacacggagccattagatgg agtggtgatttcacgcaaggaccgcagtccgccaagacacgtttctggaaaaacgtgcgct atcatatgcccgtgcagaggagatccccctccagtaaacatcagctgttatctccggcgact aaggaaaagcttcagcgcgaagcccatgttcctcttgga **(SEQ ID NO: 50)**	Signal peptide removed. Membrane bound form
IL-1R3	Q9NPH3	tccgagcggtgcgatgattggggcttagataccatgcggcagattcaggtgttcgaagacg agcctgctcgcattaaatgcccgctctttgagcacttcctgaagtttaattacagcactgctca ctccgcaggactcacactgatctggtattggacacgccaagacagagatctggaggagcc cattaattttaggctccccgagaacaggatctctaaggagaaggacgtgctgtggtttcggc cgacactactgaacgatactgggaattacacatgtatgcttcgaaatactacctattgctccaa ggtggcttttccacttgaggtggtgcagaaagacagctgttttaatagcccaatgaaactgcc cgtgcacaagctgtacatcgaatatggcatacagagaatcacatgccctaacgtcgacggc tacttccctagctcagttaagccgaccataacttggtatatgggctgctataaaatacagaact tcaataatgtaatccccgagggtatgaacttgagtttcctgatcgcactgatatctaacaacgg gaactacacctgtgtggtgacttatcccgagaacggacgcacattccatttgacaaggacgt taactgtcaaggtagtgggtagtcctaagaatgcagttcctcccgtgattcacagccctaatg atcacgtggtgtatgaaaaagaaccaggtgaagaactcctgatcccctgcacggtgtacttc tctttttaatggactcccgtaatgaagtttggtggaccatcgacggcaaaaaacctgatgata	Signal peptide removed

		ttaccatcgacgtgacaatcaacgagagcatttcacatagtcggaccgaagatgagacaag aacccagattcttagcataaaaaaagtgacttctgaagacctgaagcgcagttacgtatgtca cgcgcgatccgcaaaaggggaagttgccaaggctgccaaggtgaagcagaaagtccctg ccccacggtacaccgtagagctggcctgtggcttcggagctacggttttgctggttgttatcc ttatcgtcgtctatcatgtgtactggttggagatggtgctttttatcgggcccatttcgggacc gatgagacgattctagacggaaaggagtacgatatttacgtctcgtacgccagaaatgcgg aggaagaggaattcgtgctcttaaccctgaggggagtactggaaaacgagtttggctacaa gttgtgtatttttgacagagattcactgccaggaggaattgtcactgacgagacactctcattc atccagaaatctaggaggttgctcgttgtcctgagtccaaattatgtgctccaaggcacccag gccttgctagaactgaaggcggggcttgaaaacatggcctctcgcgggaacatcaacgta attctggtgcagtacaaagcagtgaaggagaccaaagttaaagagctgaaacgagccaag acagtcctcactgtcatcaagtggaaaggtgaaaaatcaaagtatccacaagggagattctg gaagcagcttcaagtcgctatgcccgtgaagaagtccccccgtcgttcctcctcggacgag cagggcctgagctacagctctctcaagaatgtc **(SEQ ID NO: 51)**	
IL-6Rα	P08887	cttgcaccaagacgctgtccggctcaggaggtcgctaggggagtgctgacctcgctgccg ggcgactccgtgaccctgacatgtcctggagtggagcctgaggacaacgcaacagttcac tgggtgctacggaagcccgccgctggctcccatccttccaggtgggccgggatggggcg cagactgcttctcagatcagtgcagttacatgatagcggtaattacagctgctaccgcgctgg aaggccggcaggcactgtgcacctcctagtggatgttccacctgaggagccacagttgag ctgctttcgaaaaagtcccttgtctaacgtcgtatgcgagtggggccctagatcaactccctc cctcaccaccaaagcggttctcctcgtacgtaagttccaaaactctcctgccgaagattttca agagccatgtcagtatagccaggagagtcagaagttctcatgccagcttgcagtcccggag ggtgactcatccttctatattgttagtatgtgcgtcgcctcgtctgtggggtctaagtttagcaa gactcaaacttttcagggctgcggcatcctccaaccagacccccctgccaacattacagtga ccgcagttgccagaaaccctaggtggttgagcgtgacgtggcaggatccccattcctggaa ttcatcattctacagactgcggttcgagctccgatacagggcggaacgtagcaagacattca ccacgtggatggtcaaagacctgcagcaccactgtgtaatccatgacgcttggagcggtct gcgccacgtggtccagctgcgggcacaagaggaattcggacagggtgaatggagtgaat ggtctcctgaggctatgggcactccgtggaccgaatctcggtctccaccagccgaaaacga agtgtccacccctatgcaggctctgactactaataaggatgacgataatatcttgtttagggac tccgcaaatgctacatcactgcctgtacaggattccagtagtgttcccctaccaacctttttagt cgccggagggtctctggcgttcgggacgttgctctgtatagccattgtgctgcgtttcaaaaa gacctggaaactgcgcgccttaaaggagggaaaaacaagcatgcacccccatattctctt gggcagctggtgcccgaacggcccagaccaacaccagtcctggtgcctcttatatccccc cccgtgagcccctctagcctgggcagtgacaataccagtagccataataggcccgacgcc cgagaccctcgctccccatacgatatctcaaacacagattatttttttccccgg **(SEQ ID NO: 52)**	Signal peptide removed. Membrane bound form
gp130	P40189	gaactcctggacccctgcgggtatattagccccgagtctcccgtggtgcaactgcattctaa cttcaccgcagtttgtgtgctcaaagaaaagtgtatggattacttccatgttaacgccaactac attgtgtggaaaactaatcattttacgataccaaaggagcagtacacaattatcaacagaacc gcatcatccgtcacatttaccgatatcgcctccttgaacattcagctgacatgtaatatcttaac attcggtcaactggaacaaaacgtgtatggcatcaccatcatctctggacttcctccagaaaa acccaaaaatttgtcgtgtatcgtgaatgagggaaaaaaaatgcgctgtgaatgggacggg ggccgggagactcacctcgagacgaacttcacccttaagtcagagtgggcgacacataaa tttgccgactgcaaagcaaagagagataccccacttcctgcaccgtcgactattcaactgt gtacttcgtcaacattgaggtgtgggtggaggcggagaatgcccttggcaaggttacttccg	Signal peptide removed

		accacatcaactttgatcccgtctacaaggtgaaaccgaacccaccccacaacctgtccgtc attaattcagaggagctaagttctatactcaagttaacttggacgaatccctccataaagagtg taattattctcaagtataacatccaatataggactaaagatgcttcaacctggtcacagatccc accggaggacaccgcctctacaaggtcatcgttcaccgtgcaggatcttaagcctttcaccg agtatgtgttcagaatccgatgcatgaaagaggacggcaaggggtattggagcgattggag cgaagaagcttccggcattacctacgaggacaggccttcgaaagcaccttctttctggtaca aaatcgatccttctcacactcagggctaccggaccgtgcagcttgtgtggaagactttgcca ccattcgaggcaaatggaaagatactggattatgaggtcacactgacccgctggaaaagtc acttgcagaactatacagtaaacgccaccaaactgacagtcaatctcactaacgatagatatt tagcaaccctgactgtacgaaacctggtgggaaaatctgacgccgcggtactgactatccct gcttgtgactttcaggctacccaccctgttatggatctgaaggccttccctaaggataacatgc tatgggtcgagtggaccacaccaagggaaagcgtcaaaaagtatattctcgagtggtgcgt tctgagcgacaaggccccatgtattacagactggcaacaggaggacgggacagttcatcg gacatatctgcgcggcaatctagctgaaagtaaatgctaccttatcaccgtcacgccagtcta cgccgacggcccgggctctccagagtcaatcaaggcttacctaaagcaggcccctccctct aaggggccaactgtgagaacaaaaaaggtaggtaagaatgaagccgtcctggagtggga tcaactgccagtggacgtacagaacggtttcattcgcaactacaccatcttttacaggacgat cattgggaatgagacagcagtgaacgtggattcttcccataccgaatacacgctcagcagtc tgacgtcggacacattgtacatggtcaggatggctgcatatacagacgaaggagggaagg atgggcctgagttcacctttaccacccctaagttcgctcagggcgagattgaagcaattgtg gtgcccgtatgcctggcctttctccttacgacactgctgggtgttctcttttgctttaataagcgg gacctcatcaagaaacacatttggcctaatgtgcccgaccccagcaaaagtcacatagccc agtggagccctcatactccccccgtcataatttaatagcaaggatcagatgtacagcgac ggcaattttacagacgtgtccgtcgtcgaaatagaagctaatgataagaagccctttcctgaa gacctgaaatccttggacttattcaaaaaggagaagatcaataccgaagggcactcctcag ggataggggcagcagttgcatgtcctcatcccgtccctctatcagctccagcgatgagaa cgagagcagccagaatactagttccactgttcagtacagcactgtagttcacagtggctata gacatcaggtcccgagtgttcaggtgttctccaggagtgaatctacccagccgttgttagact cagaagaacgcccagaagacctgcagctggtggaccacgtggatggaggtgatggcatt ctgccgcgccagcaatactttaagcagaactgttctcagcatgaatccagccctgacatctct cactttgagcgaagcaaacaggtgtcaagcgtgaacgaagaggatttcgttcggcttaagc aacagatatctgaccacatctcacaatcctgcggaagtggacaaatgaagatgtttcaggag gttagtgcggccgatgctttcggccctggcactgagggtcaggtggaaagattcgagacag tgggtatggaagccgctacagatgagggaatgcccaaaagctacctcccacaaaccgtgc ggcagggaggatatatgccacag **(SEQ ID NO: 53)**	
IL-12-Rβ1	P42701	tgcagaactagcgaatgttgtttccaggacccccgtatcccgacgccgattccggaagcg catccggaccacgtgacctgcggtgctatcggatttctagcgataggtacgaatgctcatgg cagtacgaggggcccactgctggggtgagtcacttcttaagatgctgtttaagttccgggag gtgctgctatttcgccgcagggtcagctactcgactacagttttctgaccaggctggagtaag cgtgctttatacagtgacactgtgggtcgaatcctgggccaggaaccaaacggagaagtca cccgaggtgaccctgcaactgtataactcagtcaaatacgagcctcctctgggtgacattaa agtgtcgaaactcgccggacagcttagaatggagtgggagacccccgataaccaggttgg cgcagaggtgcagttccggcaccgaacaccctcatctccttggaaactgggcgattgtggt ccgcaggacgacgataccgagagttgcttgtgtcccctagagatgaatgtcgcacaggagt ttcagctgaggaggcgtcagctcggcagccaaggcagttcttggtcaaaatggtcctcccc cgtctgcgttcccccctgaaaatcctccacagccgcaggttcgattcagcgtggaacaactcg	Signal peptide removed

		ggcaggacgggagacgccgcttgactcttaaggagcaaccaacgcagctcgaactccca gaaggttgccagggcctggcacctggcaccgaggtgacctaccgtttgcagttacatatgc ttagttgcccttgtaaggccaaggctacacggacccttcacctaggcaaaatgccatacctа agcggtgctgcatacaacgtggcggtcatttcttccaaccagttcggacccggtctgaatca gacctggcacatccccgcagatacccataccgaacctgtggcgctgaatatcagcgtggg cacaaatggcactacgatgtattggccggcccgcgctcaatctatgacttactgcatcgaat ggcagcctgttgggcaagatggaggactcgcgacatgcagccttactgccccgcaggac cctgatccagcaggtatggccacttattcttggagccgcgagtccggggccatgggacag gagaagtgttactacatcaccatatttgcgtcagctcatccagaaaagctgaccctgtggtca accgttctgagcacataccacttcgggggcaatgcgtccgctgcaggcaccccacaccac gtgtcggtgaaaaaccactctctggacagtgtgagtgttgactgggccccaagcctgttgtc cacatgtcccggggtgctcaaggaatatgttgtccgctgtcgagacgaggactccaaacaa gtgtcggaacatcccgtacagccaacggagacccaagtcactctgtctggactgagagcc ggcgtggcctacacagtccaagtgcgggcagatacagcttggttacggggcgtatggagc cagccacaaaggttcagcattgaggtacaggtctctgattggttgatttttttgccagtctgg gcagttttctctctatcctgttggtcggagtgttgggctatctgggactgaatcgcgccgcca gacatctgtgccccccactcccaaccccatgtgcctcctccgccatagaatttcctgggggt aaagagacatggcagtggatcaaccctgtagacttccaggaggaggctagcctccaggaa gccctggttgtggaaatgtcatgggataagggcgagagaacggaacctctcgagaagact gaacttcccgagggagctcctgagctcgcacttgacacagaactgtctttagaggatgggg ataggtgtaaggctaagatg **(SEQ ID NO: 54)**	
IL-12-Rβ2	Q99665	aaaattgatgcgtgcaaacgcggcgatgtgaccgtgaaaccgagccatgtgattctgctgg gcagcaccgtgaacattacctgcagcctgaaaccgcgccagggctgctttcattatagccg ccgcaacaaactgattctgtataaatttgatcgccgcattaactttcatcatggccatagcctg aacagccaggtgaccggcctgccgctgggcaccaccctgtttgtgtgcaaactggcgtgc attaacagcgatgaaattcagatttgcggcgcggaaatttttgtgggcgtggcgccggaaca gccgcagaacctgagctgcattcagaaaggcgaacagggcaccgtggcgtgcacctggg aacgcggccgcgatacccatctgtataccgaatatacctgcagctgagcggcccgaaaa acctgacctggcagaaacagtgcaaagatatttattgcgattatctggattttggcattaacct gaccccggaaagcccggaaagcaactttaccgcgaaagtgaccgcggtgaacagcctgg gcagcagcagcagcctgccgagcacctttacctttctggatattgtgcgcccgctgccgcc gtgggatattcgcattaaatttcagaaagcgagcgtgagccgctgcaccctgtattggcgcg atgaaggcctggtgctgctgaaccgcctgcgctatcgcccgagcaacagccgcctgtgga acatggtgaacgtgaccaaagcgaaaggccgccatgatctgctggatctgaaaccgtttac cgaatatgaatttcagattagcagcaaactgcatctgtataaaggcagctggagcgattgga gcgaaagcctgcgcgcgcagaccccggaagaagaaccgaccggcatgctggatgtgtg gtatatgaaacgccatattgattatagccgccagcagattagcctgttttggaaaaacctgag cgtgagcgaagcgcgcggcaaaattctgcattatcaggtgaccctgcaggaactgaccgg cggcaaagcgatgacccagaacattaccggccataccagctggaccaccgtgattccgcg caccggcaactgggcggtggcggtgagcgcggcgaacagcaaaggcagcagcctgcc gacccgcattaacattatgaacctgtgcgaagcgggcctgctggcgccgcgccaggtgag cgcgaacagcgaaggcatggataacattctggtgacctggcagccgccgcgcaaagatc cgagcgcggtgcaggaatatgtggtggaatggcgcgaactgcatccgggcggcgatacc caggtgccgctgaactggctgcgcagccgcccgtataacgtgagcgcgctgattagcgaa aacattaaaagctatatttgctatgaaattcgcgtgtatgcgctgagcggcgatcagggcgg ctgcagcagcattctgggcaacagcaaacataaagcgccgctgagcggcccgcatattaa	Signal peptide removed

		cgcgattaccgaagaaaaaggcagcattctgattagctggaacagcattccggtgcaggaa cagatgggctgcctgctgcattatcgcatttattggaaagaacgcgatagcaacagccagc cgcagctgtgcgaaattccgtatcgcgtgagccagaacagccatccgattaacagcctgca gccgcgcgtgacctatgtgctgtggatgaccgcgctgaccgcggcgggcgaaagcagcc atggcaacgaacgcgaattttgcctgcagggcaaagcgaactggatggcgtttgtggcgc cgagcatttgcattgcgattattatggtgggcatttttagcacccattattttcagcagaaagtgt ttgtgctgctggcggcgctgcgcccgcagtggtgcagccgcgaaattccggatccggcga acagcacctgcgcgaaaaaatatccgattgcggaagaaaaaacccagctgccgctggatc gcctgctgattgattggccgaccccggaagatccggaaccgctggtgattagcgaagtgct gcatcaggtgaccccggtgtttcgccatccgccgtgcagcaactggccgcagcgcgaaaa aggcattcagggccatcaggcgagcgaaaaagatatgatgcatagcgcgagcagcccgc cgccgccgcgcgcgctgcaggcggaaagccgccagctggtggatctgtataaagtgctg gaaagccgcggcagcgatccgaaaccggaaaacccggcgtgcccgtggaccgtgctgc cggcgggcgatctgccgacccatgatggctatctgccgagcaacattgatgatctgccgag ccatgaagcgccgctggcggatagcctggaagaactggaaccgcagcatattagcctgag cgtgtttccgagcagcagcctgcatccgctgacctttagctgcggcgataaactgaccctgg atcagctgaaaatgcgctgcgatagcctgatgctg **(SEQ ID NO: 55)**	

Table 5b – Codon Optimized DNA Sequences of Endogenous Proteins (Anti-Inflammatory Cytokine Receptors)

Name	Uniprot	Codon Optimized Sequence	Notes
IL-4Rα	P24394	atgaaagtgctgcaggaaccgacctgcgtgagcgattatatgagcattagcacctgcgaat ggaaaatgaacggcccgaccaactgcagcaccgaactgcgcctgctgtatcagctggtgtt tctgctgagcgaagcgcatacctgcattccggaaaacaacggcggcgcgggctgcgtgtg ccatctgctgatggatgatgtggtgagcgcggataactataccctggatctgtgggcgggc cagcagctgctgtggaaaggcagctttaaaccgagcgaacatgtgaaaccgcgcgcgcc gggcaacctgaccgtgcataccaacgtgagcgataccctgctgctgacctggagcaaccc gtatccgccggataactatctgtataaccatctgacctatgcggtgaacatttggagcgaaaa cgatccggcggattttcgcatttataacgtgacctatctggaaccgagcctgcgcattgcgg cgagcaccctgaaaagcggcattagctatcgcgcgcgcgtgcgcgcgtgggcgcagtgc tataacaccacctggagcgaatggagcccgagcaccaaatggcataacagctatcgcgaa ccgtttgaacagcatctgctgctgggcgtgagcgtgagctgcattgtgattctggcggtgtg cctgctgtgctatgtgagcattaccaaaattaaaaaagaatggtgggatcagattccgaacc cggcgcgcagccgcctggtggcgattattattcaggatgcgcagggcagccagtgggaa aaacgcagccgcggccaggaaccggcgaaatgcccgcattggaaaaactgcctgacca aactgctgccgtgctttctggaacataacatgaaacgcgatgaagatccgcataaagcggc gaaagaaatgccgtttcagggcagcggcaaaagcgcgtggtgcccggtggaaattagca aaaccgtgctgtggccggaaagcattagcgtggtgcgctgcgtggaactgtttgaagcgcc ggtggaatgcgaagaagaagaagaagtggaagaagaaaaaggcagcttttgcgcgagc ccggaaagcagccgcgatgattttcaggaaggccgcgaaggcattgtggcgcgcctgac cgaaagcctgtttctggatctgctgggcgaagaaaacggcggcttttgccagcaggatatg ggcgaaagctgcctgctgccgccgagcggcagcaccagcgcgcatatgccgtgggatg aatttccgagcgcgggcccgaaagaagcgccgccgtggggcaaagaacagccgctgca tctggaaccgagcccgccggcgagcccgacccagagcccggataacctgacctgcacc gaaaccccgctggtgattgcgggcaacccggcgtatcgcagctttagcaacagcctgagc	Signal peptide removed. Membrane bound form

		cagagcccgtgcccgcgcgaactgggcccggatccgctgctggcgcgccatctggaaga agtggaaccggaaatgccgtgcgtgccgcagctgagcgaaccgaccaccgtgccgcag ccggaaccggaaacctgggaacagattctgcgccgcaacgtgctgcagcatggcgcggc ggcggcgccggtgagcgcgccgaccagcggctatcaggaatttgtgcatgcggtggaac agggcggcacccaggcgagcgcggtggtgggcctgggcccgccgggcgaagcgggc tataaagcgtttagcagcctgctggcgagcagcgcggtgagcccggaaaaatgcggctt ggcgcgagcagcggcgaagaaggctataaaccgtttcaggatctgattccgggctgcccg ggcgatccggcgccggtgccggtgccgctgtttacctttggcctggatcgcgaaccgccg cgcagcccgcagagcagccatctgccgagcagcagcccggaacatctgggcctggaac cgggcgaaaaagtggaagatatgccgaaaccgccgctgccgcaggaacaggcgaccga tccgctggtggatagcctgggcagcggcattgtgtatagcgcgctgacctgccatctgtgc ggccatctgaaacagtgccatggccaggaagatggcggccagaccccggtgatggcga gcccgtgctgcggctgctgctgcggcgatcgcagcagcccgccgaccaccccgctgcgc gcgccggatccgagcccgggcggcgtgccgctggaagcgagcctgtgccccggcgagc ctggcgccgagcggcattagcgaaaaaagcaaaagcagcagcagctttcatccggcgcc gggcaacgcgcagagcagcagccagaccccgaaaattgtgaactttgtgagcgtgggcc cgacctatatgcgcgtgagc **(SEQ ID NO: 56)**	
IL-2Rγc	P31785	Ctgaacacaacaattctcacccctaacggcaacgaagacactaccgcagatttttcctcac tactatgcccactgattccctttccgtgtcgaccttgccgctgccagaagtgcagtgcttcgtc tttaatgttgagtatatgaattgtacatggaattctagcagcgaaccgcagccaaccaatttga cattgcactactggtataaaaactcagataacgacaaagtgcagaagtgttcccactacttatt tagcgaggaaataacctctgggtgccagctgcagaagaaggagatccatctgtaccagac cttcgtcgtgcagctccaggatccacgggaaccacgccggcaagctacccaaatgctaaa gctgcaaaatctcgttatcccatgggcacctgagaatttgacacttcataagctgtcggaatc ccagctggagctcaattggaacaaccgtttcctcaaccattgtctggagcacctggtgcagt acagaaccgactgggaccatagttggacggagcagagtgtcgattatagacacaaattctc actaccctcagtggacgggcagaagaggtacacatttagagtaaggagtcggttcaatccc ctgtgcgggtccgcccaacactggagtgagtggtctcatcctattcactggggcagcaaca cgtccaaggagaacccttttcttgtttgctctggaagctgttgtgatttcagtaggctctatggg attaatcatcagcctcctgtgtgtctatttttggctggagcgaacaatgcccaggatccccact ctcaaaaatctggaagaccttgtgacggagtatcacggcaacttcagcgcgtggtctggcgt ctctaaaggtcttgccgagagcctgcagcctgattacagtgagcgcttatgcctggtgagcg agataccacctaaaggaggagcccttggtgaaggaccgggggcatccccctgtaatcaac actcaccatactgggcccccccctgctataccctaaagcctgaaact **(SEQ ID NO: 57)**	Signal peptide removed
IL-13Rα1	P78552	ggcggcggcggcgcggcgccgaccgaaacccagccgccggtgaccaacctgagcgtg agcgtggaaaacctgtgcaccgtgatttggacctggaacccgccggaaggcgcgagcag caactgcagcctgtggtattttagccattttggcgataaacaggataaaaaaattgcgccgga aacccgccgcagcattgaagtgccgctgaacgaacgcatttgcctgcaggtgggcagcca gtgcagcaccaacgaaagcgaaaaaccgagcattctggtggaaaaatgcattagcccgcc ggaaggcgatccggaaagcgcggtgaccgaactgcagtgcatttggcataacctgagcta tatgaaatgcagctggctgccgggccgcaacaccagcccggataccaactataccctgtat tattggcatcgcagcctggaaaaaattcatcagtgcgaaaacatttttcgcgaaggccagtat tttggctgcagctttgatctgaccaaagtgaaagatagcagctttgaacagcatagcgtgca gattatggtgaaagataacgcgggcaaaattaaaccgagctttaacattgtgccgctgacca gccgcgtgaaaccggatccgccgcatattaaaaacctgagctttcataacgatgatctgtat	Signal peptide removed

		gtgcagtgggaaaacccgcagaactttattagccgctgcctgttttatgaagtggaagtgaa caacagccagaccgaaacccataacgtgttttatgtgcaggaagcgaaatgcgaaaaccc ggaatttgaacgcaacgtggaaaacaccagctgctttatggtgccgggcgtgctgccggat accctgaacaccgtgcgcattcgcgtgaaaaccaacaaactgtgctatgaagatgataaact gtggagcaactggagccaggaaatgagcattggcaaaaaacgcaacagcaccctgtatat taccatgctgctgattgtgccggtgattgtggcgggcgcgattattgtgctgctgctgtatctg aaacgcctgaaaattattattttccgccgattccggatccgggcaaaatttttaaagaaatgtt tggcgatcagaacgatgataccctgcattggaaaaaatatgatatttatgaaaaacagacca aagaagaaaccgatagcgtggtgctgattgaaaacctgaaaaaagcgagccag **(SEQ ID NO: 58)**	
IL-10R1	Q13651	catgggaccgagctccccagtcctccttctgtttggttcgaagccgaattctttcaccatattct gcactggactcctatcccaaatcaatcagaatcaacatgttacgaggtggcactgctgaggt acggaatcgagtcttggaatagcatttcaaactgtagccaaaccctgtcttacgatcttaccg ctgtgacgctggacctgtatcatagcaacggctaccgtgccagggttagggcagttgatgg cagcagacactccaattggacagttacgaatacccgattcagtgtcgacgaggtgactttaa ctgtcgggagtgttaaccttgaaattcacaacgggttcatattgggaaagatccagctccccc ggccaaaaatggccccagccaacgacacatacgagagtatattttctcattttagagagtatg agatcgcaatccgcaaggtgcctgggaatttcacatttactcataagaaggtaaaacacgag aacttctccttgctcacctccggcgaagtgggggagttctgcgtgcaggtgaagccctcggt ggcttcacgctccaataaaggcatgtggagcaaagaagaatgtatttctctgactcggcagt actttaccgtgactaacgtaatcatatttttgccttcgtgctcctgctgtctggtgccctggcct attgcctggcgcttcaactttatgtgcggaggaggaagaagctgccgtccgtgctgttgttta agaaaccgtctcccttcatttttatcagccagcgcccctcacccgaaacacaggatactattc acccccttgacgaagaagccttccttaaagtgtcccccgagctaaaaaacctcgacctgca cgggtccaccgatagcgggtttggtagcaccaaaccatccttgcaaaccgaggagcccca gttcttgctccctgatccacacccacaggctgacagaacgttgggaaacagagagccccca gtcctgggggattcctgttcgtcagggtctagtaatagtaccgatagcgggatttgcctgcag gagccgagcctgtcaccctcaaccggtccgacctgggagcagcaagtaggatctaactcc cgcgggcaggatgactccggcatagacctcgtacagaattcggaaggccgggcgggtga cacacagggcggctccgctctgggccaccattccccaccagagcccgaggtccctggcg aggaggaccctgcagccgtcgcttttcaaggctatctgcgtcagacacgatgtgctgaaga gaaagctactaagacgggatgtcttgaagaggaatctccgcttacagacggattgggacca aagttcggcagatgcctagtggatgaggcgggactacatcctcccgcattagcaaagggct acctgaagcaggatccactagaaatgacactggcctcatctggcgcccctacaggacagt ggaaccagccaaccgaagagtggtccttgctcgctttaagctcttgcagtgacctgggtatc tcagattggagttttgcacacgacctcgcccctctgggttgcgtcgccgctcctggtggactc ttaggaagtttcaatagcgatctcgtcactctgcctctcatcagtagcttacagagcagcgaa **(SEQ ID NO: 59)**	Signal peptide removed
IL-10R2	Q08334	Atggtaccaccacctgaaaatgtgaggatgaactctgtgaattttaagaacattctccagtgg gaaagtcccgcttttgctaaggggaacctgaccttcacagcccaatacttatcctaccgaatc ttccaagacaagtgcatgaataccactttaactgaatgcgacttctcaagcctgtctaagtatg gcgatcatacactgcgggttcgtgccgagtttgccgacgagcactctgactgggtgaatata accttctgccccgtcgatgatactataattgggccaccaggtatgcaagttgaagtgttggca gattcgctgcacatgaggtttctcgcccccaaaatcgagaacgagtacgagacctggacga tgaagaatgtctacaactcttggacatataatgttcagtattggaaaaacggaaccgacgag aagtttcagatcactccgcagtatgatttcgaagtcctgagaaacctcgagccttggacaact	Signal peptide removed

		tactgtgtccaagtgcgcggctttctccctgaccggaacaaggcaggagagtggtcagaac cggtgtgtgagcagaccacccacgacgagacagtacccagctggatggtagctgtgatcc ttatggctccgtgttcatggtttgtctagctttgttgggctgttttgcccttctatggtgcgtctat aaaaagaccaaatacgcgttttcacctagaaacagccttccacagcacctcaaggagttcct ggggcatcctcatcacaatacactgctgttcttctccttccccctgagtgacgaaaacgatgt gtttgataaactgtccgtgattgcagaagacagtgagtccggcaaacagaatccaggagat agttgcagcctgggtacgcctcccggacagggcccccagagc **(SEQ ID NO: 60)**	
IL-18Rα	Q13478	gccgagagctgcactagccggccccatataactgtggtcgaaggggagccattctatctga aacattgttcctgctcccttgcccatgaaattgaaaccacaaccaagagctggtacaaatcta gtgggtctcaagagcacgtcgagttgaacccaagatcatctagtaggatcgccctgcatga ctgcgttctagagttttggccggtggaattaaatgacaccggatcttacttcttccagatgaag aattacacccagaaatggaagctgaacgtgatacgacgcaacaagcactcatgcttcacag aacgtcaggtgacctcgaaaatcgtggaagtgaaaaagttctttcagattacatgcgagaac agttactatcaaacgctagtgaatagcacgagcctgtacaaaaactgtaagaaacttctgctg gagaacaataaaaaccctactatcaaaaaaaatgcagaattcgaggatcagggctattaca gttgtgtgcattttctccaccacaatggtaagctattcaatatcaccaagacgttcaacatcacc attgtggaggatcgctccaacatagtacctgtgttattgggtcctaaacttaaccacgtggca gtggagctggggaaaaacgtgagactcaattgctcagccttgctgaacgaagaggatgtta tttattggatgtttggggaagaaaatggaagtgacccgaacattcacgaagagaaggagat gcgaatcatgacaccagaggggaaatggcacgcgagtaaggtcctcagaattgaaaatatt ggcgaatcaaatctcaacgtcctctataactgtaccgtagcatccacaggcggcactgatac taagtcctttatccttgtgcgtaaggccgatatggctgacatccccggccacgtattcacacg gggaatgatcattgctgttctgatcctggtggcagtagtgtgtttggttactgtatgtgttatcta ccgcgtggacttagttctgttttataggcacctgacccgaagagacgaaacccttacagatg gcaagacttatgacgcgttcgtgtcgtatcttaaagaatgccggcccgagaatggagagga gcacacgtttgctgtcgaaattctccccagagtcctggagaagcattttggttacaagctgtg catcttcgaaagagacgtcgtgcccggtggcgccgtggtcgacgagatacattccctgatc gagaagtcccgcaggttgatcatagtcctctcaaagtcttacatgagcaatgaggtgcggta cgaactcgagagcggactgcatgaggctttagtcgagaggaagattaagattattttgatcg agtttacacctgtgactgactttaccttcctccctcagtcactgaaactccttaagtctcacagg gtactgaagtggaaagctgataaatccctctcttataatagccggttttggaagaacctattgt acctgatgccagccaaaacagtcaagcctggacgcgatgagcccgaagttctgccagttct gagcgagtcc **(SEQ ID NO: 61)**	Signal peptide removed
IL-18Rβ	O95256	tttaatatctctggatgcagtacgaagaaattgctctggacatactctactaggagcgaggaa gagttcgtgcttttctgcgatttaccagaaccacagaaatcccatttttgtcacagaaatcgtct ttctcctaagcaggttcccgaacacctgcccttcatgggctccaacgaccttagtgacgttca atggtaccagcaaccaagcaatggcgaccctctggaagacatacgcaagagttaccccca tattatccaggataaatgcacgctacatttcctgaccccaggcgtcaacaacagtggatcttat atatgtaggcctaagatgatcaaatccccctacgacgtggcttgttgcgtcaagatgattctc gaggtgaagccccagaccaatgcctcatgtgagtactccgcctctcacaaacaggaccttc tgctggggtcgaccggcagtataagctgcccatcgctctcttgtcagagtgatgcgcagag ccctgctgtgacatggtacaaaaacggaaagctactgtcagtggagcgctcaaaccgtatt gtagtagacgaagtctacgactatcaccaaggcacctacgtgtgcgattatacacagtctga tacggtctccagttggactgtgcgggccgtggtgcaggtacggaccatcgtgggggacac aaaactgaagcccgacatccttgatccagttgaggacaccctggaggtggagctcgggaa	Signal peptide removed

		gcccctgactatctcctgtaaagcaagatttggcttcgagcgagtatttaaccctgttatcaag tggtatattaaagatagcgatctcgagtgggaggtatcagtgcctgaagccaaatccatcaa atcaactctgaaggatgaaatcattgagcgaaatattattcttgagaaggttacccagcgcga tctccgccgcaaatttgtctgcttcgtgcaaaacagcataggcaatactactcagagcgtgca gctgaaagagaagcgtggtgtcgtcttgttgtacatcctgctcggaacaattggtacactcgt agccgtgttggccgcctcagccctgctctacaggcattggattgaaatcgtgttgctttacag gacatatcagagcaaggaccagactctgggcgacaaaaaggatttcgatgcattcgttagc tatgctaaatggtcttcatttcctagcgaagctacatcctccctgagcgaggaacacttagcct tatcactgtttccagatgtgttagaaaataaatatggctatagcctgtgtttgctggagcgcga cgttgcaccaggggggtgtatgctgaagacatcgtcagcatcatcaagcggtccaggag gggaatatttatattaagccctaactacgtcaacggtccatcgattttcgaactgcaggctgca gtgaacttggcgctcgatgaccagacgctcaagctgattctcatcaagttctgctactttcaag agcccgagtctcttcctcacctagtcaagaaggcgctgagagtcctgccgaccgtgacatg gcgaggactaaagtctgtgccgccgaattccagattctgggcaaagatgcggtatcatatgc ccgttaaaaattcccaaggttttacttggaaccagctgcggattaccagtcggatcttccagtg gaaggggctgtctagaaccgagaccaccggaagatccagtcaacccaaagaatgg **(SEQ ID NO: 62)**	

Table 6 – Amino Acid Sequences of Engineered Proteins (Cytokines)

Name	Amino Acid Sequence	Notes
scIFN-γ	QDPYVKEAENLKKYFNAGHSDVADNGTLFLGILKNWKEESDRKI MQSQIVSFYFKLFKNFKDDQSIQKSVETIKEDMNVKFFNSNKKKR DDFEKLTNYSVTDLNVQRKAIHELIQVMAELGANVSGEFVKEAEN LKKYFNAGHSDVADNGTLFLGILKNWKEESDRKIMQSQIVSFYFK LFKNFKDDQSIQKSVETIKEDMNVKFFNSNKKKRDDFEKLTNYSV TDLNVQRKAIHELIQVMAELSPAAKTGKRKRSQMLFRG **(SEQ ID NO: 63)**	Single chain; Randal et al 2000
cpIL-1β (89/88)	NYPKKKMEKRFVFNKIEINNKLEFESAQFPNWYISTSQAENMPVF LGGTKGGQDITDFTMQFVSSggggsggggsggggsAPVRSLNCTLRDSQ QKSLVMSGPYELKALHLQGQDMEQQVVFSMSFVQGEESNDKIPV ALGLKEKNLYLSCVLKDDKPTLQLESVDPK **(SEQ ID NO: 64)**	Circular permutation
scIL-12	IWELKKDVYVVELDWYPDAPGEMVVLTCDTPEEDGITWTLDQSS EVLGSGKTLTIQVKEFGDAGQYTCHKGGEVLSHSLLLLHKKEDGI WSTDILKDQKEPKNKTFLRCEAKNYSGRFTCWWLTTISTDLTFSV KSSRGSSDPQGVTCGAATLSAERVRGDNKEYEYSVECQEDSACPA AEESLPIEVMVDAVHKLKYENYTSSFFIRDIIKPDPPKNLQLKPLKN SRQVEVSWEYPDTWSTPHSYFSLTFCVQVQGKSKREKKDRVFTD KTSATVICRKNASISVRAQDRYYSSSWSEWASVPCSGSTSGSGKPG SGEGSTKGRNLPVATPDPGMFPCLHHSQNLLRAVSNMLQKARQTL EFYPCTSEEIDHEDITKDKTSTVEACLPLELTKNESCLNSRETSFITN GSCLASRKTSFMMALCLSSIYEDLKMYQVEFKTMNAKLLMDPKR QIFLDQNMLAVIDELMQALNFNSETVPQKSSLEEPDFYKTKIKLCIL LHAFRIRAVTIDRVMSYLNAS **(SEQ ID NO: 65)**	Single chain; p40-linker-p35, Lee et al 2001

cpIL-4 (38-37)	NTTEKETFCRAATVLRQFYSHHEKDTRCLGATAQQFHRHKQLIRF LKRLDRNLWGLAGLNSCPVKEANQSTLENFLERLKTIMREKYSKC SSggnggHKCDITLQEIIKTLNSLTEQKTLCTELTVTDIFAASK **(SEQ ID NO: 66)**	Circular permutation; Kreitman et al 1994
mIL-10	SPGQGTQSENSCTHFPGNLPNMLRDLRDAFSRVKTFFQMKDQLD NLLLKESLLEDFKGYLGCQALSEMIQFYLEEVMPQAENQDPDIKA HVNSLGENLKTLRLRLRRCHRFLPCENGGGSGGKSKAVEQVKNA FNKLQEKGIYKAMSEFDIFINYIEAYMTMKIRN **(SEQ ID NO: 67)**	Monomeric form; Josephson et al 2000
cpIL-10 (58/57)	GYLGCQALSEMIQFYLEEVMPQAENQDPDIKAHVNSLGENLKTL RLRLRRCHRFLPCENKSKAVEQVKNAFNKLQEKGIYKAMSEFDIFI NYIEAYMTMKIRNggggsggggsggggsSPGQGTQSENSCTHFPGNLPN MLRDLRDAFSRVKTFFQMKDQLDNLLLKESLLEDFK **(SEQ ID NO: 68)**	Circular permutation
tdIL-10	SPGQGTQSENSCTHFPGNLPNMLRDLRDAFSRVKTFFQMKDQLD NLLLKESLLEDFKGYLGCQALSEMIQFYLEEVMPQAENQDPDIKA HVNSLGENLKTLRLRLRRCHRFLPCENKSKAVEQVKNAFNKLQE KGIYKAMSEFDIFINYIEAYMTMKIRNggggsggggsggggsSPGQGTQS ENSCTHFPGNLPNMLRDLRDAFSRVKTFFQMKDQLDNLLLKESLL EDFKGYLGCQALSEMIQFYLEEVMPQAENQDPDIKAHVNSLGEN LKTLRLRLRRCHRFLPCENKSKAVEQVKNAFNKLQEKGIYKAMSE FDIFINYIEAYMTMKIRN **(SEQ ID NO: 69)**	Tandem-dimer
cpIL-13 (75/74)	VSAGQFSSLHVRDTKIEVAQFVKDLLLHLKKLFREGRFNggggsLTC LGGFASPGPVPPSTALRELIEELVNITQNQKAPLCNGSMVWSINLTA GMYCAALESLINVSGCSAIEKTQRMLSGFCPHK **(SEQ ID NO: 70)**	Circular permutation

Table 7 – Codon Optimized DNA Sequences of Engineered Proteins (Cytokines)

Name	Codon Optimized Sequence	Notes
scIFN-γ	Caggatccctacgtgaaagaagccgagaacttaaagaaatatttcaacgcaggccattcagacgtcgct gataatggaacacttttttgggcattctgaaaaattggaaggaagaatcggaccgaaaaattatgcagag ccagatagtatccttttatttcaagttatttaaaaacttcaaagacgatcagtctatccaaaaaagtgtggaga ctatcaaggaggacatgaatgtgaagttcttcaacagcaataaaaagaaacgggatgactttgaaaagct caccaattactcagtcactgatctgaacgtgcagagaaaggcgattcatgagctaatccaagtgatggct gagctcggagccaacgtgagcggagagtttgtgaaggaagccgagaatctgaagaagtatttcaacgct ggtcactctgacgtggcagataacggcacgctgttcctggggatcctgaagaattggaaagaagagtcc gacaggaagattatgcaatcccagatcgtcagtttctactttaagcttttcaagaatttcaaagacgatcaga gtatccagaagtctgtcgagaccataaaagaagacatgaatgtaaagtttttttaattcaaacaaaaagaag cgtgacgatttcgaaaaactcaccaactactccgttacagatctgaacgttcagagaaaagccattcacga gttgatccaagttatggccgagctctctcctgcagctaagacaggtaagaggaaacggagccagatgct gtttcgcggg **(SEQ ID NO: 71)**	Single chain; Randal et al 2000
cpIL-1β (89/88)	Aactaccccaaaaaaaagatggagaagcggtttgtttttaacaagattgagatcaacaataagctggaatt cgagtctgcgcagttcccaaactggtatattagcacatcgcaagcagaaaatatgcccgtgttcctcggc ggaaccaaaggcgggcaggatatcacagactttacgatgcagttcgtgtcatctggtggtggtggaagc ggcgggggaggcagtgggggaggcgggtccgccccagtgaggtccctgaactgtaccttaagagact cacagcaaaagtccctggtcatgtctggcccctacgaactgaaagcccttcacctgcaggggcaagata	Circular permutation

	tggagcagcaggtggttttcagcatgagttttgtacagggcgaagagagtaatgacaagatacctgtggc tctaggactcaaggaaaagaatttgtatctcagctgcgtcctgaaggacgataaacctactcttcagttgga gtccgtcgatccgaaa **(SEQ ID NO: 72)**	
scIL-12	atctgggagctcaaaaaggatgtttatgtggtcgaacttgactggtacccggacgcaccaggggagatg gtggtgttgacctgcgacacccccgaagaggacgggattacatggactttggaccagtccagtgaagtc ctgggctcgggaaagaccctgactatccaggtgaaggagttcggagatgctggacaatatacatgccac aagggcggggaagttttgagccattccctcctgctgctgcataaaaaagaggatggtatttggagcactg atattctgaaagaccagaaggaacccaagaacaaaacttttctgcggtgtgaggccaagaattacagtgg aagattcacctgttggtggttaaccacaatctctaccgatcttacctttccgtcaaatcaagtcgcggcagc agcgatccacagggcgtgacgtgcggcgctgccacactaagcgcggagagagtgcggggtgacaac aaggaatacgagtactccgttgagtgtcaagaagactctgcatgccctgccgcagaggaatcattaccga tcgaagtaatggtggatgctgttcacaaactgaagtatgaaaactacacttcttcatttttcataagggacatt atcaagcctgatcctccaaagaacctccaacttaaaccactcaagaatagccgtcaggtagaggtgtcct gggagtaccccgatacctggtcaacgccccactcatatttctccctgacgttctgtgtgcaggtgcaggg gaaatccaagagggagaagaaagacagggtctttacagataagacatctgccactgtcatctgcagaaa aaatgcctctatatccgtgcgagcccaggaccgctactattctagtagctggagcgagtgggctagtgta ccttgttcgggctcaaccagcggatccgggaaacccggttctggcgaggggagtacaaagggacgaa atctgccagtggctacccccgacccgggcatgtttccctgcctccatcatagccagaatctgctcagagc ggtcagcaacatgctacagaaggcccgccagaccttagagttttacccttgcacctctgaggaaatcgat cacgaagacatcaccaaagataagactagcaccgttgaagcctgtctcccattggaacttacaaaaaatg aatcttgtctgaattccagagagacatcttttatcactaatggaagttgcctcgccagtcggaaaacttccttc atgatggccctgtgtctgagttcaatctacgaggatcttaagatgtatcaagtggaattcaaaacgatgaac gcaaaactgttgatggatcctaagaggcagatattttggatcagaacatgttagctgtgatcgacgagctg atgcaagcactcaacttcaactcagagacagtcccccagaagtcctccctggaggagcctgacttctaca agacgaaaattaagctatgcattctgcttcacgcattcaggatacgggccgtaacaattgaccgtgtgatg agctatctgaacgcttcg **(SEQ ID NO: 73)**	Single Chain; p40-linker-p35, Lee et al 2001
cpIL-4 (38-37)	Aatacgactgagaaagagacctttgtagggctgccacagtcctgcggcagttctatagtcaccatgaga aagacaccagatgtctgggggcaaccgctcagcaattccatagacacaagcagttaatccgatttctgaa gcggcttgatcgtaacttgtggggactagccggcctgaactcatgccccgtgaaagaagcgaatcagtc cactcttgagaacttcctcgaaaggctcaagacaattatgcgcgaaaagtacagcaagtgcagctctggc ggaaacggtgggcacaagtgtgatattacgctccaagaaatcatcaagactctgaactccctgaccgag cagaaaacactttgcactgagttgacagtgaccgacatattcgccgctagcaaa **(SEQ ID NO: 74)**	Circular permutation; Kreitman et al 1994
mIL-10	Tcgcctggccagggaacgcagagtgaaaatagctgtacccactttcccggcaacctaccaaatatgctc agagatctgcgggatgcattctccccgggtgaagacatttttccaaatgaaggatcagttggacaaccttct gttgaaggagtcactcttagaggacttcaagggatacctggggtgccaagccctgtctgagatgattcagt tctacctcgaagaggtaatgccacaggccgaaaaccaggaccctgatataaaagctcatgtcaatagttt aggcgagaatctgaaaactctcaggctgcgtctgcgaagatgccaccgctttctgccctgtgagaacgg gggagggtctggtggcaaaagcaaagctgtggagcaagttaaaaatgcattcaacaaacttcaggaga agggtatttataaggcgatgtccgaatttgacatctttattaattacatcgaagcctatatgaccatgaagatc aggaac **(SEQ ID NO: 75)**	Monomeric form; Josephson et al 2000
cpIL-10 (58/57)	Ggttacttgggctgtcaggctctgagtgaaatgattcagttctatcttgaagaggttatgcctcaggcgga gaaccaagacccagacatcaaggcccatgtgaactctctcggggagaatctgaaaacactgcgactgc ggttaagacgttgccacaggttcctaccctgcgaaaataaaagcaaggccgtcgagcaagtgaaaaac gcattcaataaactccaggaaaagggaatttacaaggccatgtccgagtttgatatctttataaactatattg aggcttacatgaccatgaagatccgcaatggtggtggtggaagcggcgggggaggcagtgggggag	Circular permutation

	gcgggtcctcccctggccagggaactcagtcagaaaatagctgcacacactttccagggaatctcccca acatgttgagagatctgagggacgccttctctcgggtgaaaacctttttccaaatgaaagaccagctggac aacctccttctgaaggagagtttactagaggatttcaag **(SEQ ID NO: 76)**	
tdIL-10	Tctccgggacagggaacccagagcgaaaactcctgcactcattttcctggcaacctccccaatatgctg cgagacttgcgcgacgcattctcaagggtgaagacgttcttccagatgaaggatcaactggacaacttatt gctgaaagaatctctgctcgaggatttcaaaggatacctgggatgtcaggcactgagcgagatgatccaa ttttacctggaggaggtcatgcctcaggctgagaatcaggatcctgacatcaaggcccacgtgaacagtc ttggagagaatcttaagacccttaggctgagacttagacggtgtcaccgctttctgccctgcgaaaataaat caaaagcggtggaacaggttaagaacgcttttaataagctgcaggaaaagggcatttataaagctatgag tgaatttgacattttcattaactatatcgaggcctatatgacaatgaaaattaggaacgggggaggcggga gcgggggcggcggctcaggcggtgggggtcctctccaggtcaaggaacacaatctgagaactcctg cacacacttccccggcaatctaccaaacatgctcagagatctcagggacgcgttcagtcgagtgaaaact ttcttccagatgaaggatcagctggacaatctactgctgaaagaaagcttgcttgaggattttaaaggctat ctgggttgtcaggccttatcggagatgatccagttttacttggaggaagttatgcctcaggcagaaaacca agaccccgatatcaaggctcatgtgaattccctcggtgaaaacctaaagaccttacgcctgcgtctcaga cggtgtcatcggtttttgccatgcgagaataagtccaaagccgtagagcaggtcaagaatgccttcaataa gctccaggagaaggggatatacaaagcaatgagcgaatttgacattttcatcaactacatagaggcctac atgaccatgaagatccggaac **(SEQ ID NO: 77)**	Tandem-dimer
cpIL-13 (75/74)	Gtgagcgcgggccagtttagcagcctgcatgtgcgcgataccaaaattgaagtggcgcagtttgtgaaa gatctgctgctgcatctgaaaaaactgtttcgcgaaggccgctttaacggaggaggtggatctctgacctg cctgggcggctttgcgagcccgggcccggtgccgccgagcaccgcgctgcgcgaactgattgaagaa ctggtgaacattacccagaaccagaaagcgccgctgtgcaacggcagcatggtgtggagcattaacctg accgcgggcatgtattgcgcggcgctggaaagcctgattaacgtgagcggctgcagcgcgattgaaaa aacccagcgcatgctgagcggcttttgcccgcataaa **(SEQ ID NO: 78)**	Circular permutation

Table 8 – Sequences of Linkers and Signal Peptide

Name	Amino Acid Sequence	Codon Optimized
(G4S)3 linker	GGGGSGGGGSGGGGS **(SEQ ID NO: 171)**	Ggtggtggtggaagcggcgggggaggcagtgggggaggcgg gtcc **(SEQ ID NO: 79)**
Whitlow linker	GSTSGSGKPGSGEGSTKG **(SEQ ID NO: 172)**	Ggctcaaccagcggatccgggaaacccggttctggcgagggg agtacaaaggga **(SEQ ID NO: 80)**
Linker 26	SGGGSGGGGSGGGGSGGGGSGGG SLQ **(SEQ ID NO: 173)**	Tctggaggcggaagcgggggtggcggcagcggcggtggagg atcaggtggcgggggtccgggggcggaagtctgcag **(SEQ ID NO: 81)**
CD8a signal peptide	MALPVTALLLPLALLLHAARP **(SEQ ID NO: 174)**	ATGGCCTTGCCTGTGACCGCATTACTGCT TCCACTCGCCCTGCTCCTGCACGCTGCG AGACCC **(SEQ ID NO: 82)**

Table 9 – Amino Acid Sequences of Full Fusion Proteins (all constructs designed with representative signal peptide (CD8a) and flexible linker (linker 26))

Cytokine	Receptor	Amino Acid Sequence
IFN-α2	IFNAR1	MALPVTALLLPLALLLHAARPCDLPQTHSLGSRRTLMLLAQMRKIS LFSCLKDRHDFGFPQEEFGNQFQKAETIPVLHEMIQQIFNLFSTKDSS AAWDETLLDKFYTELYQQLNDLEACVIQGVGVTETPLMKEDSILAV RKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNLQESLRSKES GGGSGGGGSGGGGSGGGGSGGGGSLQKNLKSPQKVEVDIIDDNFILR WNRSDESVGNVTFSFDYQKTGMDNWIKLSGCQNITSTKCNFSSLK LNVYEEIKLRIRAEKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDK AIVIHISPGTKDSVMWALDGLSFTYSLVIWKNSSGVEERIENIYSRHK IYKLSPETTYCLKVKAALLTSWKIGVYSPVHCIKTTVENELPPPENIE VSVQNQNYVLKWDYTYANMTFQVQWLHAFLKRNPGNHLYKWKQ IPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSEEIKFDT EIQAFLLPPVFNIRSLSDSFHIYIGAPKQSGNTPVIQDYPLIYEIIFWEN TSNAERKIIEKKTDVTVPNLKPLTVYCVKARAHTMDEKLNKSSVFS DAVCEKTKPGNTSKIWLIVGICIALFALPFVIYAAKVFLRCINYVFFPS LKPSSSIDEYFSEQPLKNLLLSTSEEQIEKCFIIENISTIATVEETNQTD EDHKKYSSQTSQDSGNYSNEDESESKTSEELQQDFV **(SEQ ID NO: 83)**
IFN-α2	IFNAR2	MALPVTALLLPLALLLHAARPCDLPQTHSLGSRRTLMLLAQMRKIS LFSCLKDRHDFGFPQEEFGNQFQKAETIPVLHEMIQQIFNLFSTKDSS AAWDETLLDKFYTELYQQLNDLEACVIQGVGVTETPLMKEDSILAV RKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNLQESLRSKES GGGSGGGGSGGGGSGGGGSGGGGSLQISYDSPDYTDESCTFKISLRN FRSILSWELKNHSIVPTHYTLLYTIMSKPEDLKVVKNCANTTRSFCD LTDEWRSTHEAYVTVLEGFSGNTTLFSCSHNFWLAIDMSFEPPEFEI VGFTNHINVMVKFPSIVEEELQFDLSLVIEEQSEGIVKKHKPEIKGN MSGNFTYIIDKLIPNTNYCVSVYLEHSDEQAVIKSPLKCTLLPPGQES ESAESAKIGGIITVFLIALVLTSTIVTLKWIGYICLRNSLPKVLNFHNF LAWPFPNLPPLEAMDMVEVIYINRKKKVWDYNYDDESDSDTEAAP RTSGGGYTMHGLTVRPLGQASATSTESQLIDPESEEEPDLPEVDVEL PTMPKDSPQQLELLSGPCERRKSPLQDPFPEEDYSSTEGSGGRITFN VDLNSVFLRVLDDEDSDDLEAPLMLSSHLEEMVDPEDPDNVQSNH LLASGEGTQPTFPSPSSEGLWSEDAPSDQSDTSESDVDLGDGYIMR **(SEQ ID NO: 84)**
IFN-β	IFNAR1	MALPVTALLLPLALLLHAARPMSYNLLGFLQRSSNFQCQKLLWQL NGRLEYCLKDRMNFDIPEEIKQLQQFQKEDAALTIYEMLQNIFAIFR QDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLM SSLHLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYL RNSGGGSGGGGSGGGGSGGGGSGGGSLQKNLKSPQKVEVDIIDDN FILRWNRSDESVGNVTFSFDYQKTGMDNWIKLSGCQNITSTKCNFS SLKLNVYEEIKLRIRAEKENTSSWYEVDSFTPFRKAQIGPPEVHLEA EDKAIVIHISPGTKDSVMWALDGLSFTYSLVIWKNSSGVEERIENIYS RHKIYKLSPETTYCLKVKAALLTSWKIGVYSPVHCIKTTVENELPPP

		ENIEVSVQNQNYVLKWDYTYANMTFQVQWLHAFLKRNPGNHLYK WKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSEEI KFDTEIQAFLLPPVFNIRSLSDSFHIYIGAPKQSGNTPVIQDYPLIYEII FWENTSNAERKIIEKKTDVTVPNLKPLTVYCVKARAHTMDEKLNK SSVFSDAVCEKTKPGNTSKIWLIVGICIALFALPFVIYAAKVFLRCINY VFFPSLKPSSSIDEYFSEQPLKNLLLSTSEEQIEKCFIIENISTIATVEET NQTDEDHKKYSSQTSQDSGNYSNEDESESKTSEELQQDFV **(SEQ ID NO: 85)**
IFN-β	IFNAR2	MALPVTALLLPLALLLHAARPMSYNLLGFLQRSSNFQCQKLLWQL NGRLEYCLKDRMNFDIPEEIKQLQQFQKEDAALTIYEMLQNIFAIFR QDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLM SSLHLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYL RNSGGGSGGGGSGGGGSGGGGSGGGSLQISYDSPDYTDESCTFKIS LRNFRSILSWELKNHSIVPTHYTLLYTIMSKPEDLKVVKNCANTTRS FCDLTDEWRSTHEAYVTVLEGFSGNTTLFSCSHNFWLAIDMSFEPPE FEIVGFTNHINVMVKFPSIVEEELQFDLSLVIEEQSEGIVKKHKPEIKG NMSGNFTYIIDKLIPNTNYCVSVYLEHSDEQAVIKSPLKCTLLPPGQE SESAESAKIGGIITVFLIALVLTSTIVTLKWIGYICLRNSLPKVLNFHN FLAWPFPNLPPLEAMDMVEVIYINRKKKVWDYNYDDESDSDTEAA PRTSGGGYTMHGLTVRPLGQASATSTESQLIDPESEEEPDLPEVDVE LPTMPKDSPQQLELLSGPCERRKSPLQDPFPEEDYSSTEGSGGRITFN VDLNSVFLRVLDDEDSDDLEAPLMLSSHLEEMVDPEDPDNVQSNH LLASGEGTQPTFPSPSSEGLWSEDAPSDQSDTSESDVDLGDGYIMR **(SEQ ID NO: 86)**
IFN-γ	IFNGR1	MALPVTALLLPLALLLHAARPQDPYVKEAENLKKYFNAGHSDVAD NGTLFLGILKNWKEESDRKIMQSQIVSFYFKLFKNFKDDQSIQKSVE TIKEDMNVKFFNSNKKKRDDFEKLTNYSVTDLNVQRKAIHELIQV MAELSPAAKTGKRKRSQMLFRGSGGGSGGGGSGGGGSGGGGSGG GSLQEMGTADLGPSSVPTPTNVTIESYNMNPIVYWEYQIMPQVPVF TVEVKNYGVKNSEWIDACINISHHYCNISDHVGDPSNSLWVRVKA RVGQKESAYAKSEEFAVCRDGKIGPPKLDIRKEEKQIMIDIFHPSVFV NGDEQEVDYDPETTCYIRVYNVYVRMNGSEIQYKILTQKEDDCDEI QCQLAIPVSSLNSQYCVSAEGVLHVWGVTTEKSKEVCITIFNSSIKG SLWIPVVAALLLFLVLSLVFICFYIKKINPLKEKSIILPKSLISVVRSAT LETKPESKYVSLITSYQPFSLEKEVVCEEPLSPATVPGMHTEDNPGK VEHTEELSSITEVVTTEENIPDVVPGSHLTPIERESSSPLSSNQSEPGSI ALNSYHSRNCSESDHSRNGFDTDSSCLESHSSLSDSEFPPNNKGEIK TEGQELITVIKAPTSFGYDKPHVLVDLLVDDSGKESLIGYRPTEDSK EFS **(SEQ ID NO: 87)**
IFN-γ	IFNGR2	MALPVTALLLPLALLLHAARPQDPYVKEAENLKKYFNAGHSDVAD NGTLFLGILKNWKEESDRKIMQSQIVSFYFKLFKNFKDDQSIQKSVE TIKEDMNVKFFNSNKKKRDDFEKLTNYSVTDLNVQRKAIHELIQV MAELSPAAKTGKRKRSQMLFRGSGGGSGGGGSGGGGSGGGGSGG GSLQAPPDPLSQLPAPQHPKIRLYNAEQVLSWEPVALSNSTRPVVYQ VQFKYTDSKWFTADIMSIGVNCTQITATECDFTAASPSAGFPMDFN VTLRLRAELGALHSAWVTMPWFQHYRNVTVGPPENIEVTPGEGSLI

		IRFSSPFDIADTSTAFFCYYVHYWEKGGIQQVKGPFRSNSISLDNLKP SRVYCLQVQAQLLWNKSNIFRVGHLSNISCYETMADASTELQQVILI SVGTFSLLSVLAGACFFLVLKYRGLIKYWFHTPPSIPLQIEEYLKDPT QPILEALDKDSSPKDDVWDSVSIISFPEKEQEDVLQTL **(SEQ ID NO: 88)**
scIFN-γ	IFNGR1	MALPVTALLLPLALLLHAARPQDPYVKEAENLKKYFNAGHSDVAD NGTLFLGILKNWKEESDRKIMQSQIVSFYFKLFKNFKDDQSIQKSVE TIKEDMNVKFFNSNKKKRDDFEKLTNYSVTDLNVQRKAIHELIQV MAELGANVSGEFVKEAENLKKYFNAGHSDVADNGTLFLGILKNW KEESDRKIMQSQIVSFYFKLFKNFKDDQSIQKSVETIKEDMNVKFFN SNKKKRDDFEKLTNYSVTDLNVQRKAIHELIQVMAELSPAAKTGK RKRSQMLFRGSGGGSGGGGSGGGGSGGGGSGGGSLQEMGTADLG PSSVPTPTNVTIESYNMNPIVYWEYQIMPQVPVFTVEVKNYGVKNS EWIDACINISHHYCNISDHVGDPSNSLWVRVKARVGQKESAYAKSE EFAVCRDGKIGPPKLDIRKEEKQIMIDIFHPSVFVNGDEQEVDYDPE TTCYIRVYNVYVRMNGSEIQYKILTQKEDDCDEIQCQLAIPVSSLNS QYCVSAEGVLHVWGVTTEKSKEVCITIFNSSIKGSLWIPVVAALLLF LVLSLVFICFYIKKINPLKEKSIILPKSLISVVRSATLETKPESKYVSLIT SYQPFSLEKEVVCEEPLSPATVPGMHTEDNPGKVEHTEELSSITEVV TTEENIPDVVPGSHLTPIERESSSPLSSNQSEPGSIALNSYHSRNCSES DHSRNGFDTDSSCLESHSSLSDSEFPPNNKGEIKTEGQELITVIKAPT SFGYDKPHVLVDLLVDDSGKESLIGYRPTEDSKEFS **(SEQ ID NO: 89)**
scIFN-γ	IFNGR2	MALPVTALLLPLALLLHAARPQDPYVKEAENLKKYFNAGHSDVAD NGTLFLGILKNWKEESDRKIMQSQIVSFYFKLFKNFKDDQSIQKSVE TIKEDMNVKFFNSNKKKRDDFEKLTNYSVTDLNVQRKAIHELIQV MAELGANVSGEFVKEAENLKKYFNAGHSDVADNGTLFLGILKNW KEESDRKIMQSQIVSFYFKLFKNFKDDQSIQKSVETIKEDMNVKFFN SNKKKRDDFEKLTNYSVTDLNVQRKAIHELIQVMAELSPAAKTGK RKRSQMLFRGSGGGSGGGGSGGGGSGGGGSGGGSLQAPPDPLSQL PAPQHPKIRLYNAEQVLSWEPVALSNSTRPVVYQVQFKYTDSKWFT ADIMSIGVNCTQITATECDFTAASPSAGFPMDFNVTLRLRAELGALH SAWVTMPWFQHYRNVTVGPPENIEVTPGEGSLIIRFSSPFDIADTST AFFCYYVHYWEKGGIQQVKGPFRSNSISLDNLKPSRVYCLQVQAQ LLWNKSNIFRVGHLSNISCYETMADASTELQQVILISVGTFSLLSVL AGACFFLVLKYRGLIKYWFHTPPSIPLQIEEYLKDPTQPILEALDKDS SPKDDVWDSVSIISFPEKEQEDVLQTL **(SEQ ID NO: 90)**
TNF-α	TNFR1	MALPVTALLLPLALLLHAARPVRSSSRTPSDKPVAHVVANPQAEGQ LQWLNRRANALLANGVELRDNQLVVPSEGLYLIYSQVLFKGQGCP STHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPI YLGGVFQLEKGDRLSAEINRPDYLDFAESGQVYFGIIALSGGGSGG GGSGGGGSGGGGSGGGSLQLVPHLGDREKRDSVCPQGKYIHPQNN SICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLS CSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNC SLCLNGTVHLSCQEKQNTVCTCHAGFFLRENECVSCSNCKKSLECT KLCLPQIENVKGTEDSGTTVLLPLVIFFGLCLLSLLFIGLMYRYQRW

		KSKLYSIVCGKSTPEKEGELEGTTTKPLAPNPSFSPTPGFTPTLGFSP VPSSTFTSSSTYTPGDCPNFAAPRREVAPPYQGADPILATALASDPIP NPLQKWEDSAHKPQSLDTDDPATLYAVVENVPPLRWKEFVRRLGLS DHEIDRLELQNGRCLREAQYSMLATWRRRTPRREATLELLGRVLRD MDLLGCLEDIEEALCGPAALPPAPSLLR **(SEQ ID NO: 91)**
TNF-α	TNFR2	MALPVTALLLPLALLLHAARPVRSSSRTPSDKPVAHVVANPQAEGQ LQWLNRRANALLANGVELRDNQLVVPSEGLYLIYSQVLFKGQGCP STHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPI YLGGVFQLEKGDRLSAEINRPDYLDFAESGQVYFGIIALSGGGSGG GGSGGGGSGGGGSGGGSLQLPAQVAFTPYAPEPGSTCRLREYYDQT AQMCCSKCSPGQHAKVFCTKTSDTVCDSCEDSTYTQLWNWVPECL SCGSRCSSDQVETQACTREQNRICTCRPGWYCALSKQEGCRLCAPL RKCRPGFGVARPGTETSDVVCKPCAPGTFSNTTSSTDICRPHQICNV VAIPGNASMDAVCTSTSPTRSMAPGAVHLPQPVSTRSQHTQPTPEPS TAPSTSFLLPMGPSPPAEGSTGDFALPVGLIVGVTALGLLIIGVVNCVI MTQVKKKPLCLQREAKVPHLPADKARGTQGPEQQHLLITAPSSSSS SLESSASALDRRAPTRNQPQAPGVEASGAGEARASTGSSDSSPGGH GTQVNVTCIVNVCSSSDHSSQCSSQASSTMGDTDSSPSESPKDEQVP FSKEECAFRSQLETPETLLGSTEEKPLPLGVPDAGMKPS **(SEQ ID NO: 92)**
IL-1β	IL-1R1	MALPVTALLLPLALLLHAARPAPVRSLNCTLRDSQQKSLVMSGPYE LKALHLQGQDMEQQVVFSMSFVQGEESNDKIPVALGLKEKNLYLS CVLKDDKPTLQLESVDPKNYPKKKMEKRFVFNKIEINNKLEFESAQ FPNWYISTSQAENMPVFLGGTKGGQDITDFTMQFVSSSGGGSGGG GSGGGGSGGGGSGGGGSLQLEADKCKEREEKIILVSSANEIDVRPCPL NPNEHKGTITWYKDDSKTPVSTEQASRIHQHKEKLWFVPAKVEDS GHYYCVVRNSSYCLRIKISAKFVENEPNLCYNAQAIFKQKLPVAGD GGLVCPYMEFFKNENNELPKLQWYKDCKPLLLDNIHFSGVKDRLIV MNVAEKHRGNYTCHASYTYLGKQYPITRVIEFITLEENKPTRPVIVS PANETMEVDLGSQIQLICNVTGQLSDIAYWKWNGSVIDEDDPVLGE DYYSVENPANKRRSTLITVLNISEIESRFYKHPFTCFAKNTHGIDAAY IQLIYPVTNFQKHMIGICVTLTVIIVCSVFIYKIFKIDIVLWYRDSCYD FLPIKASDGKTYDAYILYPKTVGEGSTSDCDIFVFKVLPEVLEKQCG YKLFIYGRDDYVGEDIVEVINENVKKSRRLIIILVRETSGFSWLGGSS EEQIAMYNALVQDGIKVVLLELEKIQDYEKMPESIKFIKQKHGAIR WSGDFTQGPQSAKTRFWKNVRYHMPVQRRSPSSKHQLLSPATKEK LQREAHVPLG **(SEQ ID NO: 93)**
IL-1β	IL-1R3	MALPVTALLLPLALLLHAARPAPVRSLNCTLRDSQQKSLVMSGPYE LKALHLQGQDMEQQVVFSMSFVQGEESNDKIPVALGLKEKNLYLS CVLKDDKPTLQLESVDPKNYPKKKMEKRFVFNKIEINNKLEFESAQ FPNWYISTSQAENMPVFLGGTKGGQDITDFTMQFVSSSGGGSGGG GSGGGGSGGGGSGGGGSLQSERCDDWGLDTMRQIQVFEDEPARIKC PLFEHFLKFNYSTAHSAGLTLIWYWTRQDRDLEEPINFRLPENRISKE KDVLWFRPTLLNDTGNYTCMLRNTTYCSKVAFPLEVVQKDSCFNS PMKLPVHKLYIEYGIQRITCPNVDGYFPSSVKPTITWYMGCYKIQNF NNVIPEGMNLSFLIALISNNGNYTCVVTYPENGRTFHLTRTLTVKVV

		GSPKNAVPPVIHSPNDHVVYEKEPGEELLIPCTVYFSFLMDSRNEVW WTIDGKKPDDITIDVTINESISHSRTEDETRTQILSIKKVTSEDLKRSY VCHARSAKGEVAKAAKVKQKVPAPRYTVELACGFGATVLLVVILIV VYHVYWLEMVLFYRAHFGTDETILDGKEYDIYVSYARNAEEEEFV LLTLRGVLENEFGYKLCIFDRDSLPGGIVTDETLSFIQKSRRLLVVLS PNYVLQGTQALLELKAGLENMASRGNINVILVQYKAVKETKVKEL KRAKTVLTVIKWKGEKSKYPQGRFWKQLQVAMPVKKSPRRSSSDE QGLSYSSLKNV **(SEQ ID NO: 94)**
cpIL-1β (89/88)	IL-1R1	MALPVTALLLPLALLLHAARPNYPKKKMEKRFVFNKIEINNKLEFE SAQFPNWYISTSQAENMPVFLGGTKGGQDITDFTMQFVSSGGGGS GGGGSGGGGSAPVRSLNCTLRDSQQKSLVMSGPYELKALHLQGQD MEQQVVFSMSFVQGEESNDKIPVALGLKEKNLYLSCVLKDDKPTLQ LESVDPKSGGGSGGGGSGGGGSGGGGSGGGGSLQLEADKCKEREEK IILVSSANEIDVRPCPLNPNEHKGTITWYKDDSKTPVSTEQASRIHQH KEKLWFVPAKVEDSGHYYCVVRNSSYCLRIKISAKFVENEPNLCYN AQAIFKQKLPVAGDGGLVCPYMEFFKNENNELPKLQWYKDCKPLL LDNIHFSGVKDRLIVMNVAEKHRGNYTCHASYTYLGKQYPITRVIE FITLEENKPTRPVIVSPANETMEVDLGSQIQLICNVTGQLSDIAYWK WNGSVIDEDDPVLGEDYYSVENPANKRRSTLITVLNISEIESRFYKH PFTCFAKNTHGIDAAYIQLIYPVTNFQKHMIGICVTLTVIIVCSVFIYK IFKIDIVLWYRDSCYDFLPIKASDGKTYDAYILYPKTVGEGSTSDCDI FVFKVLPEVLEKQCGYKLFIYGRDDYVGEDIVEVINENVKKSRRLIII LVRETSGFSWLGGSSEEQIAMYNALVQDGIKVVLLELEKIQDYEKM PESIKFIKQKHGAIRWSGDFTQGPQSAKTRFWKNVRYHMPVQRRSP SSKHQLLSPATKEKLQREAHVPLG **(SEQ ID NO: 95)**
cpIL-1β (89/88)	IL-1R3	MALPVTALLLPLALLLHAARPNYPKKKMEKRFVFNKIEINNKLEFE SAQFPNWYISTSQAENMPVFLGGTKGGQDITDFTMQFVSSGGGGS GGGGSGGGGSAPVRSLNCTLRDSQQKSLVMSGPYELKALHLQGQD MEQQVVFSMSFVQGEESNDKIPVALGLKEKNLYLSCVLKDDKPTLQ LESVDPKSGGGSGGGGSGGGGSGGGGSGGGGSLQSERCDDWGLDT MRQIQVFEDEPARIKCPLFEHFLKFNYSTAHSAGLTLIWYWTRQDR DLEEPINFRLPENRISKEKDVLWFRPTLLNDTGNYTCMLRNTTYCSK VAFPLEVVQKDSCFNSPMKLPVHKLYIEYGIQRITCPNVDGYFPSSV KPTITWYMGCYKIQNFNNVIPEGMNLSFLIALISNNGNYTCVVTYPE NGRTFHLTRTLTVKVVGSPKNAVPPVIHSPNDHVVYEKEPGEELLIP CTVYFSFLMDSRNEVWWTIDGKKPDDITIDVTINESISHSRTEDETRT QILSIKKVTSEDLKRSYVCHARSAKGEVAKAAKVKQKVPAPRYTVE LACGFGATVLLVVILIVVYHVYWLEMVLFYRAHFGTDETILDGKEY DIYVSYARNAEEEEFVLLTLRGVLENEFGYKLCIFDRDSLPGGIVTD ETLSFIQKSRRLLVVLSPNYVLQGTQALLELKAGLENMASRGNINVI LVQYKAVKETKVKELKRAKTVLTVIKWKGEKSKYPQGRFWKQLQ VAMPVKKSPRRSSSDEQGLSYSSLKNV **(SEQ ID NO: 96)**
IL-6	IL-6Rα	MALPVTALLLPLALLLHAARPVPPGEDSKDVAAPHRQPLTSSERIDK QIRYILDGISALRKETCNKSNMCESSKEALAENNLNLPKMAEKDGC FQSGFNEETCLVKIITGLLEFEVYLEYLQNRFESSEEQARAVQMSTK VLIQFLQKKAKNLDAITTPDPTTNASLLTKLQAQNQWLQDMTTHLI

		LRSFKEFLQSSLRALRQMSGGGSGGGGSGGGGSGGGGSGGGSLQL APRRCPAQEVARGVLTSLPGDSVTLTCPGVEPEDNATVHWVLRKPA AGSHPSRWAGMGRRLLLRSVQLHDSGNYSCYRAGRPAGTVHLLVD VPPEEPQLSCFRKSPLSNVVCEWGPRSTPSLTTKAVLLVRKFQNSPA EDFQEPCQYSQESQKFSCQLAVPEGDSSFYIVSMCVASSVGSKFSKT QTFQGCGILQPDPPANITVTAVARNPRWLSVTWQDPHSWNSSFYRL RFELRYRAERSKTFTTWMVKDLQHHCVIHDAWSGLRHVVQLRAQ EEFGQGEWSEWSPEAMGTPWTESRSPPAENEVSTPMQALTTNKDD DNILFRDSANATSLPVQDSSSVPLPTFLVAGGSLAFGTLLCIAIVLRF KKTWKLRALKEGKTSMHPPYSLGQLVPERPRPTPVLVPLISPPVSPS SLGSDNTSSHNRPDARDPRSPYDISNTDYFFPR **(SEQ ID NO: 97)**
IL-6	gp130	MALPVTALLLPLALLLHAARPVPPGEDSKDVAAPHRQPLTSSERIDK QIRYILDGISALRKETCNKSNMCESSKEALAENNLNLPKMAEKDGC FQSGFNEETCLVKIITGLLEFEVYLEYLQNRFESSEEQARAVQMSTK VLIQFLQKKAKNLDAITTPDPTTNASLLTKLQAQNQWLQDMTTHLI LRSFKEFLQSSLRALRQMSGGGSGGGGSGGGGSGGGGSGGGSLQE LLDPCGYISPESPVVQLHSNFTAVCVLKEKCMDYFHVNANYIVWKT NHFTIPKEQYTIINRTASSVTFTDIASLNIQLTCNILTFGQLEQNVYGIT IISGLPPEKPKNLSCIVNEGKKMRCEWDGGRETHLETNFTLKSEWAT HKFADCKAKRDTPTSCTVDYSTVYFVNIEVWVEAENALGKVTSDH INFDPVYKVKPNPPHNLSVINSEELSSILKLTWTNPSIKSVIILKYNIQ YRTKDASTWSQIPPEDTASTRSSFTVQDLKPFTEYVFRIRCMKEDGK GYWSDWSEEASGITYEDRPSKAPSFWYKIDPSHTQGYRTVQLVWK TLPPFEANGKILDYEVTLTRWKSHLQNYTVNATKLTVNLTNDRYLA TLTVRNLVGKSDAAVLTIPACDFQATHPVMDLKAFPKDNMLWVEW TTPRESVKKYILEWCVLSDKAPCITDWQQEDGTVHRTYLRGNLAES KCYLITVTPVYADGPGSPESIKAYLKQAPPSKGPTVRTKKVGKNEAV LEWDQLPVDVQNGFIRNYTIFYRTIIGNETAVNVDSSHTEYTLSSLTS DTLYMVRMAAYTDEGGKDGPEFTFTTPKFAQGEIEAIVVPVCLAFL LTTLLGVLFCFNKRDLIKKHIWPNVPDPSKSHIAQWSPHTPPRHNFN SKDQMYSDGNFTDVSVVEIEANDKKPFPEDLKSLDLFKKEKINTEG HSSGIGGSSCMSSSRPSISSSDENESSQNTSSTVQYSTVVHSGYRHQ VPSVQVFSRSESTQPLLDSEERPEDLQLVDHVDGGDGILPRQQYFK QNCSQHESSPDISHFERSKQVSSVNEEDFVRLKQQISDHISQSCGSG QMKMFQEVSAADAFGPGTEGQVERFETVGMEAATDEGMPKSYLP QTVRQGGYMPQ **(SEQ ID NO: 98)**
scIL-12	IL-12-Rβ1	MALPVTALLLPLALLLHAARPIWELKKDVYVVELDWYPDAPGEM VVLTCDTPEEDGITWTLDQSSEVLGSGKTLTIQVKEFGDAGQYTCH KGGEVLSHSLLLLHKKEDGIWSTDILKDQKEPKNKTFLRCEAKNYS GRFTCWWLTTISTDLTFSVKSSRGSSDPQGVTCGAATLSAERVRGD NKEYEYSVECQEDSACPAAEESLPIEVMVDAVHKLKYENYTSSFFIR DIIKPDPPKNLQLKPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCVQV QGKSKREKKDRVFTDKTSATVICRKNASISVRAQDRYYSSSWSEWA SVPCSGSTSGSGKPGSGEGSTKGRNLPVATPDPGMFPCLHHSQNLLR AVSNMLQKARQTLEFYPCTSEEIDHEDITKDKTSTVEACLPLELTKN ESCLNSRETSFITNGSCLASRKTSFMMALCLSSIYEDLKMYQVEFKT

		MNAKLLMDPKRQIFLDQNMLAVIDELMQALNFNSETVPQKSSLEEP DFYKTKIKLCILLHAFRIRAVTIDRVMSYLNASSGGGSGGGGSGGGG SGGGGSGGGSLQCRTSECCFQDPPYPDADSGSASGPRDLRCYRISSD RYECSWQYEGPTAGVSHFLRCCLSSGRCCYFAAGSATRLQFSDQAG VSVLYTVTLWVESWARNQTEKSPEVTLQLYNSVKYEPPLGDIKVSK LAGQLRMEWETPDNQVGAEVQFRHRTPSSPWKLGDCGPQDDDTE SCLCPLEMNVAQEFQLRRRQLGSQGSSWSKWSSPVCVPPENPPQPQ VRFSVEQLGQDGRRRLTLKEQPTQLELPEGCQGLAPGTEVTYRLQL HMLSCPCKAKATRTLHLGKMPYLSGAAYNVAVISSNQFGPGLNQT WHIPADTHTEPVALNISVGTNGTTMYWPARAQSMTYCIEWQPVGQ DGGLATCSLTAPQDPDPAGMATYSWSRESGAMGQEKCYYITIFASA HPEKLTLWSTVLSTYHFGGNASAAGTPHHVSVKNHSLDSVSVDWA PSLLSTCPGVLKEYVVRCRDEDSKQVSEHPVQPTETQVTLSGLRAG VAYTVQVRADTAWLRGVWSQPQRFSIEVQVSDWLIFFASLGSFLSIL LVGVLGYLGLNRAARHLCPPLPTPCASSAIEFPGGKETWQWINPVD FQEEASLQEALVVEMSWDKGERTEPLEKTELPEGAPELALDTELSL EDGDRCKAKM **(SEQ ID NO: 99)**
scIL-12	IL-12-Rβ2	MALPVTALLLPLALLLHAARPIWELKKDVYVVELDWYPDAPGEM VVLTCDTPEEDGITWTLDQSSEVLGSGKTLTIQVKEFGDAGQYTCH KGGEVLSHSLLLLHKKEDGIWSTDILKDQKEPKNKTFLRCEAKNYS GRFTCWWLTTISTDLTFSVKSSRGSSDPQGVTCGAATLSAERVRGD NKEYEYSVECQEDSACPAAEESLPIEVMVDAVHKLKYENYTSSFFIR DIIKPDPPKNLQLKPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCVQV QGKSKREKKDRVFTDKTSATVICRKNASISVRAQDRYYSSSWSEWA SVPCSGSTSGSGKPGSGEGSTKGRNLPVATPDPGMFPCLHHSQNLLR AVSNMLQKARQTLEFYPCTSEEIDHEDITKDKTSTVEACLPLELTKN ESCLNSRETSFITNGSCLASRKTSFMMALCLSSIYEDLKMYQVEFKT MNAKLLMDPKRQIFLDQNMLAVIDELMQALNFNSETVPQKSSLEEP DFYKTKIKLCILLHAFRIRAVTIDRVMSYLNASSGGGSGGGGSGGGG SGGGGSGGGSLQKIDACKRGDVTVKPSHVILLGSTVNITCSLKPRQ GCFHYSRRNKLILYKFDRRINFHHGHSLNSQVTGLPLGTTLFVCKLA CINSDEIQICGAEIFVGVAPEQPQNLSCIQKGEQGTVACTWERGRDT HLYTEYTLQLSGPKNLTWQKQCKDIYCDYLDFGINLTPESPESNFTA KVTAVNSLGSSSSLPSTFTFLDIVRPLPPWDIRIKFQKASVSRCTLYW RDEGLVLLNRLRYRPSNSRLWNMVNVTKAKGRHDLLDLKPFTEYE FQISSKLHLYKGSWSDWSESLRAQTPEEEPTGMLDVWYMKRHIDY SRQQISLFWKNLSVSEARGKILHYQVTLQELTGGKAMTQNITGHTS WTTVIPRTGNWAVAVSAANSKGSSLPTRINIMNLCEAGLLAPRQVSA NSEGMDNILVTWQPPRKDPSAVQEYVVEWRELHPGGDTQVPLNW LRSRPYNVSALISENIKSYICYEIRVYALSGDQGGCSSILGNSKHKAP LSGPHINAITEEKGSILISWNSIPVQEQMGCLLHYRIYWKERDSNSQP QLCEIPYRVSQNSHPINSLQPRVTYVLWMTALTAAGESSHGNEREFC LQGKANWMAFVAPSICIAIIMVGIFSTHYFQQKVFVLLAALRPQWC SREIPDPANSTCAKKYPIAEEKTQLPLDRLLIDWPTPEDPEPLVISEVL HQVTPVFRHPPCSNWPQREKGIQGHQASEKDMMHSASSPPPPRAL QAESRQLVDLYKVLESRGSDPKPENPACPWTVLPAGDLPTHDGYLP

		SNIDDLPSHEAPLADSLEELEPQHISLSVFPSSSLHPLTFSCGDKLTLD QLKMRCDSLML **(SEQ ID NO: 100)**
IL-4	IL-4Rα	MALPVTALLLPLALLLHAARPHKCDITLQEIIKTLNSLTEQKTLCTEL TVTDIFAASKNTTEKETFCRAATVLRQFYSHHEKDTRCLGATAQQF HRHKQLIRFLKRLDRNLWGLAGLNSCPVKEANQSTLENFLERLKTI MREKYSKCSSSGGGSGGGGSGGGGSGGGGSGGGSLQMKVLQEPT CVSDYMSISTCEWKMNGPTNCSTELRLLYQLVFLLSEAHTCIPENN GGAGCVCHLLMDDVVSADNYTLDLWAGQQLLWKGSFKPSEHVKP RAPGNLTVHTNVSDTLLLTWSNPYPPDNYLYNHLTYAVNIWSENDP ADFRIYNVTYLEPSLRIAASTLKSGISYRARVRAWAQCYNTTWSEW SPSTKWHNSYREPFEQHLLLGVSVSCIVILAVCLLCYVSITKIKKEW WDQIPNPARSRLVAIIIQDAQGSQWEKRSRGQEPAKCPHWKNCLTK LLPCFLEHNMKRDEDPHKAAKEMPFQGSGKSAWCPVEISKTVLWP ESISVVRCVELFEAPVECEEEEEVEEEKGSFCASPESSRDDFQEGRE GIVARLTESLFLDLLGEENGGFCQQDMGESCLLPPSGSTSAHMPWD EFPSAGPKEAPPWGKEQPLHLEPSPPASPTQSPDNLTCTETPLVIAGN PAYRSFSNSLSQSPCPRELGPDPLLARHLEEVEPEMPCVPQLSEPTTV PQPEPETWEQILRRNVLQHGAAAAPVSAPTSGYQEFVHAVEQGGT QASAVVGLGPPGEAGYKAFSSLLASSAVSPEKCGFGASSGEEGYKP FQDLIPGCPGDPAPVPVPLFTFGLDREPPRSPQSSHLPSSSPEHLGLEP GEKVEDMPKPPLPQEQATDPLVDSLGSGIVYSALTCHLCGHLKQCH GQEDGGQTPVMASPCCGCCCGDRSSPPTTPLRAPDPSPGGVPLEAS LCPASLAPSGISEKSKSSSSFHPAPGNAQSSSQTPKIVNFVSVGPTYM RVS **(SEQ ID NO: 101)**
IL-4	IL-2Rγc	MALPVTALLLPLALLLHAARPHKCDITLQEIIKTLNSLTEQKTLCTEL TVTDIFAASKNTTEKETFCRAATVLRQFYSHHEKDTRCLGATAQQF HRHKQLIRFLKRLDRNLWGLAGLNSCPVKEANQSTLENFLERLKTI MREKYSKCSSSGGGSGGGGSGGGGSGGGGSGGGSLQLNTTILTPN GNEDTTADFFLTTMPTDSLSVSTLPLPEVQCFVFNVEYMNCTWNSS SEPQPTNLTLHYWYKNSDNDKVQKCSHYLFSEEITSGCQLQKKEIH LYQTFVVQLQDPREPRRQATQMLKLQNLVIPWAPENLTLHKLSESQ LELNWNNRFLNHCLEHLVQYRTDWDHSWTEQSVDYRHKFSLPSV DGQKRYTFRVRSRFNPLCGSAQHWSEWSHPIHWGSNTSKENPFLFA LEAVVISVGSMGLIISLLCVYFWLERTMPRIPTLKNLEDLVTEYHGN FSAWSGVSKGLAESLQPDYSERLCLVSEIPPKGGALGEGPGASPCNQ HSPYWAPPCYTLKPET **(SEQ ID NO: 102)**
IL-4	IL-13Ra1	MALPVTALLLPLALLLHAARPHKCDITLQEIIKTLNSLTEQKTLCTEL TVTDIFAASKNTTEKETFCRAATVLRQFYSHHEKDTRCLGATAQQF HRHKQLIRFLKRLDRNLWGLAGLNSCPVKEANQSTLENFLERLKTI MREKYSKCSSSGGGSGGGGSGGGGSGGGGSGGGSLQGGGGAAPT ETQPPVTNLSVSVENLCTVIWTWNPPEGASSNCSLWYFSHFGDKQD KKIAPETRRSIEVPLNERICLQVGSQCSTNESEKPSILVEKCISPPEGD PESAVTELQCIWHNLSYMKCSWLPGRNTSPDTNYTLYYWHRSLEKI HQCENIFREGQYFGCSFDLTKVKDSSFEQHSVQIMVKDNAGKIKPSF NIVPLTSRVKPDPPHIKNLSFHNDDLYVQWENPQNFISRCLFYEVEV NNSQTETHNVFYVQEAKCENPEFERNVENTSCFMVPGVLPDTLNT

		VRIRVKTNKLCYEDDKLWSNWSQEMSIGKKRNSTLYITMLLIVPVI VAGAIIVLLLYLKRLKIIIFPPIPDPGKIFKEMFGDQNDDTLHWKKYDI YEKQTKEETDSVVLIENLKKASQ **(SEQ ID NO: 103)**
cpIL-4 (38-37)	IL-4Rα	MALPVTALLLPLALLLHAARPNTTEKETFCRAATVLRQFYSHHEKD TRCLGATAQQFHRHKQLIRFLKRLDRNLWGLAGLNSCPVKEANQS TLENFLERLKTIMREKYSKCSSGGNGGHKCDITLQEIIKTLNSLTEQ KTLCTELTVTDIFAASKSGGGSGGGGSGGGGSGGGGSGGGSLQMK VLQEPTCVSDYMSISTCEWKMNGPTNCSTELRLLYQLVFLLSEAHT CIPENNGGAGCVCHLLMDDVVSADNYTLDLWAGQQLLWKGSFKP SEHVKPRAPGNLTVHTNVSDTLLLTWSNPYPPDNYLYNHLTYAVNI WSENDPADFRIYNVTYLEPSLRIAASTLKSGISYRARVRAWAQCYN TTWSEWSPSTKWHNSYREPFEQHLLLGVSVSCIVILAVCLLCYVSIT KIKKEWWDQIPNPARSRLVAIIIQDAQGSQWEKRSRGQEPAKCPHW KNCLTKLLPCFLEHNMKRDEDPHKAAKEMPFQGSGKSAWCPVEIS KTVLWPESISVVRCVELFEAPVECEEEEEVEEEKGSFCASPESSRDD FQEGREGIVARLTESLFLDLLGEENGGFCQQDMGESCLLPPSGSTSA HMPWDEFPSAGPKEAPPWGKEQPLHLEPSPPASPTQSPDNLTCTETP LVIAGNPAYRSFSNSLSQSPCPRELGPDPLLARHLEEVEPEMPCVPQL SEPTTVPQPEPETWEQILRRNVLQHGAAAAPVSAPTSGYQEFVHAV EQGGTQASAVVGLGPPGEAGYKAFSSLLASSAVSPEKCGFGASSGE EGYKPFQDLIPGCPGDPAPVPVPLFTFGLDREPPRSPQSSHLPSSSPE HLGLEPGEKVEDMPKPPLPQEQATDPLVDSLGSGIVYSALTCHLCG HLKQCHGQEDGGQTPVMASPCCGCCCGDRSSPPTTPLRAPDPSPG GVPLEASLCPASLAPSGISEKSKSSSSFHPAPGNAQSSSQTPKIVNFVS VGPTYMRVS **(SEQ ID NO: 104)**
cpIL-4 (38-37)	IL-2Rγc	MALPVTALLLPLALLLHAARPNTTEKETFCRAATVLRQFYSHHEKD TRCLGATAQQFHRHKQLIRFLKRLDRNLWGLAGLNSCPVKEANQS TLENFLERLKTIMREKYSKCSSGGNGGHKCDITLQEIIKTLNSLTEQ KTLCTELTVTDIFAASKSGGGSGGGGSGGGGSGGGGSGGGSLQLNT TILTPNGNEDTTADFFLTTMPTDSLSVSTLPLPEVQCFVFNVEYMNC TWNSSSEPQPTNLTLHYWYKNSDNDKVQKCSHYLFSEEITSGCQLQ KKEIHLYQTFVVQLQDPREPRRQATQMLKLQNLVIPWAPENLTLHK LSESQLELNWNNRFLNHCLEHLVQYRTDWDHSWTEQSVDYRHKF SLPSVDGQKRYTFRVRSRFNPLCGSAQHWSEWSHPIHWGSNTSKE NPFLFALEAVVISVGSMGLIISLLCVYFWLERTMPRIPTLKNLEDLVT EYHGNFSAWSGVSKGLAESLQPDYSERLCLVSEIPPKGGALGEGPG ASPCNQHSPYWAPPCYTLKPET **(SEQ ID NO: 105)**
cpIL-4 (38-37)	IL-13Ra1	MALPVTALLLPLALLLHAARPNTTEKETFCRAATVLRQFYSHHEKD TRCLGATAQQFHRHKQLIRFLKRLDRNLWGLAGLNSCPVKEANQS TLENFLERLKTIMREKYSKCSSGGNGGHKCDITLQEIIKTLNSLTEQ KTLCTELTVTDIFAASKSGGGSGGGGSGGGGSGGGGSGGGSLQGG GGAAPTETQPPVTNLSVSVENLCTVIWTWNPPEGASSNCSLWYFSH FGDKQDKKIAPETRRSIEVPLNERICLQVGSQCSTNESEKPSILVEKC ISPPEGDPESAVTELQCIWHNLSYMKCSWLPGRNTSPDTNYTLYYW HRSLEKIHQCENIFREGQYFGCSFDLTKVKDSSFEQHSVQIMVKDN AGKIKPSFNIVPLTSRVKPDPPHIKNLSFHNDDLYVQWENPQNFISRC

		LFYEVEVNNSQTETHNVFYVQEAKCENPEFERNVENTSCFMVPGV LPDTLNTVRIRVKTNKLCYEDDKLWSNWSQEMSIGKKRNSTLYITM LLIVPVIVAGAIIVLLLYLKRLKIIIFPPIPDPGKIFKEMFGDQNDDTLH WKKYDIYEKQTKEETDSVVLIENLKKASQ **(SEQ ID NO: 106)**
IL-10	IL-10R1	MALPVTALLLPLALLLHAARPSPGQGTQSENSCTHFPGNLPNMLRD LRDAFSRVKTFFQMKDQLDNLLLKESLLEDFKGYLGCQALSEMIQF YLEEVMPQAENQDPDIKAHVNSLGENLKTLRLRLRRCHRFLPCEN KSKAVEQVKNAFNKLQEKGIYKAMSEFDIFINYIEAYMTMKIRNSG GGSGGGGSGGGGSGGGGSGGGSLQHGTELPSPPSVWFEAEFFHHIL HWTPIPNQSESTCYEVALLRYGIESWNSISNCSQTLSYDLTAVTLDLY HSNGYRARVRAVDGSRHSNWTVTNTRFSVDEVTLTVGSVNLEIHN GFILGKIQLPRPKMAPANDTYESIFSHFREYEIAIRKVPGNFTFTHKK VKHENFSLLTSGEVGEFCVQVKPSVASRSNKGMWSKEECISLTRQY FTVTNVIIFFAFVLLLSGALAYCLALQLYVRRRKKLPSVLLFKKPSPF IFISQRPSPETQDTIHPLDEEAFLKVSPELKNLDLHGSTDSGFGSTKPS LQTEEPQFLLPDPHPQADRTLGNREPPVLGDSCSSGSSNSTDSGICL QEPSLSPSTGPTWEQQVGSNSRGQDDSGIDLVQNSEGRAGDTQGGS ALGHHSPPEPEVPGEEDPAAVAFQGYLRQTRCAEEKATKTGCLEEE SPLTDGLGPKFGRCLVDEAGLHPPALAKGYLKQDPLEMTLASSGAP TGQWNQPTEEWSLLALSSCSDLGISDWSFAHDLAPLGCVAAPGGLL GSFNSDLVTLPLISSLQSSE **(SEQ ID NO: 107)**
IL-10	IL-10R2	MALPVTALLLPLALLLHAARPSPGQGTQSENSCTHFPGNLPNMLRD LRDAFSRVKTFFQMKDQLDNLLLKESLLEDFKGYLGCQALSEMIQF YLEEVMPQAENQDPDIKAHVNSLGENLKTLRLRLRRCHRFLPCEN KSKAVEQVKNAFNKLQEKGIYKAMSEFDIFINYIEAYMTMKIRNSG GGSGGGGSGGGGSGGGGSGGGSLQMVPPPENVRMNSVNFKNILQ WESPAFAKGNLTFTAQYLSYRIFQDKCMNTTLTECDFSSLSKYGDH TLRVRAEFADEHSDWVNITFCPVDDTIIGPPGMQVEVLADSLHMRF LAPKIENEYETWTMKNVYNSWTYNVQYWKNGTDEKFQITPQYDF EVLRNLEPWTTYCVQVRGFLPDRNKAGEWSEPVCEQTTHDETVPS WMVAVILMASVFMVCLALLGCFALLWCVYKKTKYAFSPRNSLPQH LKEFLGHPHHNTLLFFSFPLSDENDVFDKLSVIAEDSESGKQNPGDS CSLGTPPGQGPQS **(SEQ ID NO: 108)**
mIL-10	IL-10R1	MALPVTALLLPLALLLHAARPSPGQGTQSENSCTHFPGNLPNMLRD LRDAFSRVKTFFQMKDQLDNLLLKESLLEDFKGYLGCQALSEMIQF YLEEVMPQAENQDPDIKAHVNSLGENLKTLRLRLRRCHRFLPCEN GGGSGGKSKAVEQVKNAFNKLQEKGIYKAMSEFDIFINYIEAYMT MKIRNSGGGSGGGGSGGGGSGGGGSGGGSLQHGTELPSPPSVWFE AEFFHHILHWTPIPNQSESTCYEVALLRYGIESWNSISNCSQTLSYDL TAVTLDLYHSNGYRARVRAVDGSRHSNWTVTNTRFSVDEVTLTVG SVNLEIHNGFILGKIQLPRPKMAPANDTYESIFSHFREYEIAIRKVPG NFTFTHKKVKHENFSLLTSGEVGEFCVQVKPSVASRSNKGMWSKE ECISLTRQYFTVTNVIIFFAFVLLLSGALAYCLALQLYVRRRKKLPSV LLFKKPSPFIFISQRPSPETQDTIHPLDEEAFLKVSPELKNLDLHGSTD SGFGSTKPSLQTEEPQFLLPDPHPQADRTLGNREPPVLGDSCSSGSS NSTDSGICLQEPSLSPSTGPTWEQQVGSNSRGQDDSGIDLVQNSEGR

		AGDTQGGSALGHHSPPEPEVPGEEDPAAVAFQGYLRQTRCAEEKAT KTGCLEEESPLTDGLGPKFGRCLVDEAGLHPPALAKGYLKQDPLEM TLASSGAPTGQWNQPTEEWSLLALSSCSDLGISDWSFAHDLAPLGC VAAPGGLLGSFNSDLVTLPLISSLQSSE **(SEQ ID NO: 109)**
mIL-10	IL-10R2	MALPVTALLLPLALLLHAARPSPGQGTQSENSCTHFPGNLPNMLRD LRDAFSRVKTFFQMKDQLDNLLLKESLLEDFKGYLGCQALSEMIQF YLEEVMPQAENQDPDIKAHVNSLGENLKTLRLRLRRCHRFLPCEN GGGSGGKSKAVEQVKNAFNKLQEKGIYKAMSEFDIFINYIEAYMT MKIRNSGGGSGGGGSGGGGSGGGGSGGGSLQMVPPPENVRMNSV NFKNILQWESPAFAKGNLTFTAQYLSYRIFQDKCMNTTLTECDFSSL SKYGDHTLRVRAEFADEHSDWVNITFCPVDDTIIGPPGMQVEVLAD SLHMRFLAPKIENEYETWTMKNVYNSWTYNVQYWKNGTDEKFQI TPQYDFEVLRNLEPWTTYCVQVRGFLPDRNKAGEWSEPVCEQTTH DETVPSWMVAVILMASVFMVCLALLGCFALLWCVYKKTKYAFSPR NSLPQHLKEFLGHPHHNTLLFFSFPLSDENDVFDKLSVIAEDSESGK QNPGDSCSLGTPPGQGPQS **(SEQ ID NO: 110)**
cpIL-10 (58/57)	IL-10R1	MALPVTALLLPLALLLHAARPGYLGCQALSEMIQFYLEEVMPQAE NQDPDIKAHVNSLGENLKTLRLRLRRCHRFLPCENKSKAVEQVKN AFNKLQEKGIYKAMSEFDIFINYIEAYMTMKIRNGGGGSGGGGSGG GGSSPGQGTQSENSCTHFPGNLPNMLRDLRDAFSRVKTFFQMKDQ LDNLLLKESLLEDFKSGGGSGGGGSGGGGSGGGGSGGGSLQHGTE LPSPPSVWFEAEFFHHILHWTPIPNQSESTCYEVALLRYGIESWNSIS NCSQTLSYDLTAVTLDLYHSNGYRARVRAVDGSRHSNWTVTNTRFS VDEVTLTVGSVNLEIHNGFILGKIQLPRPKMAPANDTYESIFSHFRE YEIAIRKVPGNFTFTHKKVKHENFSLLTSGEVGEFCVQVKPSVASRS NKGMWSKEECISLTRQYFTVTNVIIFFAFVLLLSGALAYCLALQLYV RRRKKLPSVLLFKKPSPFIFISQRPSPETQDTIHPLDEEAFLKVSPELK NLDLHGSTDSGFGSTKPSLQTEEPQFLLPDPHPQADRTLGNREPPVL GDSCSSGSSNSTDSGICLQEPSLSPSTGPTWEQQVGSNSRGQDDSGI DLVQNSEGRAGDTQGGSALGHHSPPEPEVPGEEDPAAVAFQGYLRQ TRCAEEKATKTGCLEEESPLTDGLGPKFGRCLVDEAGLHPPALAKG YLKQDPLEMTLASSGAPTGQWNQPTEEWSLLALSSCSDLGISDWSF AHDLAPLGCVAAPGGLLGSFNSDLVTLPLISSLQSSE **(SEQ ID NO: 111)**
cpIL-10 (58/57)	IL-10R2	MALPVTALLLPLALLLHAARPGYLGCQALSEMIQFYLEEVMPQAE NQDPDIKAHVNSLGENLKTLRLRLRRCHRFLPCENKSKAVEQVKN AFNKLQEKGIYKAMSEFDIFINYIEAYMTMKIRNGGGGSGGGGSGG GGSSPGQGTQSENSCTHFPGNLPNMLRDLRDAFSRVKTFFQMKDQ LDNLLLKESLLEDFKSGGGSGGGGSGGGGSGGGGSGGGSLQMVPP PENVRMNSVNFKNILQWESPAFAKGNLTFTAQYLSYRIFQDKCMNT TLTECDFSSLSKYGDHTLRVRAEFADEHSDWVNITFCPVDDTIIGPP GMQVEVLADSLHMRFLAPKIENEYETWTMKNVYNSWTYNVQYW KNGTDEKFQITPQYDFEVLRNLEPWTTYCVQVRGFLPDRNKAGEW SEPVCEQTTHDETVPSWMVAVILMASVFMVCLALLGCFALLWCVY KKTKYAFSPRNSLPQHLKEFLGHPHHNTLLFFSFPLSDENDVFDKLS VIAEDSESGKQNPGDSCSLGTPPGQGPQS **(SEQ ID NO: 112)**

tdIL-10	IL-10R1	MALPVTALLLPLALLLHAARPSPGQGTQSENSCTHFPGNLPNMLRD LRDAFSRVKTFFQMKDQLDNLLLKESLLEDFKGYLGCQALSEMIQF YLEEVMPQAENQDPDIKAHVNSLGENLKTLRLRLRRCHRFLPCEN KSKAVEQVKNAFNKLQEKGIYKAMSEFDIFINYIEAYMTMKIRNGG GGSGGGGSGGGGSSPGQGTQSENSCTHFPGNLPNMLRDLRDAFSR VKTFFQMKDQLDNLLLKESLLEDFKGYLGCQALSEMIQFYLEEVM PQAENQDPDIKAHVNSLGENLKTLRLRLRRCHRFLPCENKSKAVEQ VKNAFNKLQEKGIYKAMSEFDIFINYIEAYMTMKIRNSGGGSGGGG SGGGGSGGGGSGGGSLQHGTELPSPPSVWFEAEFFHHILHWTPIPN QSESTCYEVALLRYGIESWNSISNCSQTLSYDLTAVTLDLYHSNGYR ARVRAVDGSRHSNWTVTNTRFSVDEVTLTVGSVNLEIHNGFILGKI QLPRPKMAPANDTYESIFSHFREYEIAIRKVPGNFTFTHKKVKHENF SLLTSGEVGEFCVQVKPSVASRSNKGMWSKEECISLTRQYFTVTNVI IFFAFVLLLSGALAYCLALQLYVRRRKKLPSVLLFKKPSPFIFISQRPS PETQDTIHPLDEEAFLKVSPELKNLDLHGSTDSGFGSTKPSLQTEEP QFLLPDPHPQADRTLGNREPPVLGDSCSSGSSNSTDSGICLQEPSLSP STGPTWEQQVGSNSRGQDDSGIDLVQNSEGRAGDTQGGSALGHHS PPEPEVPGEEDPAAVAFQGYLRQTRCAEEKATKTGCLEEESPLTDGL GPKFGRCLVDEAGLHPPALAKGYLKQDPLEMTLASSGAPTGQWNQ PTEEWSLLALSSCSDLGISDWSFAHDLAPLGCVAAPGGLLGSFNSDL VTLPLISSLQSSE **(SEQ ID NO: 113)**
tdIL-10	IL-10R2	MALPVTALLLPLALLLHAARPSPGQGTQSENSCTHFPGNLPNMLRD LRDAFSRVKTFFQMKDQLDNLLLKESLLEDFKGYLGCQALSEMIQF YLEEVMPQAENQDPDIKAHVNSLGENLKTLRLRLRRCHRFLPCEN KSKAVEQVKNAFNKLQEKGIYKAMSEFDIFINYIEAYMTMKIRNGG GGSGGGGSGGGGSSPGQGTQSENSCTHFPGNLPNMLRDLRDAFSR VKTFFQMKDQLDNLLLKESLLEDFKGYLGCQALSEMIQFYLEEVM PQAENQDPDIKAHVNSLGENLKTLRLRLRRCHRFLPCENKSKAVEQ VKNAFNKLQEKGIYKAMSEFDIFINYIEAYMTMKIRNSGGGSGGGG SGGGGSGGGGSGGGSLQMVPPPENVRMNSVNFKNILQWESPAFAK GNLTFTAQYLSYRIFQDKCMNTTLTECDFSSLSKYGDHTLRVRAEF ADEHSDWVNITFCPVDDTIIGPPGMQVEVLADSLHMRFLAPKIENE YETWTMKNVYNSWTYNVQYWKNGTDEKFQITPQYDFEVLRNLEP WTTYCVQVRGFLPDRNKAGEWSEPVCEQTTHDETVPSWMVAVIL MASVFMVCLALLGCFALLWCVYKKTKYAFSPRNSLPQHLKEFLGH PHHNTLLFFSFPLSDENDVFDKLSVIAEDSESGKQNPGDSCSLGTPP GQGPQS **(SEQ ID NO: 114)**
IL-13	IL-13Rα1	MALPVTALLLPLALLLHAARPLTCLGGFASPGPVPPSTALRELIEELV NITQNQKAPLCNGSMVWSINLTAGMYCAALESLINVSGCSAIEKTQ RMLSGFCPHKVSAGQFSSLHVRDTKIEVAQFVKDLLLHLKKLFREG RFNSGGGSGGGGSGGGGSGGGGSGGGSLQGGGGAAPTETQPPVTN LSVSVENLCTVIWTWNPPEGASSNCSLWYFSHFGDKQDKKIAPETR RSIEVPLNERICLQVGSQCSTNESEKPSILVEKCISPPEGDPESAVTEL QCIWHNLSYMKCSWLPGRNTSPDTNYTLYYWHRSLEKIHQCENIF REGQYFGCSFDLTKVKDSSFEQHSVQIMVKDNAGKIKPSFNIVPLTS RVKPDPPHIKNLSFHNDDLYVQWENPQNFISRCLFYEVEVNNSQTE

		THNVFYVQEAKCENPEFERNVENTSCFMVPGVLPDTLNTVRIRVKT NKLCYEDDKLWSNWSQEMSIGKKRNSTLYITMLLIVPVIVAGAIIVL LLYLKRLKIIIFPPIPDPGKIFKEMFGDQNDDTLHWKKYDIYEKQTK EETDSVVLIENLKKASQ **(SEQ ID NO: 115)**
IL-13	IL-4Rα	MALPVTALLLPLALLLHAARPLTCLGGFASPGPVPPSTALRELIEELV NITQNQKAPLCNGSMVWSINLTAGMYCAALESLINVSGCSAIEKTQ RMLSGFCPHKVSAGQFSSLHVRDTKIEVAQFVKDLLLHLKKLFREG RFNSGGGSGGGGSGGGGSGGGGSGGGSLQMKVLQEPTCVSDYMSI STCEWKMNGPTNCSTELRLLYQLVFLLSEAHTCIPENNGGAGCVCH LLMDDVVSADNYTLDLWAGQQLLWKGSFKPSEHVKPRAPGNLTV HTNVSDTLLLTWSNPYPPDNYLYNHLTYAVNIWSENDPADFRIYNV TYLEPSLRIAASTLKSGISYRARVRAWAQCYNTTWSEWSPSTKWHN SYREPFEQHLLLGVSVSCIVILAVCLLCYVSITKIKKEWWDQIPNPAR SRLVAIIIQDAQGSQWEKRSRGQEPAKCPHWKNCLTKLLPCFLEHN MKRDEDPHKAAKEMPFQGSGKSAWCPVEISKTVLWPESISVVRCV ELFEAPVECEEEEEVEEEKGSFCASPESSRDDFQEGREGIVARLTESL FLDLLGEENGGFCQQDMGESCLLPPSGSTSAHMPWDEFPSAGPKE APPWGKEQPLHLEPSPPASPTQSPDNLTCTETPLVIAGNPAYRSFSNS LSQSPCPRELGPDPLLARHLEEVEPEMPCVPQLSEPTTVPQPEPETW EQILRRNVLQHGAAAAPVSAPTSGYQEFVHAVEQGGTQASAVVGL GPPGEAGYKAFSSLLASSAVSPEKCGFGASSGEEGYKPFQDLIPGCP GDPAPVPVPLFTFGLDREPPRSPQSSHLPSSSPEHLGLEPGEKVEDMP KPPLPQEQATDPLVDSLGSGIVYSALTCHLCGHLKQCHGQEDGGQT PVMASPCCGCCCGDRSSPPTTPLRAPDPSPGGVPLEASLCPASLAPS GISEKSKSSSSFHPAPGNAQSSSQTPKIVNFVSVGPTYMRVS **(SEQ ID NO: 116)**
cpIL-13 (75/74)	IL-13Rα1	MALPVTALLLPLALLLHAARPVSAGQFSSLHVRDTKIEVAQFVKDL LLHLKKLFREGRFNGGGGSLTCLGGFASPGPVPPSTALRELIEELVNI TQNQKAPLCNGSMVWSINLTAGMYCAALESLINVSGCSAIEKTQR MLSGFCPHKSGGGSGGGGSGGGGSGGGGSGGGGSLQGGGGAAPTE TQPPVTNLSVSVENLCTVIWTWNPPEGASSNCSLWYFSHFGDKQD KKIAPETRRSIEVPLNERICLQVGSQCSTNESEKPSILVEKCISPPEGD PESAVTELQCIWHNLSYMKCSWLPGRNTSPDTNYTLYYWHRSLEKI HQCENIFREGQYFGCSFDLTKVKDSSFEQHSVQIMVKDNAGKIKPS FNIVPLTSRVKPDPPHIKNLSFHNDDLYVQWENPQNFISRCLFYEVE VNNSQTETHNVFYVQEAKCENPEFERNVENTSCFMVPGVLPDTLN TVRIRVKTNKLCYEDDKLWSNWSQEMSIGKKRNSTLYITMLLIVPVI VAGAIIVLLLYLKRLKIIIFPPIPDPGKIFKEMFGDQNDDTLHWKKYD IYEKQTKEETDSVVLIENLKKASQ **(SEQ ID NO: 117)**
cpIL-13 (75/74)	IL-4Rα	MALPVTALLLPLALLLHAARPVSAGQFSSLHVRDTKIEVAQFVKDL LLHLKKLFREGRFNGGGGSLTCLGGFASPGPVPPSTALRELIEELVNI TQNQKAPLCNGSMVWSINLTAGMYCAALESLINVSGCSAIEKTQR MLSGFCPHKSGGGSGGGGSGGGGSGGGGSGGGGSLQMKVLQEPTC VSDYMSISTCEWKMNGPTNCSTELRLLYQLVFLLSEAHTCIPENNG GAGCVCHLLMDDVVSADNYTLDLWAGQQLLWKGSFKPSEHVKPR APGNLTVHTNVSDTLLLTWSNPYPPDNYLYNHLTYAVNIWSENDPA

		DFRIYNVTYLEPSLRIAASTLKSGISYRARVRAWAQCYNTTWSEWS PSTKWHNSYREPFEQHLLLGVSVSCIVILAVCLLCYVSITKIKKEWW DQIPNPARSRLVAIIQDAQGSQWEKRSRGQEPAKCPHWKNCLTKLL PCFLEHNMKRDEDPHKAAKEMPFQGSGKSAWCPVEISKTVLWPESI SVVRCVELFEAPVECEEEEEVEEEKGSFCASPESSRDDFQEGREGIV ARLTESLFLDLLGEENGGFCQQDMGESCLLPPSGSTSAHMPWDEFP SAGPKEAPPWGKEQPLHLEPSPPASPTQSPDNLTCTETPLVIAGNPAY RSFSNSLSQSPCPRELGPDPLLARHLEEVEPEMPCVPQLSEPTTVPQP EPETWEQILRRNVLQHGAAAAPVSAPTSGYQEFVHAVEQGGTQAS AVVGLGPPGEAGYKAFSSLLASSAVSPEKCGFGASSGEEGYKPFQD LIPGCPGDPAPVPVPLFTFGLDREPPRSPQSSHLPSSSPEHLGLEPGEK VEDMPKPPLPQEQATDPLVDSLGSGIVYSALTCHLCGHLKQCHGQE DGGQTPVMASPCCGCCCGDRSSPPTTPLRAPDPSPGGVPLEASLCP ASLAPSGISEKSKSSSSFHPAPGNAQSSSQTPKIVNFVSVGPTYMRVS **(SEQ ID NO: 118)**
IL-18	IL-18Rα	MALPVTALLLPLALLLHAARPYFGKLESKLSVIRNLNDQVLFIDQG NRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGMAVTISVKCEKIS TLSCENKIISFKEMNPPDNIKDTKSDIIFFQRSVPGHDNKMQFESSSY EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEDSGGGSGGGG SGGGGSGGGGSGGGSLQAESCTSRPHITVVEGEPFYLKHCSCSLAH EIETTTKSWYKSSGSQEHVELNPRSSSRIALHDCVLEFWPVELNDTG SYFFQMKNYTQKWKLNVIRRNKHSCFTERQVTSKIVEVKKFFQITC ENSYYQTLVNSTSLYKNCKKLLLENNKNPTIKKNAEFEDQGYYSCV HFLHHNGKLFNITKTFNITIVEDRSNIVPVLLGPKLNHVAVELGKNV RLNCSALLNEEDVIYWMFGEENGSDPNIHEEKEMRIMTPEGKWHA SKVLRIENIGESNLNVLYNCTVASTGGTDTKSFILVRKADMADIPGH VFTRGMIIAVLILVAVVCLVTVCVIYRVDLVLFYRHLTRRDETLTDGK TYDAFVSYLKECRPENGEEHTFAVEILPRVLEKHFGYKLCIFERDVV PGGAVVDEIHSLIEKSRRLIIVLSKSYMSNEVRYELESGLHEALVERK IKIILIEFTPVTDFTFLPQSLKLLKSHRVLKWKADKSLSYNSRFWKNL LYLMPAKTVKPGRDEPEVLPVLSES **(SEQ ID NO: 119)**
IL-18	IL-18Rβ	MALPVTALLLPLALLLHAARPYFGKLESKLSVIRNLNDQVLFIDQG NRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGMAVTISVKCEKIS TLSCENKIISFKEMNPPDNIKDTKSDIIFFQRSVPGHDNKMQFESSSY EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEDSGGGSGGGG SGGGGSGGGGSGGGSLQFNISGCSTKKLLWTYSTRSEEEFVLFCDL PEPQKSHFCHRNRLSPKQVPEHLPFMGSNDLSDVQWYQQPSNGDP LEDIRKSYPHIIQDKCTLHFLTPGVNNSGSYICRPKMIKSPYDVACCV KMILEVKPQTNASCEYSASHKQDLLLGSTGSISCPSLSCQSDAQSPA VTWYKNGKLLSVERSNRIVVDEVYDYHQGTYVCDYTQSDTVSSW TVRAVVQVRTIVGDTKLKPDILDPVEDTLEVELGKPLTISCKARFGF ERVFNPVIKWYIKDSDLEWEVSVPEAKSIKSTLKDEIIERNIILEKVT QRDLRRKFVCFVQNSIGNTTQSVQLKEKRGVVLLYILLGTIGTLVAV LAASALLYRHWIEIVLLYRTYQSKDQTLGDKKDFDAFVSYAKWSSF PSEATSSLSEEHLALSLFPDVLENKYGYSLCLLERDVAPGGVYAEDI VSIIKRSRRGIFILSPNYVNGPSIFELQAAVNLALDDQTLKLILIKFCY

		FQEPESLPHLVKKALRVLPTVTWRGLKSVPPNSRFWAKMRYHMPV KNSQGFTWNQLRITSRIFQWKGLSRTETTGRSSQPKEW **(SEQ ID NO: 120)**

Table 10 – Codon Optimized DNA Sequences for Full Constructs (all constructs designed with representative signal peptide (CD8a) and flexible linker (linker 26))

Cytokine	Receptor	Codon Optimized Sequence
IFN-α2	IFNAR1	atggccttaccagtgaccgccttgctcctgccgctggccttgctgctccacgccgccaggccgtgcgacct tccacagacccattccctcggctctcgaagaactctgatgttgctggcccagatgcggaagatttctcttttct catgtctgaaagacaggcacgactttggttttccccaggaggagttcggaaaccagttccagaaagcgga aaccattcctgtgctgcacgaaatgatccaacaaattttcaacctgttttcaactaaagatagctccgctgcat gggacgagacactcctcgataagttttatacagagctttaccagcagttaaatgatctggaagcttgtgtcat ccaaggggtcggcgtaaccgagacgcccctgatgaaggaggatagcatactggcagtgcggaagtactt ccagaggatcaccctctatctaaaggaaaaaaagtacagtccgtgcgcctgggaagtggttagagccgaa atcatgcgtagcttttccttatctacaaatttgcaggagtcgttgcgcagtaaagagtctggaggcggaagc gggggtggcggcagcggcggtggaggatcaggtggcgggggggtccgggggcggaagtctgcagaa gaacctgaaatccccacagaaagtcgaggtggacatcatcgatgacaatttcatcttaagatggaaccgta gcgatgagtccgtcggaaatgtcacattttctttgattatcagaagaccgggatggacaactggattaagct gtccggttgccagaacataaccagtaccaagtgtaacttcagcagcctcaaactcaatgtatatgaggaaat caagctgaggatccgggccgagaaggaaaacacaagctcctggtatgaagttgattcatttactccatttcg aaaagcgcaaataggacccccggaagttcacctcgaggctgaagataaagcaattgtaatacacatatcg cctggcaccaaggactctgtgatgtgggctttagatgggctgtcattcacgtacagcctggtgatctggaag aacagttctggggtggaggagagaatagaaaacatttatagtcgccacaaaatctacaaattgtcacccga aacaacctattgcctgaaggtcaaggcggcactattgacgtcctggaagatcggcgtgtactcaccagtgc attgtataaagacaacagtggaaaacgagcttcccccgccggagaatattgaggtttccgtgcagaatcag aattatgtgttgaagtgggactacacatatgccaatatgaccttccaggttcaatggcttcatgcatttctgaaa agaaaccctggtaaccacctttacaaatggaagcagattcctgactgcgagaatgtcaagaccacacagtg cgtgtttcctcaaaacgttttccagaaaggcatctatctgctacgggtccaggcttccgatggcaataatacct cattttggagcgaggaaattaaattcgacactgaaatccaagccttcctactccctcccgtatttaacatcagg agtctgtctgatagcttccatatttacatcggtgctcccaagcagtctggaaacactcccgtgatccaggatta ccccctcatctacgagatcattttctgggaaaacacctctaacgccgaacggaagattatagagaagaaaa ctgacgtcactgtgcctaacctgaaaccattaactgtctattgcgtcaaagctagggcccacaccatggatg aaaaactgaacaagtctagcgtgttcagcgacgcagtttgtgagaaaacgaagccaggaaatacttctaag atttggcttatcgtgggcatttgtatcgctctgttcgcactgccctttgtaatctacgccgccaaggtttttctcc gctgtattaattatgtgtttttcccatccctgaagccatcatcgtcgattgacgagtacttctctgagcaacctct taaaaacctgttgttgtccaccagtgaagagcagattgagaaatgcttcattatcgaaaatatttcaacaatcg ccacagtggaggagacgaatcagaccgacgaggaccataagaagtacagcagtcagacatctcaggatt ccgggaattacagcaatgaagatgaaagtgaatccaaaactagcgaggagctccaacaggactttgtg **(SEQ ID NO: 121)**
IFN-α2	IFNAR2	atggccttaccagtgaccgccttgctcctgccgctggccttgctgctccacgccgccaggccgtgcgacct tccacagacccattccctcggctctcgaagaactctgatgttgctggcccagatgcggaagatttctcttttct catgtctgaaagacaggcacgactttggttttccccaggaggagttcggaaaccagttccagaaagcgga aaccattcctgtgctgcacgaaatgatccaacaaattttcaacctgttttcaactaaagatagctccgctgcat gggacgagacactcctcgataagttttatacagagctttaccagcagttaaatgatctggaagcttgtgtcat

		ccaaggggtcggcgtaaccgagacgcccctgatgaaggaggatagcatactggcagtgcggaagtactt ccagaggatcaccctctatctaaaggaaaaaaagtacagtccgtgcgcctgggaagtggttagagccgaa atcatgcgtagcttttccttatctacaaatttgcaggagtcgttgcgcagtaaagagtctggaggcggaagc gggggtggcggcagcggcggtggaggatcaggtggcgggggggtccgggggcggaagtctgcagatc agctacgactcccccgattacaccgacgagtcctgtacctttaaaatctccctacgtaacttcaggtccattct ctcctgggaactgaaaaaccatagcattgtgccgactcactatacactgctgtataccataatgtctaaaccc gaggatctgaaggtggtgaagaactgtgcgaacaccacaagatccttctgcgacctgacagatgagtggc gatctacccatgaagcctacgtcacggtcctcgagggcttcagcggtaataccacacttttcagctgctcac ataacttttggttggccatcgatatgtcctttgaaccacccgagttcgagattgtcggtttcacaaaccacatc aatgtcatggtgaaatttccttctattgtcgaggaagaactccagtttgatttgagcctcgtgattgaggagca gtcagagggaatcgtgaagaagcataagcccgaaataaagggaaatatgagtgggaacttcacttacata atcgacaagctcatccccaacacgaattattgtgtgtcagtgtatctcgagcactcggatgagcaagccgtg atcaagtctccacttaagtgcactctcctgccgccaggccaggagtcagagagcgctgaatcggctaagat aggcgggatcattaccgtcttcctcatcgcactggtgttgacttctactattgttaccctgaagtggatcggat acatctgcttgcgcaactctctgccaaaagttctaaactttcacaattttctggcctggcccttccccaatcttc ctcctctggaggccatggacatggttgaggttatctatataaatcggaaaaaaaaagtctgggactacaatta cgatgacgaaagtgactcagacacggaggccgcaccaaggacctctggagggggctatactatgcacg gccttaccgtgagacctttaggacaggcatctgctacaagcactgaaagccagctgattgacccagagag cgaggaagagcctgatctaccagaagtggatgtagagctgccgacaatgcctaaggactccccccaaca gctcgaactgttgagcggcccttgtgaaaggcgcaaaagtcccttgcaagatccgttccctgaagaagact atagcagtaccgaaggatccggcggtcggattacattcaacgtggatttaaatagtgtatttttacgggttctg gacgatgaggacagtgatgatctggaggcgcccttatgctgtcctcccatctggaggagatggtagacc ccgaagatccagataacgtgcagtctaatcaccttctggcttccggggaaggtactcagccaacctttccta gtccttcttcagagggcttatggtcagaagacgcaccaagcgatcagtcagacacaagtgagagcgacgt agacctcggggacgggtacattatgaga **(SEQ ID NO: 122)**
IFN-β	IFNAR1	atggccttaccagtgaccgccttgctcctgccgctggccttgctgctccacgccgccaggccgatgagttat aatttactcggatttctacagcggtctagcaacttccaatgtcagaagctgctgtggcaactcaacggcagg ctggagtactgcctcaaagatagaatgaactttgatattcccgaagaaatcaagcagcttcagcagttccag aaagaggacgccgcactaaccatatacgagatgctgcagaacattttcgctatattcagacaggactcgtc ctctactggatggaatgagaccatcgtcgagaatttgctggccaatgtgtatcatcaaattaaccacctcaag acggtgcttgaagaaaagttggaaaaagaggacttcactagaggcaaactgatgtcatcccttcacctcaa acgctactatgggaggatcctgcactacttaaaggcgaaggagtatagccattgcgcttggacaatcgttc gcgtagagattctgcggaatttttactttatcaatcgtttgacaggttacctgcgaaactctggaggcggaag cgggggtggcggcagcggcggtggaggatcaggtggcgggggggtccgggggcggaagtctgcaga agaacctgaaatccccacagaaagtcgaggtggacatcatcgatgacaatttcatcttaagatggaaccgt agcgatgagtccgtcggaaatgtcacattttcttttgattatcagaagaccgggatggacaactggattaagc tgtccggttgccagaacataaccagtaccaagtgtaacttcagcagcctcaaactcaatgtatatgaggaaa tcaagctgaggatccgggccgagaaggaaaacacaagctcctggtatgaagttgattcatttactccatttc gaaaagcgcaaataggacccccggaagttcacctcgaggctgaagataaagcaattgtaatacacatatc gcctggcaccaaggactctgtgatgtgggctttagatgggctgtcattcacgtacagcctggtgatctggaa gaacagttctggggtggaggagagaatagaaaacatttatagtcgccacaaaatctacaaattgtcacccg aaacaacctattgcctgaaggtcaaggcggcactattgacgtcctggaagatcggcgtgtactcaccagtg cattgtataaagacaacagtggaaaacgagcttcccccgccggagaatattgaggtttccgtgcagaatca gaattatgtgttgaagtgggactacacatatgccaatatgaccttccaggttcaatggcttcatgcatttctgaa aagaaaccctggtaaccacctttacaaatggaagcagattcctgactgcgagaatgtcaagaccacacagt gcgtgtttcctcaaaacgttttccagaaaggcatctatctgctacgggtccaggcttccgatggcaataatac

		ctcattttggagcgaggaaattaaattcgacactgaaatccaagccttcctactccctcccgtatttaacatca ggagtctgtctgatagcttccatatttacatcggtgctcccaagcagtctggaaacactcccgtgatccagga ttacccccctcatctacgagatcattttctgggaaaacacctctaacgccgaacggaagattatagagaagaa aactgacgtcactgtgcctaacctgaaaccattaactgtctattgcgtcaaagctagggcccacaccatgga tgaaaaactgaacaagtctagcgtgttcagcgacgcagtttgtgagaaaacgaagccaggaaatacttcta agatttggcttatcgtgggcatttgtatcgctctgttcgcactgccctttgtaatctacgccgccaaggttttct ccgctgtattaattatgtgtttttcccatccctgaagccatcatcgtcgattgacgagtacttctctgagcaacct cttaaaaacctgttgttgtccaccagtgaagagcagattgagaaatgcttcattatcgaaaatatttcaacaat cgccacagtggaggagacgaatcagaccgacgaggaccataagaagtacagcagtcagacatctcagg attccgggaattacagcaatgaagatgaaagtgaatccaaaactagcgaggagctccaacaggactttgtg **(SEQ ID NO: 123)**
IFN-β	IFNAR2	atggccttaccagtgaccgccttgctcctgccgctggccttgctgctccacgccgccaggccgatgagttat aatttactcggatttctacagcggtctagcaacttccaatgtcagaagctgctgtggcaactcaacggcagg ctggagtactgcctcaaagatagaatgaactttgatattcccgaagaaatcaagcagcttcagcagttccag aaagaggacgccgcactaaccatatacgagatgctgcagaacattttcgctatattcagacaggactcgtc ctctactggatggaatgagaccatcgtcgagaatttgctggccaatgtgtatcatcaaattaaccacctcaag acggtgcttgaagaaaagttggaaaaagaggacttcactagaggcaaactgatgtcatcccttcacctcaa acgctactatgggaggatcctgcactacttaaaggcgaaggagtatagccattgcgcttggacaatcgttc gcgtagagattctgcggaatttttactttatcaatcgtttgacaggttacctgcgaaactctggaggcggaag cgggggtggcggcagcggcggtggaggatcaggtggcgggggggtccgggggcggaagtctgcagat cagctacgactcccccgattacaccgacgagtcctgtacctttaaaatctccctacgtaacttcaggtccatt ctctcctgggaactgaaaaaccatagcattgtgccgactcactatacactgctgtataccataatgtctaaac ccgaggatctgaaggtggtgaagaactgtgcgaacaccacaagatccttctgcgacctgacagatgagtg gcgatctacccatgaagcctacgtcacggtcctcgagggcttcagcggtaataccacacttttcagctgctc acataacttttggttggccatcgatatgtcctttgaaccacccgagttcgagattgtcggtttcacaaaccaca tcaatgtcatggtgaaatttccttctattgtcgaggaagaactccagtttgatttgagcctcgtgattgaggagc agtcagagggaatcgtgaagaagcataagcccgaaataaagggaaatatgagtgggaacttcacttacat aatcgacaagctcatccccaacacgaattattgtgtgtcagtgtatctcgagcactcggatgagcaagccgt gatcaagtctccacttaagtgcactctcctgccgccaggccaggagtcagagagcgctgaatcggctaag ataggcgggatcattaccgtcttcctcatcgcactggtgttgacttctactattgttaccctgaagtggatcgg atacatctgcttgcgcaactctctgccaaaagttctaaactttcacaattttctggcctggcccttccccaatctt cctcctctggaggccatggacatggttgaggttatctatataaatcggaaaaaaaaagtctgggactacaatt acgatgacgaaagtgactcagacacggaggccgcaccaaggacctctggagggggctatactatgcac ggccttaccgtgagacctttaggacaggcatctgctacaagcactgaaagccagctgattgacccagaga gcgaggaagagcctgatctaccagaagtggatgtagagctgccgacaatgcctaaggactccccccaac agctcgaactgttgagcggcccttgtgaaaggcgcaaaagtcccttgcaagatccgttccctgaagaaga ctatagcagtaccgaaggatccggcggtcggattacattcaacgtggatttaaatagtgtatttttacgggttc tggacgatgaggacagtgatgatctggaggcgccccttatgctgtcctcccatctggaggagatggtagac cccgaagatccagataacgtgcagtctaatcaccttctggcttccggggaaggtactcagccaacctttcct agtccttcttcagagggcttatggtcagaagacgcaccaagcgatcagtcagacacaagtgagagcgacg tagacctcggggacgggtacattatgaga **(SEQ ID NO: 124)**
IFN-γ	IFNGR1	atggccttaccagtgaccgccttgctcctgccgctggccttgctgctccacgccgccaggccgcaggatc cctacgtgaaggaagcagaaaatctcaaaaagtatttcaatgcgggccatagcgatgtggccgataacgg caccctgtttctggggattcttaagaattggaaagaggagtctgataggaagattatgcagtcccagatcgt gagcttctatttcaagctgttcaaaaacttcaaagacgaccagtcgatccaaaaatctgttgagacaataaaa gaggacatgaatgtgaagtttttttaattcaaacaaaaagaagcgcgacgattttgagaaattaacgaactact

		ccgtcaccgacttgaacgtacaacgaaaggctattcacgaactaatccaggtcatggctgaactgagtcct gccgccaagactggtaagcgtaaacggagtcagatgctctttagaggatctggaggcggaagcgggggt ggcggcagcggcggtggaggatcaggtggcgggggggtccgggggcggaagtctgcaggaaatggg gactgccgacttgggacctagcagtgtccccactcccaccaacgtgaccatcgagtcttataatatgaatcc tattgtttattgggaatatcagatcatgcctcaggttccagtgttcactgttgaagtgaaaaattacggagtgaa gaactcagagtggatagacgcttgcataaacatatctcaccattactgcaatatttccgaccacgtgggcga ccccagcaacagtttgtgggtcagagtgaaagctcgcgtgggccagaaggagagtgcttatgccaaaag cgaagaattcgccgtttgtagagatggcaagatcgggccccccaaattagacattcgcaaagaagaaaaa caaattatgatcgatatcttccatccctctgtcttcgtcaacggcgacgaacaggaggtagattatgatccag agacaacgtgttacatcagggtatacaacgtttacgtgaggatgaatgggtcagagatccagtataagatcc tcactcaaaaggaggacgactgtgacgaaattcagtgtcaactcgccatcccagtgtcttcgctgaatagcc agtactgcgtgtctgccgagggtgtgcttcacgtttggggagtcacaactgaaaagtccaaagaagtttgta ttaccatttttaacagctctatcaagggctccctgtggataccagtggtggcggcactgctgctgttccttgta ctcagcctggtcttcatctgcttctatattaagaagatcaaccctctgaaggagaagagcatcatactaccca agtcgcttatctcagtcgtgcggtccgccaccctagaaactaagcccgaatcaaaatatgtatccctgatca caagctaccagccattttcattagagaaagaagtcgtgtgcgaggagcctctgtccccagcaactgtgcca ggtatgcatacggaggacaatccgggtaaagtagagcacaccgaggagctgtccagcattacagaggtc gtcaccacagaggagaacatacccgatgtggtgcctggaagtcatctcacacctattgagcgtgaatctag cagtcccttgtcttctaatcagagtgaaccggggagtattgcattaaactcctaccactcccggaattgcagc gaaagcgaccactcgagaaatgggtttgataccgatagttcttgtctggaatcccactcatcactgagcgatt ctgagtttccgccaaacaacaagggcgaaattaaaacggagggacaagagctcatcaccgtcatcaagg ctccaaccagttttggttacgacaagcctcatgttttggtggatctgcttgtggatgactcaggcaaggagtc cctcattggataccgacctacagaggattccaaagagtttagc **(SEQ ID NO: 125)**
IFN-γ	IFNGR2	atggccttaccagtgaccgccttgctcctgccgctggccttgctgctccacgccgccaggccgcaggatc cctacgtgaaggaagcagaaaatctcaaaaagtatttcaatgcgggccatagcgatgtggccgataacgg caccctgtttctggggattcttaagaattggaaagaggagtctgataggaagattatgcagtcccagatcgt gagcttctatttcaagctgttcaaaaacttcaaagacgaccagtcgatccaaaaatctgttgagacaataaaa gaggacatgaatgtgaagttttttaattcaaacaaaaagaagcgcgacgattttgagaaattaacgaactact ccgtcaccgacttgaacgtacaacgaaaggctattcacgaactaatccaggtcatggctgaactgagtcct gccgccaagactggtaagcgtaaacggagtcagatgctctttagaggatctggaggcggaagcgggggt ggcggcagcggcggtggaggatcaggtggcgggggggtccgggggcggaagtctgcaggcccccccct gatcctctctcacagctacccgccccacagcatcccaagataagactgtacaatgccgagcaggtgcttag ctgggagcccgtggcactatcaaacagtacgagacccgtggtgtaccaggtacagttcaagtacacagac agcaagtggtttaccgctgacattatgagcattggagtcaattgcactcagatcaccgcaaccgagtgtgac tttacagcagcttcaccctccgccggattccctatggacttcaacgtcactctgcggcttcgtgcagaactgg gcgctcttcattccgcctgggtgacaatgccttggttccagcactatcggaacgtcaccgtagggccccctg aaaatatcgaagtaacccctggagaaggttcgctgataataaggttcagctctccgtttgacattgctgatac atccactgcgttcttctgctactatgtgcactactgggagaagggcgggattcaacaagtgaaagggccatt caggagcaacagtatcagtctcgacaacctgaaaccttctcgcgtctattgcctccaagtgcaggctcaact gctgtggaacaaaagtaatattttccgagttggccacctgtctaatatctcctgttatgagaccatggccgac gcatctacggagttgcagcaggtcatcctcatttctgtgggcacattttccctgctgtcggttctggccggtgc ctgtttttttctcgttttgaaataccgcggcttgatcaaatactggtttcataccccaccatcaataccattacag atcgaagagtatcttaaagatccaactcagccaattttagaggcgctcgataaggactctagcccgaagga cgatgtgtgggattccgtgtccatcatcagctttcccgaaaaggagcaggaagatgttctgcaaactttg **(SEQ ID NO: 126)**

scIFN-γ	IFNGR1	atggccttaccagtgaccgccttgctcctgccgctggccttgctgctccacgccgccaggccgcaggatc cctacgtgaaagaagccgagaacttaaagaaatatttcaacgcaggccattcagacgtcgctgataatgga acacttttttgggcattctgaaaaattggaaggaagaatcggaccgaaaaattatgcagagccagatagtat ccttttatttcaagttatttaaaaacttcaaagacgatcagtctatccaaaaaagtgtggagactatcaaggag gacatgaatgtgaagttcttcaacagcaataaaaagaaacgggatgactttgaaaagctcaccaattactca gtcactgatctgaacgtgcagagaaaggcgattcatgagctaatccaagtgatggctgagctcggagcca acgtgagcggagagtttgtgaaggaagccgagaatctgaagaagtatttcaacgctggtcactctgacgtg gcagataacggcacgctgttcctggggatcctgaagaattggaaagaagagtccgacaggaagattatgc aatcccagatcgtcagtttctactttaagcttttcaagaatttcaaagacgatcagagtatccagaagtctgtcg agaccataaaagaagacatgaatgtaaagtttttttaattcaaacaaaaagaagcgtgacgatttcgaaaaac tcaccaactactccgttacagatctgaacgttcagagaaaagccattcacgagttgatccaagttatggccg agctctctcctgcagctaagacaggtaagaggaaacggagccagatgctgtttcgcgggtctggaggcg gaagcgggggtggcggcagcggcggtggaggatcaggtggcgggggggtccgggggcggaagtctg caggaaatggggactgccgacttgggacctagcagtgtccccactcccaccaacgtgaccatcgagtctt ataatatgaatcctattgtttattgggaatatcagatcatgcctcaggttccagtgttcactgttgaagtgaaaa attacggagtgaagaactcagagtggatagacgcttgcataaacatatctcaccattactgcaatatttccga ccacgtgggcgaccccagcaacagtttgtgggtcagagtgaaagctcgcgtgggccagaaggagagtg cttatgccaaaagcgaagaattcgccgtttgtagagatggcaagatcgggccccccaaattagacattcgc aaagaagaaaaacaaattatgatcgatatcttccatccctctgtcttcgtcaacggcgacgaacaggaggta gattatgatccagagacaacgtgttacatcagggtatacaacgtttacgtgaggatgaatgggtcagagatc cagtataagatcctcactcaaaaggaggacgactgtgacgaaattcagtgtcaactcgccatcccagtgtct tcgctgaatagccagtactgcgtgtctgccgagggtgtgcttcacgtttggggagtcacaactgaaaagtcc aaagaagtttgtattaccatttttaacagctctatcaagggctccctgtggataccagtggtggcggcactgct gctgttccttgtactcagcctggtcttcatctgcttctatattaagaagatcaaccctctgaaggagaagagca tcatactacccaagtcgcttatctcagtcgtgcggtccgccaccctagaaactaagcccgaatcaaaatatg tatccctgatcacaagctaccagccattttcattagagaaagaagtcgtgtgcgaggagcctctgtccccag caactgtgccaggtatgcatacggaggacaatccgggtaaagtagagcacaccgaggagctgtccagca ttacagaggtcgtcaccacagaggagaacatacccgatgtggtgcctggaagtcatctcacacctattgag cgtgaatctagcagtcccttgtcttctaatcagagtgaaccggggagtattgcattaaactcctaccactccc ggaattgcagcgaaagcgaccactcgagaaatgggtttgataccgatagttcttgtctggaatcccactcat cactgagcgattctgagtttccgccaaacaacaagggcgaaattaaaacggagggacaagagctcatcac cgtcatcaaggctccaaccagttttggttacgacaagcctcatgttttggtggatctgcttgtggatgactcag gcaaggagtccctcattggataccgacctacagaggattccaaagagtttagc **(SEQ ID NO: 127)**
scIFN-γ	IFNGR2	atggccttaccagtgaccgccttgctcctgccgctggccttgctgctccacgccgccaggccgcaggatc cctacgtgaaagaagccgagaacttaaagaaatatttcaacgcaggccattcagacgtcgctgataatgga acacttttttgggcattctgaaaaattggaaggaagaatcggaccgaaaaattatgcagagccagatagtat ccttttatttcaagttatttaaaaacttcaaagacgatcagtctatccaaaaaagtgtggagactatcaaggag gacatgaatgtgaagttcttcaacagcaataaaaagaaacgggatgactttgaaaagctcaccaattactca gtcactgatctgaacgtgcagagaaaggcgattcatgagctaatccaagtgatggctgagctcggagcca acgtgagcggagagtttgtgaaggaagccgagaatctgaagaagtatttcaacgctggtcactctgacgtg gcagataacggcacgctgttcctggggatcctgaagaattggaaagaagagtccgacaggaagattatgc aatcccagatcgtcagtttctactttaagcttttcaagaatttcaaagacgatcagagtatccagaagtctgtcg agaccataaaagaagacatgaatgtaaagtttttttaattcaaacaaaaagaagcgtgacgatttcgaaaaac tcaccaactactccgttacagatctgaacgttcagagaaaagccattcacgagttgatccaagttatggccg agctctctcctgcagctaagacaggtaagaggaaacggagccagatgctgtttcgcgggtctggaggcg

		gaagcgggggtggcggcagcggcggtggaggatcaggtggcgggggggtccgggggcggaagtctg caggcccccccctgatcctctctcacagctacccgccccacagcatcccaagataagactgtacaatgccg agcaggtgcttagctgggagcccgtggcactatcaaacagtacgagacccgtggtgtaccaggtacagtt caagtacacagacagcaagtggtttaccgctgacattatgagcattggagtcaattgcactcagatcaccgc aaccgagtgtgactttacagcagcttcaccctccgccggattccctatggacttcaacgtcactctgcggctt cgtgcagaactgggcgctcttcattccgcctgggtgacaatgccttggttccagcactatcggaacgtcacc gtagggcccccctgaaaatatcgaagtaacccctggagaaggttcgctgataataaggttcagctctccgttt gacattgctgatacatccactgcgttcttctgctactatgtgcactactgggagaagggcgggattcaacaa gtgaaagggccattcaggagcaacagtatcagtctcgacaacctgaaaccttctcgcgtctattgcctccaa gtgcaggctcaactgctgtggaacaaaagtaatattttccgagttggccacctgtctaatatctcctgttatga gaccatggccgacgcatctacggagttgcagcaggtcatcctcatttctgtgggcacattttccctgctgtcg gttctggccggtgcctgttttttctcgttttgaaataccgcggcttgatcaaatactggtttcataccccaccat caataccattacagatcgaagagtatcttaaagatccaactcagccaattttagaggcgctcgataaggact ctagcccgaaggacgatgtgtgggattccgtgtccatcatcagctttcccgaaaaggagcaggaagatgtt ctgcaaactttg **(SEQ ID NO: 128)**
TNF-α	TNFR1	atggccttaccagtgaccgccttgctcctgccgctggccttgctgctccacgccgccaggccggtgcgatc ttcaagccggacaccctcagacaagccagtggcacacgtggtagcgaacccacaagctgaggggcagc tccagtggctcaatcggcgtgccaacgccctgttagccaatggggtcgagcttagggacaaccaacttgtg gtaccctcggaaggattatacttgatttacagtcaggtgctgttcaaaggacagggctgcccttccacacat gttctgctcactcacacgatctcccgcattgcagtgtcttatcagaccaaggtcaacttgctaagcgctatca aaagtccatgtcagagagagaccccggagggtgctgaggctaagccttggtacgaacctatttatctggg cggagtctttcaactggaaaaaggtgatagactgagcgcagagatcaataggcccgattacctggacttcg ccgaatccggccaggtttattttgggataatcgccctctctggaggcggaagcgggggtggcggcagcg gcggtggaggatcaggtggcgggggggtccgggggcggaagtctgcagttggtaccccatcttggcgac cgagagaaacgggatagtgtctgtccccaagggaaatatatacacccacagaataactctatctgctgcac taagtgccataaaggaacgtacctttataacgactgcccaggccccggccaagatactgactgcagagag tgcgagtctgggagcttcaccgcctccgagaatcacttgagacattgcctgagttgtagcaagtgcaggaa ggagatggggcaggttgagatctcatcatgtaccgttgatcgggacaccgtctgtggatgccgcaaaaatc agtatcggcattattggtccgaaaacctatttcagtgttttaactgttctttgtgcctgaacggaacagtccacc tgagttgccaggaaaaacagaatacagtttgcacttgccacgctggctttttctccgcgagaacgaatgtgt gtcctgttccaattgtaagaagtctctagaatgtacaaagctgtgtctgccccaaatcgagaacgtgaaagg aactgaggacagtggtacaaccgtgttgctgcctctggtgatcttcttcgggctctgcctcctcagtctgcttt cattgggctaatgtaccggtaccagcgttggaaatctaagttatactcaattgtctgtgggaagtccaccct gagaaggaaggagaactggaaggtactaccaccaaaccactggctccaaacccctccttctctcctacac ccggctttactcctaccctgggcttctcaccggtgcccagctcaacgttcaccagctcgagcacatacaccc ctggcgattgtcccaacttcgcagcaccaaggcgtgaagtggccccaccctaccagggtgctgatccaat acttgccaccgcattagccagcgatccgattcctaatcctttacagaagtgggaggattcggcccacaaac cccagagcctggacactgacgaccccgccacgctgtatgctgtggtcgagaatgtaccgcctctcagatg gaaggaatttgtgaggcgactgggcctgtccgatcacgagatcgacagactggagttgcaaaatggtcga tgcctccgggaggcccagtacagcatgctggctacatggaggaggcgcacacctcgcagggaggcga ctcttgaattgctgggacgcgtgctcagagatatggacttactcggatgtcttgaagacattgaagaggcgc tctgcggcccagcagccctgcctccggcaccatccctgctcaga **(SEQ ID NO: 129)**
TNF-α	TNFR2	atggccttaccagtgaccgccttgctcctgccgctggccttgctgctccacgccgccaggccggtgcgatc ttcaagccggacaccctcagacaagccagtggcacacgtggtagcgaacccacaagctgaggggcagc tccagtggctcaatcggcgtgccaacgccctgttagccaatggggtcgagcttagggacaaccaacttgtg gtaccctcggaaggattatacttgatttacagtcaggtgctgttcaaaggacagggctgcccttccacacat

		gttctgctcactcacacgatctcccgcattgcagtgtcttatcagaccaaggtcaacttgctaagcgctatca aaagtccatgtcagagagagaccccggagggtgctgaggctaagccttggtacgaacctatttatctggg cggagtctttcaactggaaaaaggtgatagactgagcgcagagatcaataggcccgattacctggacttcg ccgaatccggccaggtttattttgggataatcgccctctctggaggcggaagcgggggtggcggcagcg gcggtggaggatcaggtggcgggggggtccgggggcggaagtctgcagctgcctgcccaggtcgctttt acaccatatgcacctgagcctggttccacgtgtaggcttagggagtactacgatcaaaccgctcagatgtgt tgctccaagtgtagtccaggccagcacgcaaaagtcttttgtacaaagacgtcagataccgtgtgcgacag ctgcgaagatagcacctatacccagctgtggaattgggttcccgaatgtttgtcttgtggctcccgctgctct agtgaccaggtggaaacacaggcctgcactcgggaacagaaccgtatttgtacctgcaggcccggttggt actgcgcactgtccaaacaagaggggtgtagactgtgtgccccttgcgcaagtgtcgtccaggcttcggt gtggcaagacctggaacagagacttcagacgtcgtttgtaagccctgcgcccctggcacattctccaatac cacctcatctaccgacatatgcagaccccaccaaatatgcaacgtggtggctatccctgggaacgcctcca tggacgctgtttgcacttccacttctcccactcggtctatggctcccggtgccgtgcatttaccccaacccgt gagcactcggagccaacacacacagccaacacccgagccaagtaccgccccgagtaccagcttcctact ccccatgggcccatctccaccggctgagggatctaccggggattttgctctgcctgtcgggctaatcgtcg gggtgacggcgctcggattgctcattatcggagtggtaaactgcgtgattatgactcaggtgaaaaagaag cctttatgcctccagagagaagcgaaagttccccacctgcctgcagacaaggccaggggtacacagggc ccggaacagcaacatctgctgatcaccgccccctcttcaagctccagcagcctggaatccagtgccagtg cacttgatcggcgcgcaccaacgcgaaaccagccccaggcccctggggtagaggcatcaggcgctgg agaagcgcgcgctagcacaggcagttccgattccagccctggagggcatggaacacaggtaaatgtcac ctgcatcgttaatgtgtgctcgtcctcggaccacagctctcaatgttcaagccaggcctcaagcactatggg cgacactgatagctctccctccgagtcaccgaaggacgagcaggtcccatttagtaaagaggagtgtgcc ttccgaagtcagctggagacaccagaaaccctgcttgggtctactgaagagaaaccactccctcttggcgt gccagatgcgggaatgaagccgtcg **(SEQ ID NO: 130)**
IL-1β	IL-1R1	atggccttaccagtgaccgccttgctcctgccgctggccttgctgctccacgccgccaggccggcgcctgt cagaagcctcaactgcacgctgagggactcacagcaaaagagcctggtcatgagtggcccctacgagct gaaagcactccaccttcaggggcaggacatggaacaacaggtggttttctccatgtctttcgtacagggag aggagtctaacgataagatccccgtggctttgggcttaaaagagaaaaacctgtatctgagctgtgtgctaa aggacgataagcccacacttcagctcgagtccgttgatccaaaaaattatccaaagaagaaaatggaaaa gcggtttgtgtttaacaagattgagattaataacaaattggaattcgaatcagcccagttccctaattggtacat cagtacctctcaagccgaaaatatgccggtgtttctgggagggaccaagggtggccaggatataacagac ttcactatgcagtttgtctcgtcctctggaggcggaagcgggggtggcggcagcggcggtggaggatca ggtggcgggggggtccgggggcggaagtctgcagctcgaggccgataagtgcaaagaaagagaggaa aaaatcattctggtttctagcgccaacgaaatcgatgtccgcccctgtccactgaatcctaacgagcataag gggactataacatggtataaggacgacagcaagacccctgtgtctacagaacaagcaagcaggatacac cagcacaaagaaaagctttggtttgtaccagcaaaggtcgaggacagcgggcattattattgcgtggtacg aaacagttcttactgcctcagaatcaagatttccgctaagtttgtcgagaacgaacctaacttatgttacaacg cacaggctatttttaaacagaagctcccagttgctggggatggcggcctggtgtgtccctacatggagttttt aaaaatgagaataatgagctacctaaactgcaatggtacaaggactgcaaacccctttttgctcgacaatatt cacttcagcggagtgaaagatcggctgattgtgatgaacgtggctgagaaacaccgcgggaactatacat gccacgcctcttatacgtacctgggcaagcagtacccgatcactagagtgattgaatttataacactggaag agaacaagccaactcgtcctgtcatagtatcccccgcaaacgaaaccatggaggtggacttgggttctcag atccagctgatttgcaatgttaccgggcaattgagtgatatcgcctattggaagtggaatggttctgtcattga cgaagacgatccagtgttaggagaggactattatagcgtagaaaatcctgcgaacaagaggcggtcgact ctgataactgtcctgaacatcagtgagatcgagagccgattttataaacatccattcacatgtttcgccaaaaa tacacacgggatcgacgccgcctacattcagctgatctaccccgtaaccaatttccagaagcacatgatcg

		ggatatgcgtgacgctaaccgtgatcattgtttgctcagtgttcatttacaagatcttcaagatcgacatcgtcc tttggtatagggatagctgttacgactttctgcccattaaggcatcggatggcaaaacctacgacgcttacat cttgtacccaaagaccgtgggagaaggctcaacctccgactgtgacattttcgtctttaaggtgctccctga ggtcctcgagaaacagtgtggctataaactgttcatctatggccgggatgactacgtgggcgaggatatag ttgaagtcataaatgaaaatgttaagaaatcacggaggctgatcatcattctagtgcgggagacctcaggttt ttcctggctcggcggctcctcagaggagcagattgcgatgtacaacgctctggtgcaagatggaatcaag gtggttctgttggagctcgaaaagatccaggattacgagaaaatgcccgagagcattaagttcatcaaaca aaaacacggagccattagatggagtggtgatttcacgcaaggaccgcagtccgccaagacacgtttctgg aaaaacgtgcgctatcatatgcccgtgcagaggagatccccctccagtaaacatcagctgttatctccggc gactaaggaaaagcttcagcgcgaagcccatgttcctcttgga **(SEQ ID NO: 131)**
IL-1β	IL-1R3	atggccttaccagtgaccgccttgctcctgccgctggccttgctgctccacgccgccaggccggcgcctgt cagaagcctcaactgcacgctgagggactcacagcaaaagagcctggtcatgagtggcccctacgagct gaaagcactccaccttcaggggcaggacatggaacaacaggtggttttctccatgtctttcgtacagggag aggagtctaacgataagatccccgtggctttgggcttaaaagagaaaaacctgtatctgagctgtgtgctaa aggacgataagcccacacttcagctcgagtccgttgatccaaaaaattatccaaagaagaaaatggaaaa gcggtttgtgtttaacaagattgagattaataacaaattggaattcgaatcagcccagttccctaattggtacat cagtacctctcaagccgaaaatatgccggtgtttctgggagggaccaagggtggccaggatataacagac ttcactatgcagtttgtctcgtcctctggaggcggaagcgggggtggcggcagcggcggtggaggatca ggtggcgggggggtccgggggcggaagtctgcagtccgagcggtgcgatgattggggcttagataccat gcggcagattcaggtgttcgaagacgagcctgctcgcattaaatgcccgctctttgagcacttcctgaagttt aattacagcactgctcactccgcaggactcacactgatctggtattggacacgccaagacagagatctgga ggagcccattaattttaggctccccgagaacaggatctctaaggagaaggacgtgctgtggtttcggccga cactactgaacgatactgggaattacacatgtatgcttcgaaatactacctattgctccaaggtggcttttcca cttgaggtggtgcagaaagacagctgttttaatagcccaatgaaactgcccgtgcacaagctgtacatcga atatggcatacagagaatcacatgccctaacgtcgacggctacttccctagctcagttaagccgaccataac ttggtatatgggctgctataaaatacagaacttcaataatgtaatccccgagggtatgaacttgagtttcctgat cgcactgatatctaacaacgggaactacacctgtgtggtgacttatcccgagaacggacgcacattccattt gacaaggacgttaactgtcaaggtagtgggtagtcctaagaatgcagttcctcccgtgattcacagccctaa tgatcacgtggtgtatgaaaaagaaccaggtgaagaactcctgatcccctgcacggtgtacttctctttttaa tggactcccgtaatgaagtttggtggaccatcgacggcaaaaaacctgatgatattaccatcgacgtgaca atcaacgagagcatttcacatagtcggaccgaagatgagacaagaacccagattcttagcataaaaaaagt gacttctgaagacctgaagcgcagttacgtatgtcacgcgcgatccgcaaaaggggaagttgccaaggct gccaaggtgaagcagaaagtccctgccccacggtacaccgtagagctggcctgtggcttcggagctacg gttttgctggttgttatccttatcgtcgtctatcatgtgtactggttggagatggtgctttttatcgggcccatttc gggaccgatgagacgattctagacggaaaggagtacgatatttacgtctcgtacgccagaaatgcggagg aagaggaattcgtgctcttaaccctgaggggagtactggaaaacgagtttggctacaagttgtgtatttttga cagagattcactgccaggaggaattgtcactgacgagacactctcattcatccagaaatctaggaggttgct cgttgtcctgagtccaaattatgtgctccaaggcacccaggccttgctagaactgaaggcggggcttgaaa acatggcctctcgcgggaacatcaacgtaattctggtgcagtacaaagcagtgaaggagaccaaagttaa agagctgaaacgagccaagacagtcctcactgtcatcaagtggaaaggtgaaaaatcaaagtatccacaa gggagattctggaagcagcttcaagtcgctatgcccgtgaagaagtccccccgtcgttcctcctcggacga gcagggcctgagctacagctctctcaagaatgtc **(SEQ ID NO: 132)**
cpIL-1β (89/88)	IL-1R1	atggccttaccagtgaccgccttgctcctgccgctggccttgctgctccacgccgccaggccgaactaccc caaaaaaaagatggagaagcggtttgtttttaacaagattgagatcaacaataagctggaattcgagtctgc gcagttcccaaactggtatattagcacatcgcaagcagaaaatatgcccgtgttcctcggcggaaccaaag gcgggcaggatatcacagactttacgatgcagttcgtgtcatctggtggtggtggaagcggcgggggag

		gcagtgggggaggcgggtccgccccagtgaggtccctgaactgtaccttaagagactcacagcaaaagt ccctggtcatgtctggcccctacgaactgaaagcccttcacctgcaggggcaagatatggagcagcaggt ggttttcagcatgagttttgtacagggcgaagagagtaatgacaagatacctgtggctctaggactcaagga aaagaatttgtatctcagctgcgtcctgaaggacgataaacctactcttcagttggagtccgtcgatccgaaa tctggaggcggaagcgggggtggcggcagcggcggtggaggatcaggtggcgggggggtccggggg cggaagtctgcagctcgaggccgataagtgcaaagaaagagaggaaaaaatcattctggtttctagcgcc aacgaaatcgatgtccgcccctgtccactgaatcctaacgagcataaggggactataacatggtataagga cgacagcaagacccctgtgtctacagaacaagcaagcaggatacaccagcacaaagaaaagctttggttt gtaccagcaaaggtcgaggacagcgggcattattattgcgtggtacgaaacagttcttactgcctcagaatc aagatttccgctaagtttgtcgagaacgaacctaacttatgttacaacgcacaggctatttttaaacagaagct cccagttgctggggatggcggcctggtgtgtccctacatggagttttttaaaaatgagaataatgagctacct aaactgcaatggtacaaggactgcaaacccctttgctcgacaatattcacttcagcggagtgaaagatcgg ctgattgtgatgaacgtggctgagaaacaccgcgggaactatacatgccacgcctcttatacgtacctggg caagcagtacccgatcactagagtgattgaatttataacactggaagagaacaagccaactcgtcctgtcat agtatcccccgcaaacgaaaccatggaggtggacttgggttctcagatccagctgatttgcaatgttaccgg gcaattgagtgatatcgcctattggaagtggaatggttctgtcattgacgaagacgatccagtgttaggaga ggactattatagcgtagaaaatcctgcgaacaagaggcggtcgactctgataactgtcctgaacatcagtg agatcgagagccgattttataaacatccattcacatgtttcgccaaaaatacacacgggatcgacgccgcct acattcagctgatctaccccgtaaccaatttccagaagcacatgatcgggatatgcgtgacgctaaccgtga tcattgtttgctcagtgttcatttacaagatcttcaagatcgacatcgtcctttggtatagggatagctgttacga ctttctgcccattaaggcatcggatggcaaaacctacgacgcttacatcttgtacccaaagaccgtgggaga aggctcaacctccgactgtgacattttcgtctttaaggtgctccctgaggtcctcgagaaacagtgtggctat aaactgttcatctatggccgggatgactacgtgggcgaggatatagttgaagtcataaatgaaaatgttaag aaatcacggaggctgatcatcattctagtgcgggagacctcaggtttttcctggctcggcggctcctcagag gagcagattgcgatgtacaacgctctggtgcaagatggaatcaaggtggttctgttggagctcgaaaagat ccaggattacgagaaaatgcccgagagcattaagttcatcaaacaaaaacacggagccattagatggagt ggtgatttcacgcaaggaccgcagtccgccaagacacgtttctggaaaaacgtgcgctatcatatgcccgt gcagaggagatccccctccagtaaacatcagctgttatctccggcgactaaggaaaagcttcagcgcgaa gcccatgttcctcttgga **(SEQ ID NO: 133)**
cpIL-1β (89/88)	IL-1R3	atggccttaccagtgaccgccttgctcctgccgctggccttgctgctccacgccgccaggccgaactaccc caaaaaaaagatggagaagcggtttgtttttaacaagattgagatcaacaataagctggaattcgagtctgc gcagttcccaaactggtatattagcacatcgcaagcagaaaatatgcccgtgttcctcggcggaaccaaag gcgggcaggatatcacagactttacgatgcagttcgtgtcatctggtggtggtggaagcggcgggggag gcagtgggggaggcgggtccgccccagtgaggtccctgaactgtaccttaagagactcacagcaaaagt ccctggtcatgtctggcccctacgaactgaaagcccttcacctgcaggggcaagatatggagcagcaggt ggttttcagcatgagttttgtacagggcgaagagagtaatgacaagatacctgtggctctaggactcaagga aaagaatttgtatctcagctgcgtcctgaaggacgataaacctactcttcagttggagtccgtcgatccgaaa tctggaggcggaagcgggggtggcggcagcggcggtggaggatcaggtggcgggggggtccggggg cggaagtctgcagtccgagcggtgcgatgattggggcttagataccatgcggcagattcaggtgttcgaa gacgagcctgctcgcattaaatgcccgctctttgagcacttcctgaagtttaattacagcactgctcactccg caggactcacactgatctggtattggacacgccaagacagagatctggaggagcccattaattttaggctc cccgagaacaggatctctaaggagaaggacgtgctgtggtttcggccgacactactgaacgatactggga attacacatgtatgcttcgaaatactacctattgctccaaggtggcttttccacttgaggtggtgcagaaagac agctgttttaatagcccaatgaaactgcccgtgcacaagctgtacatcgaatatggcatacagagaatcaca tgccctaacgtcgacggctacttccctagctcagttaagccgaccataacttggtatatgggctgctataaaa tacagaacttcaataatgtaatccccgagggtatgaacttgagtttcctgatcgcactgatatctaacaacgg

		gaactacacctgtgtggtgacttatcccgagaacggacgcacattccatttgacaaggacgttaactgtcaa ggtagtgggtagtcctaagaatgcagttcctcccgtgattcacagccctaatgatcacgtggtgtatgaaaa agaaccaggtgaagaactcctgatcccctgcacggtgtacttctctttttaatggactcccgtaatgaagttt ggtggaccatcgacggcaaaaaacctgatgatattaccatcgacgtgacaatcaacgagagcatttcacat agtcggaccgaagatgagacaagaacccagattcttagcataaaaaaagtgacttctgaagacctgaagc gcagttacgtatgtcacgcgcgatccgcaaaaggggaagttgccaaggctgccaaggtgaagcagaaa gtccctgccccacggtacaccgtagagctggcctgtggcttcggagctacggttttgctggttgttatccttat cgtcgtctatcatgtgtactggttggagatggtgctttttatcgggcccatttcgggaccgatgagacgattct agacggaaaggagtacgatatttacgtctcgtacgccagaaatgcggaggaagaggaattcgtgctcttaa ccctgaggggagtactggaaaacgagtttggctacaagttgtgtatttttgacagagattcactgccaggag gaattgtcactgacgagacactctcattcatccagaaatctaggaggttgctcgttgtcctgagtccaaattat gtgctccaaggcacccaggccttgctagaactgaaggcggggcttgaaaacatggcctctcgcgggaac atcaacgtaattctggtgcagtacaaagcagtgaaggagaccaaagttaaagagctgaaacgagccaag acagtcctcactgtcatcaagtggaaaggtgaaaaatcaaagtatccacaagggagattctggaagcagct tcaagtcgctatgcccgtgaagaagtccccccgtcgttcctcctcggacgagcagggcctgagctacagc tctctcaagaatgtc **(SEQ ID NO: 134)**
IL-6	IL-6Rα	atggccttaccagtgaccgccttgctcctgccgctggccttgctgctccacgccgccaggccggtgccgc ccggggaagatagcaaggatgtggctgctcctcacaggcagccactgacaagcagcgagagaatcgac aagcaaataaggtatattcttgatggaatcagcgcgctgcgaaaggagacatgtaacaagtcgaatatgtg cgagtcttccaaagaagcacttgctgaaaataatctgaacctcccaaaaatggccgagaaagacggctgct ttcagtccggttttaacgaggagacttgtttagtaaagattataacgggcttgttggaattcgaagtctacctag aatacctccaaaatagattcgagagtagtgaggaacaggcccgcgctgttcagatgtcaacaaaagtgttg atccaattcctgcagaaaaaagccaagaacttagatgcaatcaccacacctgaccccactaccaatgcctct ctgctcaccaagctgcaagcccagaaccagtggctgcaggacatgactacccatctaattctgcggtctttt aaggagttcctccagtcatccctgcgtgcacttcggcagatgtctggaggcggaagcgggggtggcggc agcggcggtggaggatcaggtggcgggggtccgggggcggaagtctgcagcttgcaccaagacgct gtccggctcaggaggtcgctaggggagtgctgacctcgctgccgggcgactccgtgaccctgacatgtc ctggagtggagcctgaggacaacgcaacagttcactgggtgctacggaagcccgccgctggctcccatc cttccaggtgggccgggatggggcgcagactgcttctcagatcagtgcagttacatgatagcggtaattac agctgctaccgcgctggaaggccggcaggcactgtgcacctcctagtggatgttccacctgaggagcca cagttgagctgctttcgaaaaagtcccttgtctaacgtcgtatgcgagtggggccctagatcaactccctccc tcaccaccaaagcggttctcctcgtacgtaagttccaaaactctcctgccgaagattttcaagagccatgtca gtatagccaggagagtcagaagttctcatgccagcttgcagtcccggagggtgactcatccttctatattgtt agtatgtgcgtcgcctcgtctgtggggtctaagtttagcaagactcaaacttttcagggctgcggcatcctcc aaccagacccccctgccaacattacagtgaccgcagttgccagaaaccctaggtggttgagcgtgacgtg gcaggatccccattcctggaattcatcattctacagactgcggttcgagctccgatacagggcggaacgta gcaagacattcaccacgtggatggtcaaagacctgcagcaccactgtgtaatccatgacgcttggagcgg tctgcgccacgtggtccagctgcgggcacaagaggaattcggacagggtgaatggagtgaatggtctcct gaggctatgggcactccgtggaccgaatctcggtctccaccagccgaaaacgaagtgtccacccctatgc aggctctgactactaataaggatgacgataatatcttgtttagggactccgcaaatgctacatcactgcctgta caggattccagtagtgttcccctaccaacctttttagtcgccggagggtctctggcgttcgggacgttgctct gtatagccattgtgctgcgtttcaaaaagacctggaaactgcgcgccttaaaggagggaaaaacaagcat gcacccccccatattctcttgggcagctggtgcccgaacggcccagaccaacaccagtcctggtgcctctta tatcccccccccgtgagcccctctagcctgggcagtgacaataccagtagccataataggcccgacgcccg agaccctcgctccccatacgatatctcaaacacagattatttttttccccgg **(SEQ ID NO: 135)**

IL-6	gp130	atggccttaccagtgaccgccttgctcctgccgctggccttgctgctccacgccgccaggccggtgccgc ccggggaagatagcaaggatgtggctgctcctcacaggcagccactgacaagcagcgagagaatcgac aagcaaataaggtatattcttgatggaatcagcgcgctgcgaaaggagacatgtaacaagtcgaatatgtg cgagtcttccaaagaagcacttgctgaaaataatctgaacctcccaaaaatggccgagaaagacggctgct ttcagtccggttttaacgaggagacttgtttagtaaagattataacgggcttgttggaattcgaagtctacctag aatacctccaaaatagattcgagagtagtgaggaacaggcccgcgctgttcagatgtcaacaaaagtgttg atccaattcctgcagaaaaaagccaagaacttagatgcaatcaccacacctgaccccactaccaatgcctct ctgctcaccaagctgcaagcccagaaccagtggctgcaggacatgactacccatctaattctgcggtctttt aaggagttcctccagtcatccctgcgtgcacttcggcagatgtctggaggcggaagcgggggtggcggc agcggcggtggaggatcaggtggcgggggtccgggggcggaagtctgcaggaactcctggacccct gcgggtatattagccccgagtctcccgtggtgcaactgcattctaacttcaccgcagtttgtgtgctcaaaga aaagtgtatggattacttccatgttaacgccaactacattgtgtggaaaactaatcattttacgataccaaagg agcagtacacaattatcaacagaaccgcatcatccgtcacatttaccgatatcgcctccttgaacattcagct gacatgtaatatcttaacattcggtcaactggaacaaaacgtgtatggcatcaccatcatctctggacttcctc cagaaaaacccaaaaatttgtcgtgtatcgtgaatgagggaaaaaaaatgcgctgtgaatgggacgggggg ccgggagactcacctcgagacgaacttcacccttaagtcagagtgggcgacacataaatttgccgactgc aaagcaaagagagataccccacttcctgcaccgtcgactattcaactgtgtacttcgtcaacattgaggtgt gggtggaggcggagaatgcccttggcaaggttacttccgaccacatcaactttgatcccgtctacaaggtg aaaccgaacccacccccacaacctgtccgtcattaattcagaggagctaagttctatactcaagttaacttgga cgaatccctccataaagagtgtaattattctcaagtataacatccaatataggactaaagatgcttcaacctgg tcacagatcccaccggaggacaccgcctctacaaggtcatcgttcaccgtgcaggatcttaagcctttcac cgagtatgtgttcagaatccgatgcatgaaagaggacggcaaggggtattggagcgattggagcgaaga agcttccggcattacctacgaggacaggccttcgaaagcaccttctttctggtacaaaatcgatccttctcac actcagggctaccggaccgtgcagcttgtgtggaagactttgccaccattcgaggcaaatggaaagatact ggattatgaggtcacactgacccgctggaaaagtcacttgcagaactatacagtaaacgccaccaaactga cagtcaatctcactaacgatagatatttagcaaccctgactgtacgaaacctggtgggaaaatctgacgccg cggtactgactatccctgcttgtgactttcaggctacccaccctgttatggatctgaaggccttccctaaggat aacatgctatgggtcgagtggaccacaccaagggaaagcgtcaaaaagtatattctcgagtggtgcgttct gagcgacaaggccccatgtattacagactggcaacaggaggacgggacagttcatcggacatatctgcg cggcaatctagctgaaagtaaatgctaccttatcaccgtcacgccagtctacgccgacggcccgggctctc cagagtcaatcaaggcttacctaaagcaggcccctccctctaaggggccaactgtgagaacaaaaaaggt aggtaagaatgaagccgtcctggagtgggatcaactgccagtggacgtacagaacggtttcattcgcaact acaccatcttttacaggacgatcattgggaatgagacagcagtgaacgtggattcttcccataccgaataca cgctcagcagtctgacgtcggacacattgtacatggtcaggatggctgcatatacagacgaaggagggaa ggatgggcctgagttcacctttaccaccctaagttcgctcagggcgagattgaagcaattgtggtgcccgt atgcctggcctttctccttacgacactgctgggtgttctcttttgctttaataagcgggacctcatcaagaaaca catttggcctaatgtgcccgaccccagcaaaagtcacatagcccagtggagccctcatactcccccccgtc ataattttaatagcaaggatcagatgtacagcgacggcaattttacagacgtgtccgtcgtcgaaatagaag ctaatgataagaagccctttcctgaagacctgaaatccttggacttattcaaaaaggagaagatcaataccg aagggcactcctcagggataggggcagcagttgcatgtcctcatcccgtccctctatcagctccagcgat gagaacgagagcagccagaatactagttccactgttcagtacagcactgtagttcacagtggctatagaca tcaggtcccgagtgttcaggtgttctccaggagtgaatctacccagccgttgttagactcagaagaacgccc agaagacctgcagctggtggaccacgtggatggaggtgatggcattctgccgcgccagcaatactttaag cagaactgttctcagcatgaatccagccctgacatctctcactttgagcgaagcaaacaggtgtcaagcgtg aacgaagaggatttcgttcggcttaagcaacagatatctgaccacatctcacaatcctgcggaagtggaca aatgaagatgtttcaggaggttagtgcggccgatgctttcggccctggcactgagggtcaggtggaaagat

		tcgagacagtgggtatggaagccgctacagatgagggaatgcccaaaagctacctcccacaaaccgtgc ggcagggaggatatatgccacag **(SEQ ID NO: 136)**
scIL-12	IL-12-Rβ1	atggccttaccagtgaccgccttgctcctgccgctggccttgctgctccacgccgccaggccgatctggga gctcaaaaaggatgtttatgtggtcgaacttgactggtacccggacgcaccaggggagatggtggtgttga cctgcgacacccccgaagaggacgggattacatggactttggaccagtccagtgaagtcctgggctcgg gaaagaccctgactatccaggtgaaggagttcggagatgctggacaatatacatgccacaagggcgggg aagttttgagccattccctcctgctgctgcataaaaaagaggatggtatttggagcactgatattctgaaaga ccagaaggaacccaagaacaaaacttttctgcggtgtgaggccaagaattacagtggaagattcacctgtt ggtggttaaccacaatctctaccgatcttacctttccgtcaaatcaagtcgcggcagcagcgatccacagg gcgtgacgtgcggcgctgccacactaagcgcggagagagtgcggggtgacaacaaggaatacgagta ctccgttgagtgtcaagaagactctgcatgccctgccgcagaggaatcattaccgatcgaagtaatggtgg atgctgttcacaaactgaagtatgaaaactacacttcttcatttttcataagggacattatcaagcctgatcctc caaagaacctccaacttaaaccactcaagaatagccgtcaggtagaggtgtcctgggagtaccccgatac ctggtcaacgccccactcatatttctccctgacgttctgtgtgcaggtgcaggggaaatccaagagggaga agaaagacagggtctttacagataagacatctgccactgtcatctgcagaaaaaatgcctctatatccgtgc gagcccaggaccgctactattctagtagctggagcgagtgggctagtgtaccttgttcgggctcaaccagc ggatccgggaaacccggttctggcgaggggagtacaaagggacgaaatctgccagtggctacccccga cccgggcatgtttccctgcctccatcatagccagaatctgctcagagcggtcagcaacatgctacagaagg cccgccagaccttagagttttacccttgcacctctgaggaaatcgatcacgaagacatcaccaaagataag actagcaccgttgaagcctgtctcccattggaacttacaaaaaatgaatcttgtctgaattccagagagacat cttttatcactaatggaagttgcctcgccagtcggaaaacttccttcatgatggccctgtgtctgagttcaatct acgaggatcttaagatgtatcaagtggaattcaaaacgatgaacgcaaaactgttgatggatcctaagagg cagatatttttggatcagaacatgttagctgtgatcgacgagctgatgcaagcactcaacttcaactcagaga cagtcccccagaagtcctccctggaggagcctgacttctacaagacgaaaattaagctatgcattctgcttc acgcattcaggatacgggccgtaacaattgaccgtgtgatgagctatctgaacgcttcgtctggaggcgga agcgggggtggcggcagcggcggtggaggatcaggtggcgggggggtccgggggcggaagtctgca gtgcagaactagcgaatgttgtttccaggacccccccgtatcccgacgccgattccggaagcgcatccgga ccacgtgacctgcggtgctatcggatttctagcgataggtacgaatgctcatggcagtacgaggggccca ctgctggggtgagtcacttcttaagatgctgtttaagttccgggaggtgctgctatttcgccgcagggtcagc tactcgactacagttttctgaccaggctggagtaagcgtgctttatacagtgacactgtgggtcgaatcctgg gccaggaaccaaacggagaagtcacccgaggtgaccctgcaactgtataactcagtcaaatacgagcct cctctgggtgacattaaagtgtcgaaactcgccggacagcttagaatggagtgggagacccccgataacc aggttggcgcagaggtgcagttccggcaccgaacaccctcatctccttggaaactgggcgattgtggtcc gcaggacgacgataccgagagttgcttgtgtcccctagagatgaatgtcgcacaggagtttcagctgagg aggcgtcagctcggcagccaaggcagttcttggtcaaaatggtcctcccccgtctgcgttcccccctgaaaa tcctccacagccgcaggttcgattcagcgtggaacaactcgggcaggacgggagacgccgcttgactctt aaggagcaaccaacgcagctcgaactcccagaaggttgccagggcctggcacctggcaccgaggtgac ctaccgtttgcagttacatatgcttagttgcccttgtaaggccaaggctacacggacccttcacctaggcaaa atgccatacctaagcggtgctgcatacaacgtggcggtcatttcttccaaccagttcggacccggtctgaat cagacctggcacatccccgcagatacccataccgaacctgtggcgctgaatatcagcgtgggcacaaatg gcactacgatgtattggccggcccgcgctcaatctatgacttactgcatcgaatggcagcctgttgggcaa gatggaggactcgcgacatgcagccttactgccccgcaggaccctgatccagcaggtatggccacttatt cttggagccgcgagtccggggccatgggacaggagaagtgttactacatcaccatatttgcgtcagctcat ccagaaaagctgaccctgtggtcaaccgttctgagcacataccacttcgggggcaatgcgtccgctgcag gcaccccacaccacgtgtcggtgaaaaaccactctctggacagtgtgagtgttgactgggccccaagcct gttgtccacatgtcccggggtgctcaaggaatatgttgtccgctgtcgagacgaggactccaaacaagtgt

		cggaacatcccgtacagccaacggagacccaagtcactctgtctggactgagagccggcgtggcctaca cagtccaagtgcgggcagatacagcttggttacggggcgtatggagccagccacaaaggttcagcattga ggtacaggtctctgattggttgatttttttgccagtctgggcagttttctctctatcctgttggtcggagtgttgg gctatctgggactgaatcgcgccgccagacatctgtgccccccactcccaaccccatgtgcctcctccgcc atagaatttcctgggggtaaagagacatggcagtggatcaaccctgtagacttccaggaggaggctagcc tccaggaagccctggttgtggaaatgtcatgggataagggcgagagaacggaacctctcgagaagactg aacttcccgagggagctcctgagctcgcacttgacacagaactgtctttagaggatggggataggtgtaag gctaagatg **(SEQ ID NO: 137)**
scIL-12	IL-12-Rβ2	atggccttaccagtgaccgccttgctcctgccgctggccttgctgctccacgccgccaggccgatctggga gctcaaaaaggatgtttatgtggtcgaacttgactggtacccggacgcaccaggggagatggtggtgttga cctgcgacacccccgaagaggacgggattacatggactttggaccagtccagtgaagtcctgggctcgg gaaagaccctgactatccaggtgaaggagttcggagatgctggacaatatacatgccacaagggcgggg aagttttgagccattccctcctgctgctgcataaaaaagaggatggtatttggagcactgatattctgaaaga ccagaaggaacccaagaacaaaacttttctgcggtgtgaggccaagaattacagtggaagattcacctgtt ggtggttaaccacaatctctaccgatcttacctttccgtcaaatcaagtcgcggcagcagcgatccacagg gcgtgacgtgcggcgctgccacactaagcgcggagagagtgcggggtgacaacaaggaatacgagta ctccgttgagtgtcaagaagactctgcatgccctgccgcagaggaatcattaccgatcgaagtaatggtgg atgctgttcacaaactgaagtatgaaaactacacttcttcatttttcataagggacattatcaagcctgatcctc caaagaacctccaacttaaaccactcaagaatagccgtcaggtagaggtgtcctgggagtaccccgatac ctggtcaacgccccactcatatttctccctgacgttctgtgtgcaggtgcaggggaaatccaagagggaga agaaagacagggtctttacagataagacatctgccactgtcatctgcagaaaaaatgcctctatatccgtgc gagcccaggaccgctactattctagtagctggagcgagtgggctagtgtaccttgttcgggctcaaccagc ggatccgggaaacccggttctggcgaggggagtacaaagggacgaaatctgccagtggctacccccga cccgggcatgtttccctgcctccatcatagccagaatctgctcagagcggtcagcaacatgctacagaagg cccgccagaccttagagttttacccttgcacctctgaggaaatcgatcacgaagacatcaccaaagataag actagcaccgttgaagcctgtctcccattggaacttacaaaaaatgaatcttgtctgaattccagagagacat cttttatcactaatggaagttgcctcgccagtcggaaaacttccttcatgatggccctgtgtctgagttcaatct acgaggatcttaagatgtatcaagtggaattcaaaacgatgaacgcaaaactgttgatggatcctaagagg cagatatttttggatcagaacatgttagctgtgatcgacgagctgatgcaagcactcaacttcaactcagaga cagtcccccagaagtcctccctggaggagcctgacttctacaagacgaaaattaagctatgcattctgcttc acgcattcaggatacgggccgtaacaattgaccgtgtgatgagctatctgaacgcttcgtctggaggcgga agcgggggtggcggcagcggcggtggaggatcaggtggcgggggggtccgggggcggaagtctgca gaagattgacgcctgtaagcgaggagatgtcacagtgaagcccagtcacgtgattctcctcggaagcaca gttaatatcacttgctccctaaagccaaggcagggctgctttcactactcccggagaaataagctcatcctgt acaagtttgaccgcagaatcaacttccatcacggtcactctctgaattcgcaggtgacagggctgccgctg ggtacgacgttatttgtgtgcaaactggcctgcatcaactctgacgagattcagatctgtggagctgaaatttt cgttggcgtggctccagagcagccacagaacctctcttgtattcagaaaggggagcagggcacagttgcc tgtacctgggagcgcggtcgagacactcacctgtacactgaatatacgctgcagctgtctgggccaaaaa acctcacctggcagaagcaatgcaaagatatctattgcgactacctggacttcggcataaacctcacccca gagtccccagaaagcaatttcacagcaaaggtgaccgcggtgaactctcttggcagctcctcatctctccct agcacctttacgtttctggacatcgttcgacccttacccccctgggacatacggatcaagtttcagaaagcca gtgtgtcacgttgcaccctttactggcgagacgagggtttggtcttgttgaaccgccttcggtatcgcccatct aacagccgcctgtggaatatggtcaacgttaccaaagcgaaaggcagacacgatctgttggatctgaaac ctttcacagagtatgagttccagattagtagcaagctacacctgtataaaggatcatggtccgactggtcaga gtcactgagggcccagacacctgaggaagagcccaccggcatgttggacgtctggtacatgaagaggc acattgactacagccggcagcaaattagcctgttctggaagaatttgagtgtcagcgaagctagagggaag

		atcctacactaccaggtaaccctccaagagctaacagggggggaaagctatgactcaaaatatcactggac atacctcctggaccactgtgatccctcgtacgggcaattgggcagtggcggttagcgcagcaaattccaag ggaagtagtttacccacaagaatcaacattatgaacctgtgtgaagctgggctgttagctccccggcaggtc agcgcgaactccgaaggtatggataatatccttgtgacctggcaacccccccgtaaggatccctccgccgt ccaggagtatgtggtggagtggagggaacttcatcctggaggcgatacacaggtaccgctgaactggctt cggagtcggccctacaacgtgagcgccctgatctctgagaatatcaagagctatatttgttatgagattcgc gtgtatgcattatcgggtgatcagggggggttgctcaagcatattgggcaattcaaaacataaggccccactc agtggcccacatattaatgctatcaccgaggaaaagggctcaattctcatcagctggaactcaatcccagta caggaacaaatgggctgcctacttcattataggatctactggaaggagagggattctaattcccagccgca actttgtgaaatcccctacagagtgtcccagaacagtcatccaatcaattccttacagcccagagtgacatat gtgctctggatgactgctctgaccgcagccggagaatccagccacgggaacgagagggagttttgtcttc agggaaaggcaaactggatggccttcgtggccccttccatttgcatcgcaataattatggtcggcatctttag tactcactactttcagcaaaaagttttcgtactgctcgccgccctgcgccctcagtggtgtagcagagaaatt ccagaccctgcgaattccacatgcgccaaaaaataccccatagctgaggagaagacccagctgcctctag ataggctgctgattgactggccaactcccgaagatcctgaaccacttgtaattagtgaggtattacatcaggt gacaccagtcttcaggcatcctccttgttcaaactggccgcagcgagaaaaaggcatacaagggcatcaa gctagcgaaaaagatatgatgcatagtgcctcgtctcctcctcctccgcgggcactgcaggcagagtcac ggcagctggtcgatctgtacaaagtgttggaatctcgcggatcggacccgaagcccgagaatcccgcctg cccgtggaccgtcctccctgctggcgacttgcctactcacgatgggtacctcccctctaacatagacgacct gcctagccacgaagcccccctcgctgactctctggaggaactggagccccagcacatatccctgtccgttt tcccatctagctcattgcacccactcacctttttcttgtggagataaattgactctcgatcaactgaagatgagat gcgattccctgatgctt **(SEQ ID NO: 138)**
IL-4	IL-4Rα	atggccttaccagtgaccgccttgctcctgccgctggccttgctgctccacgccgccaggccgcacaagt gtgatattacactccaagaaataatcaagaccctgaacagcctaaccgagcagaaaactctctgtacggaa ttgaccgttaccgatatcttcgcagctagtaagaatacaactgaaaaagagacgttttgtcgtgccgccaca gtcctgaggcagttttattcacatcacgagaaagacacccggtgccttggggcaactgcccaacagtttcat cgccacaaacagctgatcagattcttgaagcggctggacaggaatctctggggattagctggcctgaattc ttgccccgtgaaggaggcgaaccagagcactctggagaacttcctggaacgacttaagacaattatgaga gagaagtactccaaatgctcctcttctggaggcggaagcgggggtggcggcagcggcggtggaggatc aggtggcgggggtccgggggcggaagtctgcagatgaaagtgctgcaggaaccgacctgcgtgagc gattatatgagcattagcacctgcgaatggaaaatgaacggcccgaccaactgcagcaccgaactgcgcc tgctgtatcagctggtgtttctgctgagcgaagcgcatacctgcattccggaaaacaacggcggcgcggg ctgcgtgtgccatctgctgatggatgatgtggtgagcgcggataactataccctggatctgtgggcgggcc agcagctgctgtggaaaggcagctttaaaccgagcgaacatgtgaaaccgcgcgcgccgggcaacctg accgtgcataccaacgtgagcgataccctgctgctgacctggagcaacccgtatccgccggataactatct gtataaccatctgacctatgcggtgaacatttggagcgaaaacgatccggcggattttcgcatttataacgtg acctatctggaaccgagcctgcgcattgcggcgagcaccctgaaaagcggcattagctatcgcgcgcgc gtgcgcgcgtgggcgcagtgctataacaccacctggagcgaatggagcccgagcaccaaatggcataa cagctatcgcgaaccgtttgaacagcatctgctgctgggcgtgagcgtgagctgcattgtgattctggcggt gtgcctgctgtgctatgtgagcattaccaaaattaaaaaagaatggtgggatcagattccgaacccggcgc gcagccgcctggtggcgattattattcaggatgcgcagggcagccagtgggaaaaacgcagccgcggc caggaaccggcgaaatgcccgcattggaaaaactgcctgaccaaactgctgccgtgctttctggaacata acatgaaacgcgatgaagatccgcataaagcggcgaaagaaatgccgtttcagggcagcggcaaaagc gcgtggtgcccggtggaaattagcaaaaccgtgctgtggccggaaagcattagcgtggtgcgctgcgtg gaactgtttgaagcgccggtggaatgcgaagaagaagaagaagtggaagaagaaaaaggcagcttttgc gcgagcccggaaagcagccgcgatgattttcaggaaggccgcgaaggcattgtggcgcgcctgaccga

		aagcctgtttctggatctgctgggcgaagaaaacggcggcttttgccagcaggatatgggcgaaagctgc ctgctgccgccgagcggcagcaccagcgcgcatatgccgtgggatgaatttccgagcgcgggcccgaa agaagcgccgccgtggggcaaagaacagccgctgcatctggaaccgagcccgccggcgagcccgac ccagagcccggataacctgacctgcaccgaaaccccgctggtgattgcgggcaacccggcgtatcgca gctttagcaacagcctgagccagagcccgtgcccgcgcgaactgggcccggatccgctgctggcgcgc catctggaagaagtggaaccggaaatgccgtgcgtgccgcagctgagcgaaccgaccaccgtgccgca gccggaaccggaaacctgggaacagattctgcgccgcaacgtgctgcagcatggcgcggcggcggcgg ccggtgagcgcgccgaccagcggctatcaggaatttgtgcatgcggtggaacagggcggcacccaggc gagcgcggtggtgggcctgggcccgccgggcgaagcgggctataaagcgtttagcagcctgctggcga gcagcgcggtgagcccggaaaaatgcggctttggcgcgagcagcggcgaagaaggctataaaccgttt caggatctgattccgggctgcccgggcgatccggcgccggtgccggtgccgctgtttacctttggcctgg atcgcgaaccgccgcgcagcccgcagagcagccatctgccgagcagcagcccggaacatctgggcct ggaaccgggcgaaaaagtggaagatatgccgaaaccgccgctgccgcaggaacaggcgaccgatccg ctggtggatagcctgggcagcggcattgtgtatagcgcgctgacctgccatctgtgcggccatctgaaaca gtgccatggccaggaagatggcggccagaccccggtgatggcgagcccgtgctgcggctgctgctgcg gcgatcgcagcagcccgccgaccaccccgctgcgcgcgccggatccgagcccgggcggcgtgccgc tggaagcgagcctgtgcccggcgagcctggcgccgagcggcattagcgaaaaaagcaaaagcagcag cagctttcatccggcgccgggcaacgcgcagagcagcagccagaccccgaaaattgtgaactttgtgag cgtgggcccgacctatatgcgcgtgagc **(SEQ ID NO: 139)**
IL-4	IL-2Rγc	atggccttaccagtgaccgccttgctcctgccgctggccttgctgctccacgccgccaggccgcacaagt gtgatattacactccaagaaataatcaagaccctgaacagcctaaccgagcagaaaactctctgtacggaa ttgaccgttaccgatatcttcgcagctagtaagaatacaactgaaaaagagacgttttgtcgtgccgccaca gtcctgaggcagttttattcacatcacgagaaagacacccggtgccttggggcaactgcccaacagtttcat cgccacaaacagctgatcagattcttgaagcggctggacaggaatctctggggattagctggcctgaattc ttgccccgtgaaggaggcgaaccagagcactctggagaacttcctggaacgacttaagacaattatgaga gagaagtactccaaatgctcctcttctggaggcggaagcgggggtggcggcagcggcggtggaggatc aggtggcgggggtccgggggcggaagtctgcagctgaacacaacaattctcacccctaacggcaacg aagacactaccgcagatttttcctcactactatgcccactgattccctttccgtgtcgaccttgccgctgcca gaagtgcagtgcttcgtctttaatgttgagtatatgaattgtacatggaattctagcagcgaaccgcagccaa ccaatttgacattgcactactggtataaaaactcagataacgacaaagtgcagaagtgttcccactacttattt agcgaggaaataacctctgggtgccagctgcagaagaaggagatccatctgtaccagaccttcgtcgtgc agctccaggatccacgggaaccacgccggcaagctacccaaatgctaaagctgcaaaatctcgttatccc atgggcacctgagaatttgacacttcataagctgtcggaatcccagctggagctcaattggaacaaccgttt cctcaaccattgtctggagcacctggtgcagtacagaaccgactgggaccatagttggacggagcagagt gtcgattatagacacaaattctcactaccctcagtggacgggcagaagaggtacacatttagagtaaggag tcggttcaatcccctgtgcgggtccgcccaacactggagtgagtggtctcatcctattcactggggcagca acacgtccaaggagaacccttttcttgtttgctctggaagctgttgtgatttcagtaggctctatgggattaatca tcagcctcctgtgtgtctatttttggctggagcgaacaatgcccaggatccccactctcaaaaatctggaaga ccttgtgacggagtatcacggcaacttcagcgcgtggtctggcgtctctaaaggtcttgccgagagcctgc agcctgattacagtgagcgcttatgcctggtgagcgagataccacctaaaggaggagcccttggtgaagg accgggggcatccccctgtaatcaacactcaccatactgggcccccccctgctataccctaaagcctgaaa ct **(SEQ ID NO: 140)**
IL-4	IL-13Ra1	atggccttaccagtgaccgccttgctcctgccgctggccttgctgctccacgccgccaggccgcacaagt gtgatattacactccaagaaataatcaagaccctgaacagcctaaccgagcagaaaactctctgtacggaa ttgaccgttaccgatatcttcgcagctagtaagaatacaactgaaaaagagacgttttgtcgtgccgccaca gtcctgaggcagttttattcacatcacgagaaagacacccggtgccttggggcaactgcccaacagtttcat

		cgccacaaacagctgatcagattcttgaagcggctggacaggaatctctggggattagctggcctgaattc ttgccccgtgaaggaggcgaaccagagcactctggagaacttcctggaacgacttaagacaattatgaga gagaagtactccaaatgctcctcttctggaggcggaagcgggggtggcggcagcggcggtggaggatc aggtggcgggggtccgggggcggaagtctgcagggcggcggcggcgcggcgccgaccgaaaccc agccgccggtgaccaacctgagcgtgagcgtggaaaacctgtgcaccgtgatttggacctggaacccgc cggaaggcgcgagcagcaactgcagcctgtggtattttagccattttggcgataaacaggataaaaaaatt gcgccggaaacccgccgcagcattgaagtgccgctgaacgaacgcatttgcctgcaggtgggcagcca gtgcagcaccaacgaaagcgaaaaaccgagcattctggtggaaaaatgcattagcccgccggaaggcg atccggaaagcgcggtgaccgaactgcagtgcatttggcataacctgagctatatgaaatgcagctggctg ccgggccgcaacaccagcccggataccaactataccctgtattattggcatcgcagcctggaaaaaattca tcagtgcgaaaacatttttcgcgaaggccagtattttggctgcagctttgatctgaccaaagtgaaagatagc agctttgaacagcatagcgtgcagattatggtgaaagataacgcgggcaaaattaaaccgagctttaacatt gtgccgctgaccagccgcgtgaaaccggatccgccgcatattaaaaacctgagctttcataacgatgatct gtatgtgcagtgggaaaacccgcagaactttattagccgctgcctgttttatgaagtggaagtgaacaacag ccagaccgaaacccataacgtgttttatgtgcaggaagcgaaatgcgaaaacccggaatttgaacgcaac gtggaaaacaccagctgctttatggtgccgggcgtgctgccggataccctgaacaccgtgcgcattcgcg tgaaaaccaacaaactgtgctatgaagatgataaactgtggagcaactggagccaggaaatgagcattgg caaaaaacgcaacagcaccctgtatattaccatgctgctgattgtgccggtgattgtggcgggcgcgattat tgtgctgctgctgtatctgaaacgcctgaaaattattattttccgccgattccggatccgggcaaaatttttaa agaaatgtttggcgatcagaacgatgataccctgcattggaaaaaatatgatatttatgaaaaacagaccaa agaagaaaccgatagcgtggtgctgattgaaaacctgaaaaaagcgagccag **(SEQ ID NO: 141)**
cpIL-4(38-37)	IL-4Rα	atggccttaccagtgaccgccttgctcctgccgctggccttgctgctccacgccgccaggccgaatacgac tgagaaagagacctttgtagggctgccacagtcctgcggcagttctatagtcaccatgagaaagacacca gatgtctgggggcaaccgctcagcaattccatagacacaagcagttaatccgatttctgaagcggcttgatc gtaacttgtggggactagccggcctgaactcatgccccgtgaaagaagcgaatcagtccactcttgagaa cttcctcgaaaggctcaagacaattatgcgcgaaaagtacagcaagtgcagctctggcggaaacggtgg gcacaagtgtgatattacgctccaagaaatcatcaagactctgaactccctgaccgagcagaaaacactttg cactgagttgacagtgaccgacatattcgccgctagcaaatctggaggcggaagcgggggtggcggca gcggcggtggaggatcaggtggcgggggtccgggggcggaagtctgcagatgaaagtgctgcagga accgacctgcgtgagcgattatatgagcattagcacctgcgaatggaaaatgaacggcccgaccaactgc agcaccgaactgcgcctgctgtatcagctggtgtttctgctgagcgaagcgcatacctgcattccggaaaa caacggcggcgcgggctgcgtgtgccatctgctgatggatgatgtggtgagcgcggataactataccctg gatctgtgggcgggccagcagctgctgtggaaaggcagctttaaaccgagcgaacatgtgaaaccgcgc gcgccgggcaacctgaccgtgcataccaacgtgagcgataccctgctgctgacctggagcaacccgtat ccgccggataactatctgtataaccatctgacctatgcggtgaacatttggagcgaaaacgatccggcgga ttttcgcatttataacgtgacctatctggaaccgagcctgcgcattgcggcgagcaccctgaaaagcggcat tagctatcgcgcgcgcgtgcgcgcgtgggcgcagtgctataacaccacctggagcgaatggagcccga gcaccaaatggcataacagctatcgcgaaccgtttgaacagcatctgctgctgggcgtgagcgtgagctg cattgtgattctggcggtgtgcctgctgtgctatgtgagcattaccaaaattaaaaaagaatggtgggatcag attccgaacccggcgcgcagccgcctggtggcgattattattcaggatgcgcagggcagccagtgggaa aaacgcagccgcggccaggaaccggcgaaatgcccgcattggaaaaactgcctgaccaaactgctgcc gtgctttctggaacataacatgaaacgcgatgaagatccgcataaagcggcgaaagaaatgccgtttcag ggcagcggcaaaagcgcgtggtgcccggtggaaattagcaaaaccgtgctgtggccggaaagcattag cgtggtgcgctgcgtggaactgtttgaagcgccggtggaatgcgaagaagaagaagaagtggaagaag aaaaaggcagcttttgcgcgagcccggaaagcagccgcgatgattttcaggaaggccgcgaaggcattg

		tggcgcgcctgaccgaaagcctgtttctggatctgctgggcgaagaaaacggcggcttttgccagcagga tatgggcgaaagctgcctgctgccgccgagcggcagcaccagcgcgcatatgccgtgggatgaatttcc gagcgcgggcccgaaagaagcgccgccgtggggcaaagaacagccgctgcatctggaaccgagccc gccggcgagcccgacccagagcccggataacctgacctgcaccgaaaccccgctggtgattgcgggca acccggcgtatcgcagctttagcaacagcctgagccagagcccgtgcccgcgcgaactgggcccggat ccgctgctggcgcgccatctggaagaagtggaaccggaaatgccgtgcgtgccgcagctgagcgaacc gaccaccgtgccgcagccggaaccggaaacctgggaacagattctgcgccgcaacgtgctgcagcatg gcgcggcggcggcgccggtgagcgcgccgaccagcggctatcaggaatttgtgcatgcggtggaaca gggcggcacccaggcgagcgcggtggtgggcctgggcccgccgggcgaagcgggctataaagcgttt agcagcctgctggcgagcagcgcggtgagcccggaaaaatgcggctttggcgcgagcagcggcgaag aaggctataaaccgtttcaggatctgattccgggctgcccgggcgatccggcgccggtgccggtgccgct gtttacctttggcctggatcgcgaaccgccgcgcagcccgcagagcagccatctgccgagcagcagccc ggaacatctgggcctggaaccgggcgaaaaagtggaagatatgccgaaaccgccgctgccgcaggaa caggcgaccgatccgctggtggatagcctgggcagcggcattgtgtatagcgcgctgacctgccatctgt gcggccatctgaaacagtgccatggccaggaagatggcggccagaccccggtgatggcgagcccgtg ctgcggctgctgctgcggcgatcgcagcagcccgccgaccaccccgctgcgcgcgccggatccgagc ccgggcggcgtgccgctggaagcgagcctgtgcccggcgagcctggcgccgagcggcattagcgaaa aaagcaaaagcagcagcagctttcatccggcgccgggcaacgcgcagagcagcagccagaccccgaa aattgtgaactttgtgagcgtgggcccgacctatatgcgcgtgagc **(SEQ ID NO: 142)**
cpIL-4(38-37)	IL-2Rγc	atggccttaccagtgaccgccttgctcctgccgctggccttgctgctccacgccgccaggccgaatacgac tgagaaagagacctttgtagggctgccacagtcctgcggcagttctatagtcaccatgagaaagacacca gatgtctgggggcaaccgctcagcaattccatagacacaagcagttaatccgatttctgaagcggcttgatc gtaacttgtggggactagccggcctgaactcatgccccgtgaaagaagcgaatcagtccactcttgagaa cttcctcgaaaggctcaagacaattatgcgcgaaaagtacagcaagtgcagctctggcggaaacggtgg gcacaagtgtgatattacgctccaagaaatcatcaagactctgaactccctgaccgagcagaaaacactttg cactgagttgacagtgaccgacatattcgccgctagcaaatctggaggcggaagcgggggtggcggca gcggcggtggaggatcaggtggcgggggtccgggggcggaagtctgcagctgaacacaacaattctc acccctaacggcaacgaagacactaccgcagatttttcctcactactatgcccactgattccctttccgtgtc gaccttgccgctgccagaagtgcagtgcttcgtctttaatgttgagtatatgaattgtacatggaattctagca gcgaaccgcagccaaccaatttgacattgcactactggtataaaaactcagataacgacaaagtgcagaa gtgttcccactacttatttagcgaggaaataacctctgggtgccagctgcagaagaaggagatccatctgta ccagaccttcgtcgtgcagctccaggatccacgggaaccacgccggcaagctacccaaatgctaaagct gcaaaatctcgttatcccatgggcacctgagaatttgacacttcataagctgtcggaatcccagctggagct caattggaacaaccgtttcctcaaccattgtctggagcacctggtgcagtacagaaccgactgggaccata gttggacggagcagagtgtcgattatagacacaaattctcactaccctcagtggacgggcagaagaggta cacatttagagtaaggagtcggttcaatcccctgtgcgggtccgcccaacactggagtgagtggtctcatc ctattcactggggcagcaacacgtccaaggagaacccttttcttgtttgctctggaagctgttgtgatttcagta ggctctatgggattaatcatcagcctcctgtgtgtctatttttggctggagcgaacaatgcccaggatcccca ctctcaaaaatctggaagaccttgtgacggagtatcacggcaacttcagcgcgtggtctggcgtctctaaag gtcttgccgagagcctgcagcctgattacagtgagcgcttatgcctggtgagcgagataccacctaaagga ggagcccttggtgaaggaccgggggcatccccctgtaatcaacactcaccatactgggcccccccctgct ataccctaaagcctgaaact **(SEQ ID NO: 143)**
cpIL-4(38-37)	IL-13Ra1	atggccttaccagtgaccgccttgctcctgccgctggccttgctgctccacgccgccaggccgaatacgac tgagaaagagacctttgtagggctgccacagtcctgcggcagttctatagtcaccatgagaaagacacca gatgtctgggggcaaccgctcagcaattccatagacacaagcagttaatccgatttctgaagcggcttgatc gtaacttgtggggactagccggcctgaactcatgccccgtgaaagaagcgaatcagtccactcttgagaa

		cttcctcgaaaggctcaagacaattatgcgcgaaaagtacagcaagtgcagctctggcggaaacggtgg gcacaagtgtgatattacgctccaagaaatcatcaagactctgaactccctgaccgagcagaaaacactttg cactgagttgacagtgaccgacatattcgccgctagcaaatctggaggcggaagcgggggtggcggca gcggcggtggaggatcaggtggcgggggtccgggggcggaagtctgcagggcggcggcggcgcg gcgccgaccgaaacccagccgccggtgaccaacctgagcgtgagcgtggaaaacctgtgcaccgtgat ttggacctggaacccgccggaaggcgcgagcagcaactgcagcctgtggtattttagccattttggcgata aacaggataaaaaaattgcgccggaaacccgccgcagcattgaagtgccgctgaacgaacgcatttgcct gcaggtgggcagccagtgcagcaccaacgaaagcgaaaaaccgagcattctggtggaaaaatgcatta gcccgccggaaggcgatccggaaagcgcggtgaccgaactgcagtgcatttggcataacctgagctata tgaaatgcagctggctgccgggccgcaacaccagcccggataccaactataccctgtattattggcatcgc agcctggaaaaaattcatcagtgcgaaaacatttttcgcgaaggccagtattttggctgcagctttgatctga ccaaagtgaaagatagcagctttgaacagcatagcgtgcagattatggtgaaagataacgcgggcaaaat taaaccgagctttaacattgtgccgctgaccagccgcgtgaaaccggatccgccgcatattaaaaacctga gctttcataacgatgatctgtatgtgcagtgggaaaacccgcagaactttattagccgctgcctgttttatgaa gtggaagtgaacaacagccagaccgaaacccataacgtgttttatgtgcaggaagcgaaatgcgaaaac ccggaatttgaacgcaacgtggaaaacaccagctgctttatggtgccgggcgtgctgccggataccctga acaccgtgcgcattcgcgtgaaaaccaacaaactgtgctatgaagatgataaactgtggagcaactggag ccaggaaatgagcattggcaaaaaacgcaacagcaccctgtatattaccatgctgctgattgtgccggtga ttgtggcgggcgcgattattgtgctgctgctgtatctgaaacgcctgaaaattattattttccgccgattccgg atccgggcaaaatttttaaagaaatgtttggcgatcagaacgatgataccctgcattggaaaaaatatgatatt tatgaaaaacagaccaaagaagaaaccgatagcgtggtgctgattgaaaacctgaaaaaagcgagccag **(SEQ ID NO: 144)**
IL-10	IL-10R1	atggccttaccagtgaccgccttgctcctgccgctggccttgctgctccacgccgccaggccgtcacccg gacagggtactcaatctgaaaatagttgcacccattttccaggaaatctgcctaacatgctgagggacttac gcgatgcattttcgcgtgtaaaaacattctttcagatgaaagatcaactggataacctgttgctaaaagagag cctgcttgaggatttcaagggctatctgggctgtcaggcgctctccgaaatgattcaattctacctcgaagag gtgatgccccaggccgagaaccaggacccagacatcaaggcccacgtgaattctctgggggagaatctg aaaacgctcagattgcgactcagacggtgccacaggtttttaccttgtgaaaacaagagcaaagccgttga gcaggtcaagaacgcttttaataagcttcaggaaaaagggatctataaggcaatgtccgagttcgacatatt cattaattacattgaggcttacatgaccatgaagatccggaactctggaggcggaagcgggggtggcggc agcggcggtggaggatcaggtggcgggggtccgggggcggaagtctgcagcatgggaccgagctc cccagtcctccttctgtttggttcgaagccgaattctttcaccatattctgcactggactcctatcccaaatcaat cagaatcaacatgttacgaggtggcactgctgaggtacggaatcgagtcttggaatagcatttcaaactgta gccaaaccctgtcttacgatcttaccgctgtgacgctggacctgtatcatagcaacggctaccgtgccagg gttagggcagttgatggcagcagacactccaattggacagttacgaatacccgattcagtgtcgacgaggt gactttaactgtcgggagtgttaaccttgaaattcacaacgggttcatattgggaaagatccagctcccccg gccaaaaatggccccagccaacgacacatacgagagtatattttctcattttagagagtatgagatcgcaat ccgcaaggtgcctgggaatttcacatttactcataagaaggtaaaacacgagaacttctccttgctcacctcc ggcgaagtgggggagttctgcgtgcaggtgaagccctcggtggcttcacgctccaataaaggcatgtgg agcaaagaagaatgtatttctctgactcggcagtactttaccgtgactaacgtaatcatatttttgccttcgtgc tcctgctgtctggtgccctggcctattgcctggcgcttcaactttatgtgcggaggaggaagaagctgccgt ccgtgctgttgtttaagaaaccgtctcccttcatttttatcagccagcgcccctcacccgaaacacaggatact attcacccccttgacgaagaagccttccttaaagtgtcccccgagctaaaaaacctcgacctgcacgggtc caccgatagcgggtttggtagcaccaaaccatccttgcaaaccgaggagccccagttcttgctcctgatc cacacccacaggctgacagaacgttgggaaacagagagcccccagtcctgggggattcctgttcgtcag ggtctagtaatagtaccgatagcgggatttgcctgcaggagccgagcctgtcaccctcaaccggtccgac

		ctgggagcagcaagtaggatctaactcccgcgggcaggatgactccggcatagacctcgtacagaattc ggaaggccgggcgggtgacacacagggcggctccgctctgggccaccattccccaccagagcccgag gtccctggcgaggaggaccctgcagccgtcgcttttcaaggctatctgcgtcagacacgatgtgctgaag agaaagctactaagacgggatgtcttgaagaggaatctccgcttacagacggattgggaccaaagttcgg cagatgcctagtggatgaggcgggactacatcctcccgcattagcaaagggctacctgaagcaggatcca ctagaaatgacactggcctcatctggcgcccctacaggacagtggaaccagccaaccgaagagtggtcc ttgctcgctttaagctcttgcagtgacctgggtatctcagattggagttttgcacacgacctcgcccctctggg ttgcgtcgccgctcctggtggactcttaggaagtttcaatagcgatctcgtcactctgcctctcatcagtagct tacagagcagcgaa **(SEQ ID NO: 145)**
IL-10	IL-10R2	atggccttaccagtgaccgccttgctcctgccgctggccttgctgctccacgccgccaggccgtcacccg gacagggtactcaatctgaaaatagttgcacccattttccaggaaatctgcctaacatgctgagggacttac gcgatgcattttcgcgtgtaaaaacattctttcagatgaaagatcaactggataacctgttgctaaaagagag cctgcttgaggatttcaagggctatctgggctgtcaggcgctctccgaaatgattcaattctacctcgaagag gtgatgccccaggccgagaaccaggacccagacatcaaggcccacgtgaattctctgggggagaatctg aaaacgctcagattgcgactcagacggtgccacaggtttttaccttgtgaaaacaagagcaaagccgttga gcaggtcaagaacgcttttaataagcttcaggaaaaagggatctataaggcaatgtccgagttcgacatatt cattaattacattgaggcttacatgaccatgaagatccggaactctggaggcggaagcgggggtggcggc agcggcggtggaggatcaggtggcgggggggtccgggggcggaagtctgcagatggtaccaccacctg aaaatgtgaggatgaactctgtgaattttaagaacattctccagtgggaaagtcccgcttttgctaaggggaa cctgaccttcacagcccaatacttatcctaccgaatcttccaagacaagtgcatgaataccactttaactgaat gcgacttctcaagcctgtctaagtatggcgatcatacactgcgggttcgtgccgagtttgccgacgagcact ctgactgggtgaatataaccttctgccccgtcgatgatactataattgggccaccaggtatgcaagttgaagt gttggcagattcgctgcacatgaggtttctcgcccccaaaatcgagaacgagtacgagacctggacgatg aagaatgtctacaactcttggacatataatgttcagtattggaaaaacggaaccgacgagaagtttcagatc actccgcagtatgatttcgaagtcctgagaaacctcgagccttggacaacttactgtgtccaagtgcgcggc tttctccctgaccggaacaaggcaggagagtggtcagaaccggtgtgtgagcagaccacccacgacgag acagtacccagctggatggtagctgtgatccttatggcctccgtgttcatggtttgtctagctttgttgggctgt tttgcccttctatggtgcgtctataaaaagaccaaatacgcgttttcacctagaaacagccttccacagcacct caaggagttcctggggcatcctcatcacaatacactgctgttcttctccttccccctgagtgacgaaaacgat gtgtttgataaactgtccgtgattgcagaagacagtgagtccggcaaacagaatccaggagatagttgcag cctgggtacgcctcccggacagggcccccagagc **(SEQ ID NO: 146)**
mIL-10	IL-10R1	atggccttaccagtgaccgccttgctcctgccgctggccttgctgctccacgccgccaggccgtcgcctgg ccagggaacgcagagtgaaaatagctgtacccactttcccggcaacctaccaaatatgctcagagatctgc gggatgcattctcccgggtgaagacatttttccaaatgaaggatcagttggacaaccttctgttgaaggagtc actcttagaggacttcaagggatacctggggtgccaagccctgtctgagatgattcagttctacctcgaaga ggtaatgccacaggccgaaaaccaggaccctgatataaaagctcatgtcaatagtttaggcgagaatctga aaactctcaggctgcgtctgcgaagatgccaccgctttctgccctgtgagaacgggggagggtctggtgg caaaagcaaagctgtggagcaagttaaaaatgcattcaacaaacttcaggagaagggtatttataaggcga tgtccgaatttgacatctttattaattacatcgaagcctatatgaccatgaagatcaggaactctggaggcgg aagcgggggtggcggcagcggcggtggaggatcaggtggcgggggggtccgggggcggaagtctgc agcatgggaccgagctccccagtcctccttctgtttggttcgaagccgaattctttcaccatattctgcactgg actcctatcccaaatcaatcagaatcaacatgttacgaggtggcactgctgaggtacggaatcgagtcttgg aatagcatttcaaactgtagccaaaccctgtcttacgatcttaccgctgtgacgctggacctgtatcatagca acggctaccgtgccagggttagggcagttgatggcagcagacactccaattggacagttacgaatacccg attcagtgtcgacgaggtgactttaactgtcgggagtgttaaccttgaaattcacaacgggttcatattggga aagatccagctcccccggccaaaaatggccccagccaacgacacatacgagagtatattttctcattttaga

		gagtatgagatcgcaatccgcaaggtgcctgggaatttcacatttactcataagaaggtaaaacacgagaa cttctccttgctcacctccggcgaagtgggggagttctgcgtgcaggtgaagccctcggtggcttcacgct ccaataaaggcatgtggagcaaagaagaatgtatttctctgactcggcagtactttaccgtgactaacgtaat catatttttgccttcgtgctcctgctgtctggtgccctggcctattgcctggcgcttcaactttatgtgcggagg aggaagaagctgccgtccgtgctgttgtttaagaaaccgtctcccttcatttttatcagccagcgcccctcac ccgaaacacaggatactattcacccccttgacgaagaagccttccttaaagtgtcccccgagctaaaaaac ctcgacctgcacgggtccaccgatagcgggtttggtagcaccaaaccatccttgcaaaccgaggagccc cagttcttgctccctgatccacacccacaggctgacagaacgttgggaaacagagagcccccagtcctgg gggattcctgttcgtcagggtctagtaatagtaccgatagcgggatttgcctgcaggagccgagcctgtca ccctcaaccggtccgacctgggagcagcaagtaggatctaactcccgcgggcaggatgactccggcata gacctcgtacagaattcggaaggccgggcgggtgacacacagggcggctccgctctgggccaccattc cccaccagagcccgaggtccctggcgaggaggaccctgcagccgtcgcttttcaaggctatctgcgtca gacacgatgtgctgaagagaaagctactaagacgggatgtcttgaagaggaatctccgcttacagacggga ttgggaccaaagttcggcagatgcctagtggatgaggcgggactacatcctcccgcattagcaaagggct acctgaagcaggatccactagaaatgacactggcctcatctggcgcccctacaggacagtggaaccagc caaccgaagagtggtccttgctcgctttaagctcttgcagtgacctgggtatctcagattggagttttgcaca cgacctcgcccctctgggttgcgtcgccgctcctggtggactcttaggaagtttcaatagcgatctcgtcact ctgcctctcatcagtagcttacagagcagcgaa **(SEQ ID NO: 147)**
mIL-10	IL-10R2	atggccttaccagtgaccgccttgctcctgccgctggccttgctgctccacgccgccaggccgtcgcctgg ccagggaacgcagagtgaaaatagctgtacccactttcccggcaacctaccaaatatgctcagagatctgc gggatgcattctcccgggtgaagacatttttccaaatgaaggatcagttggacaaccttctgttgaaggagtc actcttagaggacttcaagggatacctggggtgccaagccctgtctgagatgattcagttctacctcgaaga ggtaatgccacaggccgaaaaccaggaccctgatataaaagctcatgtcaatagtttaggcgagaatctga aaactctcaggctgcgtctgcgaagatgccaccgctttctgccctgtgagaacgggggagggtctggtgg caaaagcaaagctgtggagcaagttaaaaatgcattcaacaaacttcaggagaagggtatttataaggcga tgtccgaatttgacatctttattaattacatcgaagcctatatgaccatgaagatcaggaactctggaggcgg aagcgggggtggcggcagcggcggtggaggatcaggtggcgggggggtccgggggcggaagtctgc agatggtaccaccacctgaaaatgtgaggatgaactctgtgaattttaagaacattctccagtgggaaagtc ccgcttttgctaaggggaacctgaccttcacagcccaatacttatcctaccgaatcttccaagacaagtgcat gaataccactttaactgaatgcgacttctcaagcctgtctaagtatggcgatcatacactgcgggttcgtgcc gagtttgccgacgagcactctgactgggtgaatataaccttctgccccgtcgatgatactataattgggcca ccaggtatgcaagttgaagtgttggcagattcgctgcacatgaggtttctcgcccccaaaatcgagaacga gtacgagacctggacgatgaagaatgtctacaactcttggacatataatgttcagtattggaaaaacggaac cgacgagaagtttcagatcactccgcagtatgatttcgaagtcctgagaaacctcgagccttggacaactta ctgtgtccaagtgcgcggctttctccctgaccggaacaaggcaggagagtggtcagaaccggtgtgtgag cagaccacccacgacgagacagtacccagctggatggtagctgtgatccttatggcctccgtgttcatggtt tgtctagctttgttgggctgttttgcccttctatggtgcgtctataaaaagaccaaatacgcgttttcacctagaa acagccttccacagcacctcaaggagttcctggggcatcctcatcacaatacactgctgttcttctccttccc cctgagtgacgaaaacgatgtgtttgataaactgtccgtgattgcagaagacagtgagtccggcaaacaga atccaggagatagttgcagcctgggtacgcctcccggacagggcccccagagc **(SEQ ID NO: 148)**
cpIL-10(58/57)	IL-10R1	atggccttaccagtgaccgccttgctcctgccgctggccttgctgctccacgccgccaggccgggttactt gggctgtcaggctctgagtgaaatgattcagttctatcttgaagaggttatgcctcaggcggagaaccaaga cccagacatcaaggcccatgtgaactctctcggggagaatctgaaaacactgcgactgcggttaagacgtt gccacaggttcctaccctgcgaaaataaaagcaaggccgtcgagcaagtgaaaaacgcattcaataaact ccaggaaaagggaatttacaaggccatgtccgagtttgatatctttataaactatattgaggcttacatgacca

		tgaagatccgcaatggtggtggtggaagcggcgggggaggcagtgggggaggcgggtcctcccctgg ccagggaactcagtcagaaaatagctgcacacactttccagggaatctccccaacatgttgagagatctga gggacgccttctctcgggtgaaaaccttttccaaatgaaagaccagctggacaacctccttctgaaggag agtttactagaggatttcaagtctggaggcggaagcgggggtggcggcagcggcggtggaggatcagg tggcgggggggtccgggggcggaagtctgcagcatgggaccgagctccccagtcctccttctgtttggttc gaagccgaattctttcaccatattctgcactggactcctatcccaaatcaatcagaatcaacatgttacgaggt ggcactgctgaggtacggaatcgagtcttggaatagcatttcaaactgtagccaaaccctgtcttacgatctt accgctgtgacgctggacctgtatcatagcaacggctaccgtgccagggttagggcagttgatggcagca gacactccaattggacagttacgaatacccgattcagtgtcgacgaggtgactttaactgtcgggagtgtta accttgaaattcacaacgggttcatattgggaaagatccagctccccggccaaaaatggccccagccaa cgacacatacgagagtatattttctcattttagagagtatgagatcgcaatccgcaaggtgcctgggaatttc acatttactcataagaaggtaaaacacgagaacttctccttgctcacctccggcgaagtgggggagttctgc gtgcaggtgaagccctcggtggcttcacgctccaataaaggcatgtggagcaaagaagaatgtatttctct gactcggcagtactttaccgtgactaacgtaatcatatttttgccttcgtgctcctgctgtctggtgccctggc ctattgcctggcgcttcaactttatgtgcggaggaggaagaagctgccgtccgtgctgttgtttaagaaacc gtctcccttcatttttatcagccagcgcccctcacccgaaacacaggatactattcacccccttgacgaagaa gccttccttaaagtgtcccccgagctaaaaaacctcgacctgcacgggtccaccgatagcgggtttggtag caccaaaccatccttgcaaaccgaggagccccagttcttgctccctgatccacacccacaggctgacaga acgttgggaaacagagagccccccagtcctgggggattcctgttcgtcagggtctagtaatagtaccgatag cgggatttgcctgcaggagccgagcctgtcaccctcaaccggtccgacctgggagcagcaagtaggatc taactcccgcgggcaggatgactccggcatagacctcgtacagaattcggaaggccgggcgggtgaca cacagggcggctccgctctgggccaccattccccaccagagcccgaggtccctggcgaggaggaccct gcagccgtcgcttttcaaggctatctgcgtcagacacgatgtgctgaagagaaagctactaagacgggatg tcttgaagaggaatctccgcttacagacggattgggaccaaagttcggcagatgcctagtggatgaggcg ggactacatcctcccgcattagcaaagggctacctgaagcaggatccactagaaatgacactggcctcatc tggcgcccctacaggacagtggaaccagccaaccgaagagtggtccttgctcgctttaagctcttgcagtg acctgggtatctcagattggagttttgcacacgacctcgcccctctgggttgcgtcgccgctcctggtggac tcttaggaagtttcaatagcgatctcgtcactctgcctctcatcagtagcttacagagcagcgaa **(SEQ ID NO: 149)**
cpIL-10(58/57)	IL-10R2	atggccttaccagtgaccgccttgctcctgccgctggccttgctgctccacgccgccaggccgggttactt gggctgtcaggctctgagtgaaatgattcagttctatcttgaagaggttatgcctcaggcggagaaccaaga cccagacatcaaggcccatgtgaactctctcggggagaatctgaaaacactgcgactgcggttaagacgtt gccacaggttcctaccctgcgaaaataaaagcaaggccgtcgagcaagtgaaaaacgcattcaataaact ccaggaaaagggaatttacaaggccatgtccgagtttgatatctttataaactatattgaggcttacatgacca tgaagatccgcaatggtggtggtggaagcggcgggggaggcagtgggggaggcgggtcctcccctgg ccagggaactcagtcagaaaatagctgcacacactttccagggaatctccccaacatgttgagagatctga gggacgccttctctcgggtgaaaaccttttccaaatgaaagaccagctggacaacctccttctgaaggag agtttactagaggatttcaagtctggaggcggaagcgggggtggcggcagcggcggtggaggatcagg tggcgggggggtccgggggcggaagtctgcagatggtaccaccacctgaaaatgtgaggatgaactctgt gaattttaagaacattctccagtgggaaagtcccgcttttgctaaggggaacctgaccttcacagcccaata cttatcctaccgaatcttccaagacaagtgcatgaataccactttaactgaatgcgacttctcaagcctgtcta agtatggcgatcatacactgcgggttcgtgccgagtttgccgacgagcactctgactgggtgaatataacct tctgccccgtcgatgatactataattgggccaccaggtatgcaagttgaagtgttggcagattcgctgcacat gaggtttctcgcccccaaaatcgagaacgagtacgagacctggacgatgaagaatgtctacaactcttgga catataatgttcagtattggaaaaacggaaccgacgagaagtttcagatcactccgcagtatgatttcgaagt cctgagaaacctcgagccttggacaacttactgtgtccaagtgcgcggctttctccctgaccggaacaagg

		caggagagtggtcagaaccggtgtgtgagcagaccacccacgacgagacagtacccagctggatggta gctgtgatccttatggcctccgtgttcatggtttgtctagctttgttgggctgttttgcccttctatggtgcgtctat aaaaagaccaaatacgcgttttcacctagaaacagccttccacagcacctcaaggagttcctggggcatcc tcatcacaatacactgctgttcttctccttccccctgagtgacgaaaacgatgtgtttgataaactgtccgtgat tgcagaagacagtgagtccggcaaacagaatccaggagatagttgcagcctgggtacgcctcccggaca gggcccccagagc **(SEQ ID NO: 150)**
tdIL-10	IL-10R1	atggccttaccagtgaccgccttgctcctgccgctggccttgctgctccacgccgccaggccgtctccggg acagggaacccagagcgaaaactcctgcactcattttcctggcaacctccccaatatgctgcgagacttgc gcgacgcattctcaagggtgaagacgttcttccagatgaaggatcaactggacaacttattgctgaaagaat ctctgctcgaggatttcaaaggatacctgggatgtcaggcactgagcgagatgatccaattttacctggagg aggtcatgcctcaggctgagaatcaggatcctgacatcaaggcccacgtgaacagtcttggagagaatctt aagacccttaggctgagacttagacggtgtcaccgctttctgccctgcgaaaataaatcaaaagcggtgga acaggttaagaacgcttttaataagctgcaggaaaagggcatttataaagctatgagtgaatttgacattttca ttaactatatcgaggcctatatgacaatgaaaattaggaacgggggaggcgggagcgggggcggcggct caggcggtgggggtcctctccaggtcaaggaacacaatctgagaactcctgcacacacttccccggca atctaccaaacatgctcagagatctcagggacgcgttcagtcgagtgaaaactttcttccagatgaaggatc agctggacaatctactgctgaaagaaagcttgcttgaggattttaaaggctatctgggttgtcaggccttatc ggagatgatccagttttacttggaggaagttatgcctcaggcagaaaaccaagaccccgatatcaaggctc atgtgaattccctcggtgaaaacctaaagaccttacgcctgcgtctcagacggtgtcatcggtttttgccatg cgagaataagtccaaagccgtagagcaggtcaagaatgccttcaataagctccaggagaaggggatata caaagcaatgagcgaatttgacattttcatcaactacatagaggcctacatgaccatgaagatccggaactc tggaggcggaagcgggggtggcggcagcggcggtggaggatcaggtggcgggggggtccgggggcg gaagtctgcagcatgggaccgagctccccagtcctccttctgtttggttcgaagccgaattctttcaccatatt ctgcactggactcctatcccaaatcaatcagaatcaacatgttacgaggtggcactgctgaggtacggaatc gagtcttggaatagcatttcaaactgtagccaaaccctgtcttacgatcttaccgctgtgacgctggacctgt atcatagcaacggctaccgtgccagggttagggcagttgatggcagcagacactccaattggacagttac gaatacccgattcagtgtcgacgaggtgactttaactgtcgggagtgttaaccttgaaattcacaacgggttc atattgggaaagatccagctcccccggccaaaaatggccccagccaacgacacatacgagagtatattttc tcattttagagagtatgagatcgcaatccgcaaggtgcctgggaatttcacatttactcataagaaggtaaaa cacgagaacttctccttgctcacctccggcgaagtgggggagttctgcgtgcaggtgaagccctcggtgg cttcacgctccaataaaggcatgtggagcaaagaagaatgtatttctctgactcggcagtactttaccgtgac taacgtaatcatatttttgccttcgtgctcctgctgtctggtgccctggcctattgcctggcgcttcaactttatg tgcggaggaggaagaagctgccgtccgtgctgttgtttaagaaaccgtctcccttcatttttatcagccagcg cccctcacccgaaacacaggatactattcacccccttgacgaagaagccttccttaaagtgtcccccgagc taaaaaacctcgacctgcacgggtccaccgatagcgggtttggtagcaccaaaccatccttgcaaaccga ggagccccagttcttgctccctgatccacacccacaggctgacagaacgttgggaaacagagagccccc agtcctgggggattcctgttcgtcagggtctagtaatagtaccgatagcgggatttgcctgcaggagccga gcctgtcaccctcaaccggtccgacctgggagcagcaagtaggatctaactcccgcgggcaggatgact ccggcatagacctcgtacagaattcggaaggccgggcgggtgacacacagggcggctccgctctgggc caccattccccaccagagcccgaggtccctggcgaggaggaccctgcagccgtcgcttttcaaggctatc tgcgtcagacacgatgtgctgaagagaaagctactaagacgggatgtcttgaagaggaatctccgcttaca gacggattgggaccaaagttcggcagatgcctagtggatgaggcgggactacatcctcccgcattagcaa agggctacctgaagcaggatccactagaaatgacactggcctcatctggcgcccctacaggacagtgga accagccaaccgaagagtggtccttgctcgctttaagctcttgcagtgacctgggtatctcagattggagttt tgcacacgacctcgcccctctgggttgcgtcgccgctcctggtggactcttaggaagtttcaatagcgatct cgtcactctgcctctcatcagtagcttacagagcagcgaa **(SEQ ID NO: 151)**

tdIL-10	IL-10R2	atggccttaccagtgaccgccttgctcctgccgctggccttgctgctccacgccgccaggccgtctccggg acagggaacccagagcgaaaactcctgcactcattttcctggcaacctccccaatatgctgcgagacttgc gcgacgcattctcaagggtgaagacgttcttccagatgaaggatcaactggacaacttattgctgaaagaat ctctgctcgaggatttcaaaggatacctgggatgtcaggcactgagcgagatgatccaattttacctggagg aggtcatgcctcaggctgagaatcaggatcctgacatcaaggcccacgtgaacagtcttggagagaatctt aagacccttaggctgagacttagacggtgtcaccgctttctgccctgcgaaaataaatcaaaagcggtgga acaggttaagaacgcttttaataagctgcaggaaaagggcatttataaagctatgagtgaatttgacattttca ttaactatatcgaggcctatatgacaatgaaaattaggaacgggggaggcgggagcgggggcggcggct caggcggtgggggtcctctccaggtcaaggaacacaatctgagaactcctgcacacacttccccggca atctaccaaacatgctcagagatctcagggacgcgttcagtcgagtgaaaactttcttccagatgaaggatc agctggacaatctactgctgaaagaaagcttgcttgaggattttaaaggctatctgggttgtcaggccttatc ggagatgatccagttttacttggaggaagttatgcctcaggcagaaaaccaagaccccgatatcaaggctc atgtgaattccctcggtgaaaacctaaagaccttacgcctgcgtctcagacggtgtcatcggtttttgccatg cgagaataagtccaaagccgtagagcaggtcaagaatgccttcaataagctccaggagaaggggatata caaagcaatgagcgaatttgacattttcatcaactacatagaggcctacatgaccatgaagatccggaactc tggaggcggaagcgggggtggcggcagcggcggtggaggatcaggtggcgggggggtccgggggcgg gaagtctgcagatggtaccaccacctgaaaatgtgaggatgaactctgtgaattttaagaacattctccagtg ggaaagtcccgcttttgctaaggggaacctgaccttcacagcccaatacttatcctaccgaatcttccaaga caagtgcatgaataccactttaactgaatgcgacttctcaagcctgtctaagtatggcgatcatacactgcgg gttcgtgccgagtttgccgacgagcactctgactgggtgaatataaccttctgccccgtcgatgatactataa ttgggccaccaggtatgcaagttgaagtgttggcagattcgctgcacatgaggtttctcgcccccaaaatcg agaacgagtacgagacctggacgatgaagaatgtctacaactcttggacatataatgttcagtattggaaaa acggaaccgacgagaagtttcagatcactccgcagtatgatttcgaagtcctgagaaacctcgagccttgg acaacttactgtgtccaagtgcgcggctttctccctgaccggaacaaggcaggagagtggtcagaaccgg tgtgtgagcagaccacccacgacgagacagtacccagctggatggtagctgtgatccttatggcctccgtg ttcatggtttgtctagctttgttgggctgttttgcccttctatggtgcgtctataaaaagaccaaatacgcgtttc acctagaaacagccttccacagcacctcaaggagttcctggggcatcctcatcacaatacactgctgttctt ctccttcccccctgagtgacgaaaacgatgtgtttgataaactgtccgtgattgcagaagacagtgagtccgg caaacagaatccaggagatagttgcagcctgggtacgcctcccggacagggcccccagagc **(SEQ ID NO: 152)**
IL-13	IL-13Rα1	atggccttaccagtgaccgccttgctcctgccgctggccttgctgctccacgccgccaggccgttaacatgt ctgggcgggttcgcctcacctggaccagttccccttcaaccgctctcagagaactgattgaggagctcgt caatatcacccagaaccaaaaagccccactctgcaatggaagtatggtgtggtctattaacttgactgccgg catgtactgtgccgcactggagtctttgatcaacgtgtccgggtgcagtgcaatcgaaaagacgcagcgg atgctgagcggcttttgcccccacaaggtgagcgctggtcagttttccagccttcacgtgcgagatacaaa gatagaagtagcgcagttcgtcaaggacctgctgctgcatcttaaaaaactatttcgcgagggtaggttcaa ttctggaggcggaagcgggggtggcggcagcggcggtggaggatcaggtggcgggggggtccgggggg cggaagtctgcagggcggcggcggcgcggcgccgaccgaaacccagccgccggtgaccaacctgag cgtgagcgtggaaaacctgtgcaccgtgatttggacctggaacccgccggaaggcgcgagcagcaact gcagcctgtggtattttagccattttggcgataaacaggataaaaaaattgcgccggaaacccgccgcagc attgaagtgccgctgaacgaacgcatttgcctgcaggtgggcagccagtgcagcaccaacgaaagcgaa aaaccgagcattctggtggaaaaatgcattagcccgccggaaggcgatccggaaagcgcggtgaccga actgcagtgcatttggcataacctgagctatatgaaatgcagctggctgccgggccgcaacaccagcccg gataccaactataccctgtattattggcatcgcagcctggaaaaaattcatcagtgcgaaaacatttttcgcg aaggccagtattttggctgcagctttgatctgaccaaagtgaaagatagcagctttgaacagcatagcgtgc agattatggtgaaagataacgcgggcaaaattaaaccgagctttaacattgtgccgctgaccagccgcgtg

		aaaccggatccgccgcatattaaaaacctgagctttcataacgatgatctgtatgtgcagtgggaaaacccg cagaactttattagccgctgcctgttttatgaagtggaagtgaacaacagccagaccgaaacccataacgtg ttttatgtgcaggaagcgaaatgcgaaaacccggaatttgaacgcaacgtggaaaacaccagctgctttat ggtgccgggcgtgctgccggataccctgaacaccgtgcgcattcgcgtgaaaaccaacaaactgtgctat gaagatgataaactgtggagcaactggagccaggaaatgagcattggcaaaaaacgcaacagcaccctg tatattaccatgctgctgattgtgccggtgattgtggcgggcgcgattattgtgctgctgctgtatctgaaacg cctgaaaattattattttccgccgattccggatccgggcaaaatttttaaagaaatgtttggcgatcagaacg atgataccctgcattggaaaaaatatgatatttatgaaaaacagaccaaagaagaaaccgatagcgtggtg ctgattgaaaacctgaaaaaagcgagccag **(SEQ ID NO: 153)**
IL-13	IL-4Rα	atggccttaccagtgaccgccttgctcctgccgctggccttgctgctccacgccgccaggccgttaacatgt ctgggcgggttcgcctcacctggaccagttccccccttcaaccgctctcagagaactgattgaggagctcgt caatatcacccagaaccaaaaagccccactctgcaatggaagtatggtgtggtctattaacttgactgccgg catgtactgtgccgcactggagtctttgatcaacgtgtccgggtgcagtgcaatcgaaaagacgcagcgg atgctgagcggcttttgccccacaaggtgagcgctggtcagttttccagccttcacgtgcgagatacaaa gatagaagtagcgcagttcgtcaaggacctgctgctgcatcttaaaaaactatttcgcgagggtaggttcaa ttctggaggcggaagcgggggtggcggcagcggcggtggaggatcaggtggcgggggggtccgggggg cggaagtctgcagatgaaagtgctgcaggaaccgacctgcgtgagcgattatatgagcattagcacctgc gaatggaaaatgaacggcccgaccaactgcagcaccgaactgcgcctgctgtatcagctggtgtttctgct gagcgaagcgcatacctgcattccggaaaacaacggcggcgcgggctgcgtgtgccatctgctgatgga tgatgtggtgagcgcggataactatacctggatctgtgggcgggccagcagctgctgtggaaaggcag ctttaaaccgagcgaacatgtgaaaccgcgcgcgccgggcaacctgaccgtgcataccaacgtgagcga taccctgctgctgacctggagcaacccgtatccgccggataactatctgtataaccatctgacctatgcggt gaacatttggagcgaaaacgatccggcggattttcgcatttataacgtgacctatctggaaccgagcctgcg cattgcggcgagcaccctgaaaagcggcattagctatcgcgcgcgcgtgcgcgcgtgggcgcagtgcta taacaccacctggagcgaatggagcccgagcaccaaatggcataacagctatcgcgaaccgtttgaaca gcatctgctgctgggcgtgagcgtgagctgcattgtgattctggcggtgtgcctgctgtgctatgtgagcatt accaaaattaaaaaagaatggtgggatcagattccgaacccggcgcgcagccgcctggtggcgattatta ttcaggatgcgcagggcagccagtgggaaaaacgcagccgcggccaggaaccggcgaaatgcccgc attggaaaaactgcctgaccaaactgctgccgtgctttctggaacataacatgaaacgcgatgaagatccg cataaagcggcgaaagaaatgccgtttcagggcagcggcaaaagcgcgtggtgcccggtggaaattag caaaaccgtgctgtggccggaaagcattagcgtggtgcgctgcgtggaactgtttgaagcgccggtggaa tgcgaagaagaagaagaagtggaagaagaaaaaggcagcttttgcgcgagcccggaaagcagccgcg atgattttcaggaaggccgcgaaggcattgtggcgcgcctgaccgaaagcctgtttctggatctgctgggc gaagaaaacggcggcttttgccagcaggatatgggcgaaagctgcctgctgccgccgagcggcagcac cagcgcgcatatgccgtgggatgaatttccgagcgcgggcccgaaagaagcgccgccgtggggcaaa gaacagccgctgcatctggaaccgagcccgccggcgagcccgacccagagcccggataacctgacct gcaccgaaaccccgctggtgattgcgggcaacccggcgtatcgcagctttagcaacagcctgagccaga gcccgtgcccgcgcgaactgggcccggatccgctgctggcgcgccatctggaagaagtggaaccgga aatgccgtgcgtgccgcagctgagcgaaccgaccaccgtgccgcagccggaaccggaaacctgggaa cagattctgcgccgcaacgtgctgcagcatggcgcggcggcggcgccggtgagcgcgccgaccagcg gctatcaggaatttgtgcatgcggtggaacagggcggcacccaggcgagcgcggtggtgggcctgggc ccgccgggcgaagcgggctataaagcgtttagcagcctgctggcgagcagcgcggtgagcccggaaa aatgcggctttggcgcgagcagcggcgaagaaggctataaaccgtttcaggatctgattccgggctgccc gggcgatccggcgccggtgccggtgccgctgtttacctttggcctggatcgcgaaccgccgcgcagccc gcagagcagccatctgccgagcagcagcccggaacatctgggcctggaaccgggcgaaaaagtggaa gatatgccgaaaccgccgctgccgcaggaacaggcgaccgatccgctggtggatagcctgggcagcg

		gcattgtgtatagcgcgctgacctgccatctgtgcggccatctgaaacagtgccatggccaggaagatgg cggccagaccccggtgatggcgagcccgtgctgcggctgctgctgcggcgatcgcagcagcccgccg accaccccgctgcgcgcgccggatccgagcccgggcggcgtgccgctggaagcgagcctgtgcccgg cgagcctggcgccgagcggcattagcgaaaaaagcaaaagcagcagcagctttcatccggcgccggg caacgcgcagagcagcagccagaccccgaaaattgtgaactttgtgagcgtgggcccgacctatatgcg cgtgagc **(SEQ ID NO: 154)**
cpIL-13(75/74)	IL-13Rα1	atggccttaccagtgaccgccttgctcctgccgctggccttgctgctccacgccgccaggccggtgagcg cgggccagtttagcagcctgcatgtgcgcgataccaaaattgaagtggcgcagtttgtgaaagatctgctg ctgcatctgaaaaaactgtttcgcgaaggccgctttaacggaggaggtggatctctgacctgcctgggcgg ctttgcgagcccgggcccggtgccgccgagcaccgcgctgcgcgaactgattgaagaactggtgaacat tacccagaaccagaaagcgccgctgtgcaacggcagcatggtgtggagcattaacctgaccgcgggcat gtattgcgcggcgctggaaagcctgattaacgtgagcggctgcagcgcgattgaaaaaacccagcgcat gctgagcggcttttgcccgcataaatctggaggcggaagcgggggtggcggcagcggcggtggaggat caggtggcgggggtccgggggcggaagtctgcagggcggcggcggcgcggcgccgaccgaaacc cagccgccggtgaccaacctgagcgtgagcgtggaaaacctgtgcaccgtgatttggacctggaacccg ccggaaggcgcgagcagcaactgcagcctgtggtattttagccattttggcgataaacaggataaaaaaat tgcgccggaaacccgccgcagcattgaagtgccgctgaacgaacgcatttgcctgcaggtgggcagcca gtgcagcaccaacgaaagcgaaaaaccgagcattctggtggaaaaatgcattagcccgccggaaggcg atccggaaagcgcggtgaccgaactgcagtgcatttggcataacctgagctatatgaaatgcagctggctg ccgggccgcaacaccagcccggataccaactataccctgtattattggcatcgcagcctggaaaaaattca tcagtgcgaaaacatttttcgcgaaggccagtattttggctgcagctttgatctgaccaaagtgaaagatagc agctttgaacagcatagcgtgcagattatggtgaaagataacgcgggcaaaattaaaccgagctttaacatt gtgccgctgaccagccgcgtgaaaccggatccgccgcatattaaaaacctgagctttcataacgatgatct gtatgtgcagtgggaaaacccgcagaactttattagccgctgcctgttttatgaagtggaagtgaacaacag ccagaccgaaacccataacgtgttttatgtgcaggaagcgaaatgcgaaaacccggaatttgaacgcaac gtggaaaacaccagctgctttatggtgccgggcgtgctgccggataccctgaacaccgtgcgcattcgcg tgaaaaccaacaaactgtgctatgaagatgataaactgtggagcaactggagccaggaaatgagcattgg caaaaaacgcaacagcaccctgtatattaccatgctgctgattgtgccggtgattgtggcgggcgcgattat tgtgctgctgctgtatctgaaacgcctgaaaattattattttccgccgattccggatccgggcaaaatttttaa agaaatgtttggcgatcagaacgatgataccctgcattggaaaaaatatgatatttatgaaaaacagaccaa agaagaaaccgatagcgtggtgctgattgaaaacctgaaaaaagcgagccag **(SEQ ID NO: 155)**
cpIL-13(75/74)	IL-4Rα	atggccttaccagtgaccgccttgctcctgccgctggccttgctgctccacgccgccaggccggtgagcg cgggccagtttagcagcctgcatgtgcgcgataccaaaattgaagtggcgcagtttgtgaaagatctgctg ctgcatctgaaaaaactgtttcgcgaaggccgctttaacggaggaggtggatctctgacctgcctgggcgg ctttgcgagcccgggcccggtgccgccgagcaccgcgctgcgcgaactgattgaagaactggtgaacat tacccagaaccagaaagcgccgctgtgcaacggcagcatggtgtggagcattaacctgaccgcgggcat gtattgcgcggcgctggaaagcctgattaacgtgagcggctgcagcgcgattgaaaaaacccagcgcat gctgagcggcttttgcccgcataaatctggaggcggaagcgggggtggcggcagcggcggtggaggat caggtggcgggggtccgggggcggaagtctgcagatgaaagtgctgcaggaaccgacctgcgtgag cgattatatgagcattagcacctgcgaatggaaaatgaacggcccgaccaactgcagcaccgaactgcgc ctgctgtatcagctggtgtttctgctgagcgaagcgcatacctgcattccggaaaacaacggcggcgcgg gctgcgtgtgccatctgctgatggatgatgtggtgagcgcggataactataccctggatctgtgggcgggc cagcagctgctgtggaaaggcagctttaaaccgagcgaacatgtgaaaccgcgcgcgccgggcaacct gaccgtgcataccaacgtgagcgataccctgctgctgacctggagcaacccgtatccgccggataactat ctgtataaccatctgacctatgcggtgaacatttggagcgaaaacgatccggcggattttcgcatttataacg

		tgacctatctggaaccgagcctgcgcattgcggcgagcaccctgaaaagcggcattagctatcgcgcgc gcgtgcgcgcgtgggcgcagtgctataacaccacctggagcgaatggagcccgagcaccaaatggcat aacagctatcgcgaaccgtttgaacagcatctgctgctgggcgtgagcgtgagctgcattgtgattctggc ggtgtgcctgctgtgctatgtgagcattaccaaaattaaaaaagaatggtgggatcagattccgaacccgg cgcgcagccgcctggtggcgattattattcaggatgcgcagggcagccagtgggaaaaacgcagccgc ggccaggaaccggcgaaatgcccgcattggaaaaactgcctgaccaaactgctgccgtgctttctggaac ataacatgaaacgcgatgaagatccgcataaagcggcgaaagaaatgccgtttcagggcagcggcaaaa gcgcgtggtgcccggtggaaattagcaaaaccgtgctgtggccggaaagcattagcgtggtgcgctgcg tggaactgtttgaagcgccggtggaatgcgaagaagaagaagaagtggaagaagaaaaaggcagctttt gcgcgagcccggaaagcagccgcgatgattttcaggaaggccgcgaaggcattgtggcgcgcctgacc gaaagcctgtttctggatctgctgggcgaagaaaacggcggcttttgccagcaggatatgggcgaaagct gcctgctgccgccgagcggcagcaccagcgcgcatatgccgtgggatgaatttccgagcgcgggcccg aaagaagcgccgccgtggggcaaagaacagccgctgcatctggaaccgagcccgccggcgagcccg acccagagcccggataacctgacctgcaccgaaaccccgctggtgattgcgggcaacccggcgtatcgc agctttagcaacagcctgagccagagcccgtgcccgcgcgaactgggcccggatccgctgctggcgcg ccatctggaagaagtggaaccggaaatgccgtgcgtgccgcagctgagcgaaccgaccaccgtgccgc agccggaaccggaaacctgggaacagattctgcgccgcaacgtgctgcagcatggcgcggcggcggc gccggtgagcgcgccgaccagcggctatcaggaatttgtgcatgcggtggaacagggcggcacccagg cgagcgcggtggtgggcctgggcccgccgggcgaagcgggctataaagcgtttagcagcctgctggcg agcagcgcggtgagcccggaaaaatgcggctttggcgcgagcagcggcgaagaaggctataaaccgtt tcaggatctgattccgggctgcccgggcgatccggcgccggtgccggtgccgctgtttacctttggcctgg atcgcgaaccgccgcgcagcccgcagagcagccatctgccgagcagcagcccggaacatctgggcct ggaaccgggcgaaaaagtggaagatatgccgaaaccgccgctgccgcaggaacaggcgaccgatccg ctggtggatagcctgggcagcggcattgtgtatagcgcgctgacctgccatctgtgcggccatctgaaaca gtgccatggccaggaagatggcggccagaccccggtgatggcgagcccgtgctgcggctgctgctgcg gcgatcgcagcagcccgccgaccaccccgctgcgcgcgccggatccgagcccgggcggcgtgccgc tggaagcgagcctgtgcccggcgagcctggcgccgagcggcattagcgaaaaaagcaaaagcagcag cagctttcatccggcgccgggcaacgcgcagagcagcagccagaccccgaaaattgtgaactttgtgag cgtgggcccgacctatatgcgcgtgagc **(SEQ ID NO: 156)**
IL-18	IL-18Rα	atggccttaccagtgaccgccttgctcctgccgctggccttgctgctccacgccgccaggccgtattttggc aaactcgaaagtaagctgagcgtgattcggaatcttaacgatcaggtgttattcatcgatcaaggcaacaga ccactctttgaagatatgacagattcagactgtagggataatgcccctaggaccatctttattataagcatgta taaggactctcagccccgcggtatggcagtaacgattagcgttaagtgcgagaagatttctacactttcatg cgaaaacaaaatcatctccttcaaagagatgaaccctcccgataatatcaaagataccaagtcggacataat tttctttcagagatccgtcccaggacacgacaataagatgcaattcgaatccagcagttacgagggatactttt ctggcttgtgagaaggaacgtgacttgttcaaactgatcctgaagaaagaggacgagctaggggaccgat ctatcatgttcactgtgcagaacgaggactctggaggcggaagcgggggtggcggcagcggcggtgga ggatcaggtggcgggggtccgggggcggaagtctgcaggccgagagctgcactagccggccccata taactgtggtcgaaggggagccattctatctgaaacattgttcctgctcccttgcccatgaaattgaaaccac aaccaagagctggtacaaatctagtgggtctcaagagcacgtcgagttgaacccaagatcatctagtagga tcgccctgcatgactgcgttctagagttttggccggtggaattaaatgacaccggatcttacttcttccagatg aagaattacacccagaaatggaagctgaacgtgatacgacgcaacaagcactcatgcttcacagaacgtc aggtgacctcgaaaatcgtggaagtgaaaaagttctttcagattacatgcgagaacagttactatcaaacgc tagtgaatagcacgagcctgtacaaaaactgtaagaaacttctgctggagaacaataaaaaccctactatca aaaaaaatgcagaattcgaggatcagggctattacagttgtgtgcattttctccaccacaatggtaagctattc aatatcaccaagacgttcaacatcaccattgtggaggatcgctccaacatagtacctgtgttattgggtccta

		aacttaaccacgtggcagtggagctggggaaaaacgtgagactcaattgctcagccttgctgaacgaaga ggatgttatttattggatgtttggggaagaaaatggaagtgacccgaacattcacgaagagaaggagatgc gaatcatgacaccagaggggaaatggcacgcgagtaaggtcctcagaattgaaaatattggcgaatcaaa tctcaacgtcctctataactgtaccgtagcatccacaggcggcactgatactaagtcctttatccttgtgcgta aggccgatatggctgacatccccggccacgtattcacacggggaatgatcattgctgttctgatcctggtgg cagtagtgtgtttggttactgtatgtgttatctaccgcgtggacttagttctgttttataggcacctgacccgaag agacgaaacccttacagatggcaagacttatgacgcgttcgtgtcgtatcttaaagaatgccggcccgaga atggagaggagcacacgtttgctgtcgaaattctccccagagtcctggagaagcattttggttacaagctgt gcatcttcgaaagagacgtcgtgcccggtggcgccgtggtcgacgagatacattccctgatcgagaagtc ccgcaggttgatcatagtcctctcaaagtcttacatgagcaatgaggtgcggtacgaactcgagagcggac tgcatgaggctttagtcgagaggaagattaagattattttgatcgagtttacacctgtgactgactttaccttcct ccctcagtcactgaaactccttaagtctcacagggtactgaagtggaaagctgataaatccctctcttataata gccggttttggaagaacctattgtacctgatgccagccaaaacagtcaagcctggacgcgatgagcccga agttctgccagttctgagcgagtcc **(SEQ ID NO: 157)**
IL-18	IL-18Rβ	atggccttaccagtgaccgccttgctcctgccgctggccttgctgctccacgccgccaggccgtattttggc aaactcgaaagtaagctgagcgtgattcggaatcttaacgatcaggtgttattcatcgatcaaggcaacaga ccactctttgaagatatgacagattcagactgtagggataatgcccctaggaccatctttattataagcatgta taaggactctcagccccgcggtatggcagtaacgattagcgttaagtgcgagaagatttctacactttcatg cgaaaacaaaatcatctccttcaaagagatgaaccctcccgataatatcaaagataccaagtcggacataat tttctttcagagatccgtcccaggacacgacaataagatgcaattcgaatccagcagttacgagggatacttt ctggcttgtgagaaggaacgtgacttgttcaaactgatcctgaagaaagaggacgagctaggggaccgat ctatcatgttcactgtgcagaacgaggactctggaggcggaagcgggggtggcggcagcggcggtgga ggatcaggtggcgggggtccgggggcggaagtctgcagtttaatatctctggatgcagtacgaagaaat tgctctggacatactctactaggagcgaggaagagttcgtgcttttctgcgatttaccagaaccacagaaatc ccatttttgtcacagaaatcgtctttctcctaagcaggttcccgaacacctgcccttcatgggctccaacgacc ttagtgacgttcaatggtaccagcaaccaagcaatggcgaccctctggaagacatacgcaagagttaccc ccatattatccaggataaatgcacgctacatttcctgaccccaggcgtcaacaacagtggatcttatatatgta ggcctaagatgatcaaatccccctacgacgtggcttgttgcgtcaagatgattctcgaggtgaagccccag accaatgcctcatgtgagtactccgcctctcacaaacaggaccttctgctggggtcgaccggcagtataag ctgcccatcgctctcttgtcagagtgatgcgcagagccctgctgtgacatggtacaaaaacggaaagctac tgtcagtggagcgctcaaaccgtattgtagtagacgaagtctacgactatcaccaaggcacctacgtgtgc gattatacacagtctgatacggtctccagttggactgtgcgggccgtggtgcaggtacggaccatcgtggg ggacacaaaactgaagcccgacatccttgatccagttgaggacaccctggaggtggagctcgggaagcc cctgactatctcctgtaaagcaagatttggcttcgagcgagtatttaaccctgttatcaagtggtatattaaaga tagcgatctcgagtgggaggtatcagtgcctgaagccaaatccatcaaatcaactctgaaggatgaaatca ttgagcgaaatattattcttgagaaggttacccagcgcgatctccgccgcaaatttgtctgcttcgtgcaaaa cagcataggcaatactactcagagcgtgcagctgaaagagaagcgtggtgtcgtcttgttgtacatcctgct cggaacaattggtacactcgtagccgtgttggccgcctcagccctgctctacaggcattggattgaaatcgt gttgctttacaggacatatcagagcaaggaccagactctgggcgacaaaaaggatttcgatgcattcgttag ctatgctaaatggtcttcatttcctagcgaagctacatcctccctgagcgaggaacacttagccttatcactgtt tccagatgtgttagaaaataaatatggctatagcctgtgtttgctggagcgcgacgttgcaccaggggggt gtatgctgaagacatcgtcagcatcatcaagcggtccaggaggggaatatttatattaagccctaactacgt caacggtccatcgattttcgaactgcaggctgcagtgaacttggcgctcgatgaccagacgctcaagctga ttctcatcaagttctgctactttcaagagcccgagtctcttcctcacctagtcaagaaggcgctgagagtcctg ccgaccgtgacatggcgaggactaaagtctgtgccgccgaattccagattctgggcaaagatgcggtatc atatgcccgttaaaaattcccaaggttttacttggaaccagctgcggattaccagtcggatcttccagtggaa

		ggggctgtctagaaccgagaccaccggaagatccagtcaacccaaagaatgg **(SEQ ID NO: 158)**

Table 11a – Amino Acid Sequences of Exemplary anti-HER2 Chimeric Antigen Receptor (CAR)

CD8a Signal Peptide	MALPVTALLLPLALLLHAARP **(SEQ ID NO: 174)**
HER2 scFv	DIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPKLLIY SASFLYSGVPSRFSGSRSGTDFTLTISSLQPEDFATYYCQQHYTTPPTFGQ GTKVEIKRTGSTSGSGKPGSGEGSEVQLVESGGGLVQPGGSLRLSCAAS GFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTISADT SKNTAYLQMNSLRAEDTAVYYCSRWGGDGFYAMDVWGQGTLVTVSS SG **(SEQ ID NO: 159)**
CD8a Hinge	TTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACD **(SEQ ID NO: 160)**
CD8a Transmembrane Domain	IYIWAPLAGTCGVLLLSLVITLYC **(SEQ ID NO: 161)**
CD3ζ Stimulatory Domain	RVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGG KPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLS TATKDTYDALHMQALPPR **(SEQ ID NO: 162)**
Complete CAR	MALPVTALLLPLALLLHAARPDIQMTQSPSSLSASVGDRVTITCRASQDV NTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRFSGSRSGTDFTLTISSLQ PEDFATYYCQQHYTTPPTFGQGTKVEIKRTGSTSGSGKPGSGEGSEVQLV ESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPT NGYTRYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCSRWGG DGFYAMDVWGQGTLVTVSSSGTTTPAPRPPTPAPTIASQPLSLRPEACRP AAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCRVKFSRSAD APAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQE GLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDA LHMQALPPR **(SEQ ID NO: 163)**

Table 11b – DNA Sequences of Exemplary anti-HER2 Chimeric Antigen Receptor (CAR)

CD8a Signal Peptide	Atggccttaccagtgaccgccttgctcctgccgctggccttgctgctccacgccgccaggccg **(SEQ ID NO: 164)**
HER2 scFv	Gacattcaaatgacacagagtccctcatccctcagtgccagcgtgggcgatcgggtgactataacctgcagagctt ctcaggacgtgaataccgctgtggcgtggtaccagcagaagccaggcaaagcgcctaagcttctcatttatagtgc cagcttcctgtactcaggtgttccgtctcgcttttctggaagtagaagtgggaccgatttcacattgacgatcagcagc ttgcagcccgaagatttcgccacctactactgtcagcagcactacactaccccaccgacatttggtcaaggcacaaa agtagagattaaacgcactggttccaccagcgggagcgggaaacccggctctggggaggggagcgaggtcca gctggtggaatccgggggtggtcttgtgcagccaggaggatccttgaggttgtcctgcgccgcaagcggctttaac atcaaagatacatacatccattgggtccgacaggcccctggaaagggcctggagtgggtcgcccggatctaccca

	actaacgggtacactcgctacgctgatagcgtcaagggtcggtttactatttctgccgacacctcaaaaaacacagc ctacctccagatgaactctctcagagctgaggatacagccgtgtactattgcagccggtggggaggcgacgggttc tacgctatggatgtgtgggggcagggcacactggtcaccgtgagctcatccgga **(SEQ ID NO: 165)**
CD8a Hinge	Accacgacgccagcgccgcgaccaccaacaccggcgcccaccatcgcgtcgcagcccctgtccctgcgccca gaggcgtgccggccagcggcgggggggcgcagtgcacacgagggggctggacttcgcctgtgat **(SEQ ID NO: 166)**
CD8a Transmembrane Domain	Atctacatctgggcgcccttggccgggacttgtggggtccttctcctgtcactggttatcacccttactgc **(SEQ ID NO: 167)**
CD3ζ Stimulatory Domain	Agagtgaagttcagcaggagcgcagacgcccccgcgtaccagcagggccagaaccagctctataacgagctc aatctaggacgaagagaggagtacgatgttttggacaagagacgtggccgggaccctgagatgggggggaaagc cgagaaggaagaaccctcaggaaggcctgtacaatgaactgcagaaagataagatggcggaggcctacagtga gattgggatgaaaggcgagcgccggaggggcaaggggcacgatggcctttaccagggtctcagtacagccacc aaggacacctacgacgcccttcacatgcaggccctgcccctcgc **(SEQ ID NO: 168)**
Complete CAR	atggccttaccagtgaccgccttgctcctgccgctggccttgctgctccacgccgccaggccggacattcaaatga cacagagtccctcatccctcagtgccagcgtgggcgatcgggtgactataacctgcagagcttctcaggacgtgaa taccgctgtggcgtggtaccagcagaagccaggcaaagcgcctaagcttctcatttatagtgccagcttcctgtact caggtgttccgtctcgcttttctggaagtagaagtgggaccgatttcacattgacgatcagcagcttgcagcccgaa gatttcgccacctactactgtcagcagcactacactaccccaccgacatttggtcaaggcacaaaagtagagattaa acgcactggttccaccagcgggagcgggaaacccggctctggggaggggagcgaggtccagctggtggaatc cgggggtggtcttgtgcagccaggaggatccttgaggttgtcctgcgccgcaagcggctttaacatcaaagataca tacatccattgggtccgacaggcccctggaaagggcctggagtgggtcgcccggatctacccaactaacgggtac actcgctacgctgatagcgtcaagggtcggtttactatttctgccgacacctcaaaaaacacagcctacctccagatg aactctctcagagctgaggatacagccgtgtactattgcagccggtggggaggcgacgggttctacgctatggatg tgtgggggcagggcacactggtcaccgtgagctcatccggaaccacgacgccagcgccgcgaccaccaacacc ggcgcccaccatcgcgtcgcagcccctgtccctgcgcccagaggcgtgccggccagcggcgggggggcgcagt gcacacgagggggctggacttcgcctgtgatatctacatctgggcgcccttggccgggacttgtggggtccttctcc tgtcactggttatcacccttactgcagagtgaagttcagcaggagcgcagacgcccccgcgtaccagcagggcc agaaccagctctataacgagctcaatctaggacgaagagaggagtacgatgttttggacaagagacgtggccggg accctgagatgggggggaaagccgagaaggaagaaccctcaggaaggcctgtacaatgaactgcagaaagataa gatggcggaggcctacagtgagattgggatgaaaggcgagcgccggaggggcaaggggcacgatggccttta ccagggtctcagtacagccaccaaggacacctacgacgcccttcacatgcaggccctgcccctcgc **(SEQ ID NO: 169)**

Table 12 – Amino Acid Sequences of Exemplary Chemokines

hCCL19	MALLLALSLLVLWTSPAPTLSGTNDAEDCCLSVTQKPIPGYIVRNF HYLLIKDGCRVPAVVFTTLRGRQLCAPPDQPWVERIIQRLQRTSAK MKRRSS **(SEQ ID NO: 178)**
hCXCL12	MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVK HLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIQEYLEKALNK **(SEQ ID NO: 179)**

EQUIVALENTS

[0316] It is to be appreciated by those skilled in the art that various alterations, modifications, and improvements to the present disclosure will readily occur to those skilled in the art. Such alterations, modifications, and improvements are intended to be part of the present disclosure, and are intended to be within the spirit and scope of the invention. Accordingly, the foregoing description and drawing are by way of example only and any invention described in the present disclosure if further described in detail by the claims that follow.

[0317] Those skilled in the art will appreciate typical standards of deviation or error attributable to values obtained in assays or other processes as described herein. The publications, websites and other reference materials referenced herein to describe the background of the invention and to provide additional detail regarding its practice are hereby incorporated by reference in their entireties.

CLAIMS

1. A modified immune cell comprising a fusion protein comprising a cytokine, a linker, and a cytokine receptor,

wherein the modified immune cell is a stem cell, macrophage, monocyte, or dendritic cell and

the cytokine binds the cytokine receptor.

2. The modified immune cell of claim 1, wherein the fusion protein is membrane-bound.

3. The modified immune cell of claim 1 or 2, wherein the linker is a flexible linker.

4. The modified immune cell of any one of claims 1-3, wherein the linker is a cleavable linker.

5. The modified immune cell of any one of claims 1-4, further comprising a chimeric antigen receptor (CAR).

6. The modified immune cell of any one of claims 1-5, wherein the fusion protein further comprises a signal peptide.

7. The modified immune cell of claim 6, wherein the fusion protein comprises, from N-terminus to C-terminus: the signal peptide, the cytokine, the linker, and the cytokine receptor.

8. The modified immune cell of any one of claims 1-7, wherein the fusion protein comprises an amino acid sequence at least 80% identical to a sequence selected from Table 2a, Table 2b, Table 3a, Table 3b, Table 6, Table 8, or Table 9.

9. A modified immune cell comprising one or more nucleic acids encoding a fusion protein comprising a cytokine, a linker, and a cytokine receptor,

wherein the modified immune cell is a stem cell, macrophage, monocyte or dendritic cell and

the cytokine binds the cytokine receptor.

10. The modified immune cell of claim 9, wherein the fusion protein is membrane-bound.

11. The modified immune cell of claim 9 or 10, wherein the linker is a flexible linker.

12. The modified immune cell of any one of claims 9-11, wherein the linker is a cleavable linker.

13. The modified immune cell of any one of claims 9-12, further comprising a chimeric antigen receptor (CAR).

14. The modified immune cell of claim 13, wherein the fusion protein further comprises a signal peptide.

15. The modified immune cell of claims 14, wherein the fusion protein comprises, from N-terminus to C-terminus: the signal peptide, the cytokine, the linker, and the cytokine receptor.

16. The modified immune cell of any one of claims 9-15, wherein the one or more nucleic acids comprise a sequence at least 80% identical to a sequence selected from Table 10.

17. The modified immune cell of any one of claims 9-15, wherein the one or more nucleic acids comprise a sequence at least 80% identical to a sequence selected from Table 11b.

18. The modified immune cell of any one of claims 9-15, wherein the one or more nucleic acids comprise a sequence at least 80% identical to a sequence selected from Table 4a, Table 4b, or Table 7.

19. The modified immune cell of any one of claims 9-15, wherein the one or more nucleic acids comprise a sequence at least 80% identical to a sequence selected from Table 5a or Table 5b.

20. The modified immune cell of any one of claims 9-15, wherein the one or more nucleic acids comprise a sequence at least 80% identical to a signal peptide sequence selected from Table 8.

21. The modified immune cell of any one of claims 9-15, wherein the one or more nucleic acids comprise a sequence at least 80% identical to a linker sequence selected from Table 8.

22. The modified immune cell of any one of claims 1-21, wherein the signal peptide is or comprises a CD8a, IgG κ, PDGFR-β, Type I Interferon (IFN-α1, IFN-α2, IFN-α4, IFN-α5, IFN-α6, IFN-α7, IFN-α8, IFN-α10, IFN-α13, IFN-α14, IFN-α16, IFN-α17, IFN-α21, IFN-β, IFN-ω, IFN-ε, or IFN-κ), Type II Interferon (IFN-γ), Type III Interferon (IFN-λ1, IFN-λ2, IFN-λ3, or IFN-λ4), TNF-α, IL-1β, IL-6, IL-12, IL-17, IL-23, GM-CSF, IL-4, IL-10, IL-13, IL-18, M-CSF, TGF-β, IFNAR1, IFNAR2, IFNGR1, IFNGR2, IFNLR1, TNFR1, TNFR2, IL-1R1, IL-1R3, IL-6Rα, gp130, IL-12Rβ1, IL-12Rβ2, IL-17RA, IL-17RB, IL-17RC, IL-23R, CSF2-Rα, CSF2-Rβ, IL-4Rα, IL-4Rα1, IL-2Rγc, IL-10R1, IL-10R2, IL-13Rα1, IL-18Rα, IL-18Rβ, CSF1-R, TGF-βR1, or TGF-βR2 signal peptide.

23. The modified immune cell of any one of claims 1-22, wherein the cytokine is or comprises a pro-inflammatory cytokine.

24. The modified immune cell of any one of claims 1-22, wherein the cytokine is or comprises an anti-inflammatory cytokine.

25. The modified immune cell of claim 23, wherein the cytokine is or comprises a Type I Inteferon (IFN-α1, IFN-α2, IFN-α4, IFN-α5, IFN-α6, IFN-α7, IFN-α8, IFN-α10, IFN-α13, IFN-α14, IFN-α16, IFN-α17, IFN-α21, IFN-β, IFN-ω, IFN-ε, or IFN-κ), Type II Interferon (IFN-γ),

Type III Interferon (IFN-λ1, IFN-λ2, IFN-λ3, or IFN-λ4), TNF-α, IL-1β, IL-6, IL-12, IL-17, IL-23, or GM-CSF.

26. The modified immune cell of claim 24, wherein the cytokine is or comprises IL-4, IL-10, IL-13, IL-18, M-CSF, or TGF-β.

27. The modified immune cell of any one of claims 1-22, wherein the cytokine is or comprises a Type I Inteferon (IFN-α1, IFN-α2, IFN-α4, IFN-α5, IFN-α6, IFN-α7, IFN-α8, IFN-α10, IFN-α13, IFN-α14, IFN-α16, IFN-α17, IFN-α21, IFN-β, IFN-ω, IFN-ε, or IFN-κ), Type II Interferon (IFN-γ), Type III Interferon (IFN-λ1, IFN-λ2, IFN-λ3, or IFN-λ4), TNF-α, IL-1β, IL-6, IL-12, IL-17, IL-23, GM-CSF, IL-4, IL-10, IL-13, IL-18, M-CSF, or TGF-β .

28. The modified immune cell of any one of claims 1-22, wherein the cytokine receptor is or comprises a pro-inflammatory cytokine receptor.

29. The modified immune cell of any one of claims 1-22, wherein the cytokine receptor is or comprises an anti-inflammatory cytokine receptor.

30. The modified immune cell of claim 28, wherein the cytokine receptor is or comprises IFNAR1, IFNAR2, IFNGR1, IFNGR2, IFNLR1, TNFR1, TNFR2, IL-1R1, IL-1R3, IL-6Rα, gp130, IL-12Rβ1, IL-12Rβ2, IL-17RA, IL-17RB, IL-17RC, IL-23R, CSF2-Rα, or CSF2-Rβ.

31. The modified immune cell of claim 29, wherein the cytokine receptor is or comprises IL-4Rα, IL-4Rα1, IL-2Rγc, IL-10R1, IL-10R2, IL-13Rα1, IL-18Rα, IL-18Rβ, CSF1-R, TGF-βR1, or TGF-βR2.

32. The modified immune cell of any one of claims 1-3a, wherein the cytokine receptor is or comprises IFNAR1, IFNAR2, IFNGR1, IFNGR2, IFNLR1, TNFR1, TNFR2, IL-1R1, IL-1R3, IL-6Rα, gp130, IL-12Rβ1, IL-12Rβ2, IL-17RA, IL-17RB, IL-17RC, IL-23R, CSF2-Rα, CSF2-Rβ, IL-4Rα, IL-4Rα1, IL-2Rγc, IL-10R1, IL-10R2, IL-13Rα1, IL-18Rα, IL-18Rβ, CSF1-R, TGF-βR1, or TGF-βR2.

33. The modified immune cell of any one of claims 1-32, wherein the linker is or comprises a linker selected from a group consisting of: a $(G4S)_n$ linker, wherein n = 1-5 (SEQ ID NO: 170), a Whitlow linker, and Linker 26.

34. A modified immune cell comprising a fusion protein comprising interleukin 10 (IL-10), a linker, and interleukin-10 receptor (IL10R).

35. A modified immune cell comprising a fusion protein comprising interferon beta (IFNβ), a linker, and interferon-α/β receptor (IFNAR).

36. The modified immune cell of claim 34 or 35, wherein the fusion protein is membrane-bound.

37. The modified immune cell of claim 34 or 35, wherein the linker is a flexible linker.

38. The modified immune cell of any one of claims 34-37, wherein the linker is a cleavable linker.

39. The modified immune cell of any one of claims 34-38, further comprising a chimeric antigen receptor (CAR).

40. A pharmaceutical composition comprising a modified immune cell of any one of claims 1-39.

41. The pharmaceutical composition of claim 40, comprising a pharmaceutically acceptable carrier.

42. A nucleic acid construct comprising one or more nucleic acids encoding a fusion protein comprising a cytokine and a cytokine receptor.

43. The nucleic acid construct of claim 42, further comprising one or more nucleic acids encoding a chimeric antigen receptor (CAR).

44. A pharmaceutical composition comprising the nucleic acid construct of claim 42 or 43.

45. The pharmaceutical composition of claim 44, comprising a pharmaceutically acceptable carrier.

46. A method of treating or preventing a disease or disorder in a subject, comprising delivering to the subject a therapeutically effective amount of the pharmaceutical composition of any one of claims 40, 41, 44, or 45.

47. A method of modifying an immune cell, the method comprising delivering to the immune cell a nucleic acid construct comprising one or more nucleic acids encoding a fusion protein comprising a cytokine, a linker, and a cytokine receptor.

48. The method of claim 47, wherein the linker is a flexible linker.

49. The method of claim 47 or 48, wherein the linker is a cleavable linker.

50. The method of any one of claims 47-49, wherein the nucleic acid construct further comprises one or more nucleic acids encoding a chimeric antigen receptor (CAR).

51. The method of any one of claims 47-50, wherein the delivering comprises electroporation or transfection with DNA, mRNA, or chemically modified mRNA.

52. The method of any one of claims 47-50, wherein the delivering comprises transduction with an adeno-associated viral (AAV) vector, an adenoviral vector, or a retroviral vector.

53. The method of claim 52, wherein the retroviral vector comprises a lentiviral vector or a gammaretroviral vector.

54. The method of claim 53, wherein the lentiviral vector is packaged with a Vpx protein.

55. The method of claim 52, wherein the adenoviral vector comprises an Ad2 vector or an Ad5 vector.

56. The method of claim 55, wherein the Ad5 vector comprises an Ad5f35 adenoviral vector.

57. The method of any one of claims 47-50, wherein the delivery comprises transposon-based delivery or CRISPR-based targeted integration.

58. A modified immune cell comprising an exogenous cytokine and a chimeric antigen receptor (CAR),

wherein the modified immune cell is a stem cell, macrophage, monocyte, or dendritic cell and

the exogenous cytokine is or comprises a pro-inflammatory cytokine, an anti-inflammatory cytokine, or a chemoattractant chemokine.

59. The modified immune cell of claim 58, wherein the exogenous cytokine comprises a signal peptide.

60. The modified immune cell of claim 58 or 59, wherein the exogenous cytokine comprises an amino acid sequence at least 80% identical to a sequence selected from Table 2a, Table 2b, Table 6, or Table 8.

61. A modified immune cell comprising one or more nucleic acids encoding an exogenous cytokine and a chimeric antigen receptor (CAR),

wherein the modified immune cell is a stem cell, macrophage, monocyte or dendritic cell and

the exogenous cytokine is or comprises a pro-inflammatory cytokine, an anti-inflammatory cytokine, or a chemoattractant chemokine.

62. The modified immune cell of claim 61, wherein the exogenous cytokine further comprises a signal peptide.

63. The modified immune cell of claim 61 or 62, wherein the one or more nucleic acids comprise a sequence at least 80% identical to a sequence selected from Table 4a, Table 4b, Table 7, or Table 11b.

64. The modified immune cell of claim 61 or 62, wherein the one or more nucleic acids comprise a sequence at least 80% identical to a sequence selected from Table 8.

65. The modified immune cell of any one of claims 61-64, wherein the one or more nucleic acids encode a signal peptide.

66. The modified immune cell of claim 62 or 65, wherein the signal peptide is or comprises a CD8a, IgG κ, PDGFR-β, Type I Interferon (IFN-α1, IFN-α2, IFN-α4, IFN-α5, IFN-α6, IFN-α7, IFN-α8, IFN-α10, IFN-α13, IFN-α14, IFN-α16, IFN-α17, IFN-α21, IFN-β, IFN-ω, IFN-ε, or IFN-κ), Type II Interferon (IFN-γ), Type III Interferon (IFN-λ1, IFN-λ2, IFN-λ3, or IFN-λ4), TNF-α, IL-1β, IL-6, IL-12, IL-17, IL-23, GM-CSF, IL-4, IL-10, IL-13, IL-18, M-CSF, TGF-β, IFNAR1, IFNAR2, IFNGR1, IFNGR2, IFNLR1, TNFR1, TNFR2, IL-1R1, IL-1R3, IL-6Rα, gp130, IL-12Rβ1, IL-12Rβ2, IL-17RA, IL-17RB, IL-17RC, IL-23R, CSF2-Rα, CSF2-Rβ, IL-4Rα, IL-4Rα1, IL-2Rγc, IL-10R1, IL-10R2, IL-13Rα1, IL-18Rα, IL-18Rβ, CSF1-R, TGF-βR1, or TGF-βR2 signal peptide.

67. The modified immune cell of any one of claims 58-66, wherein the exogenous cytokine is or comprises a Type I Inteferon (IFN-α1, IFN-α2, IFN-α4, IFN-α5, IFN-α6, IFN-α7, IFN-α8, IFN-α10, IFN-α13, IFN-α14, IFN-α16, IFN-α17, IFN-α21, IFN-β, IFN-ω, IFN-ε, or IFN-κ), Type II Interferon (IFN-γ), Type III Interferon (IFN-λ1, IFN-λ2, IFN-λ3, or IFN-λ4), TNF-α, IL-1β, IL-6, IL-12, IL-17, IL-23, GM-CSF, IL-4, IL-10, IL-13, IL-18, M-CSF, TGF-β, CCL19, or CXCL12.

68. The modified immune cell of claim 67, wherein the exogenous cytokine is or comprises IFN-γ, IL-10, CCL19, or CXCL12.

69. A pharmaceutical composition comprising a modified immune cell of any one of claims 58-68.

70. The pharmaceutical composition of claim 69, comprising a pharmaceutically acceptable carrier.

71. A nucleic acid construct comprising one or more nucleic acids encoding an exogenous cytokine and a chimeric antigen receptor (CAR).

72. A pharmaceutical composition comprising the nucleic acid construct of claim 71.

73. The pharmaceutical composition of claim 72, comprising a pharmaceutically acceptable carrier.

74. A method of treating or preventing a disease or disorder in a subject, comprising delivering to the subject a therapeutically effective amount of the pharmaceutical composition of any one of claims 69, 70, 72, or 73.

75. A method of modifying an immune cell, the method comprising delivering to the immune cell a nucleic acid construct comprising one or more nucleic acids encoding an exogenous cytokine and a chimeric antigen receptor (CAR).

76. The method of claim 75, wherein the delivering comprises electroporation or transfection with DNA, mRNA, or chemically modified mRNA.

77. The method of claim 75, wherein the delivering comprises transduction with an adeno-associated viral (AAV) vector, an adenoviral vector, or a retroviral vector.

78. The method of claim 77, wherein the retroviral vector comprises a lentiviral vector or a gammaretroviral vector.

79. The method of claim 78, wherein the lentiviral vector is packaged with a Vpx protein.

80. The method of claim 77, wherein the adenoviral vector comprises an Ad2 vector or an Ad5 vector.

81. The method of claim 80, wherein the Ad5 vector comprises an Ad5f35 adenoviral vector.

82. The method of claim 50, wherein the delivery comprises transposon-based delivery or CRISPR-based targeted integration.

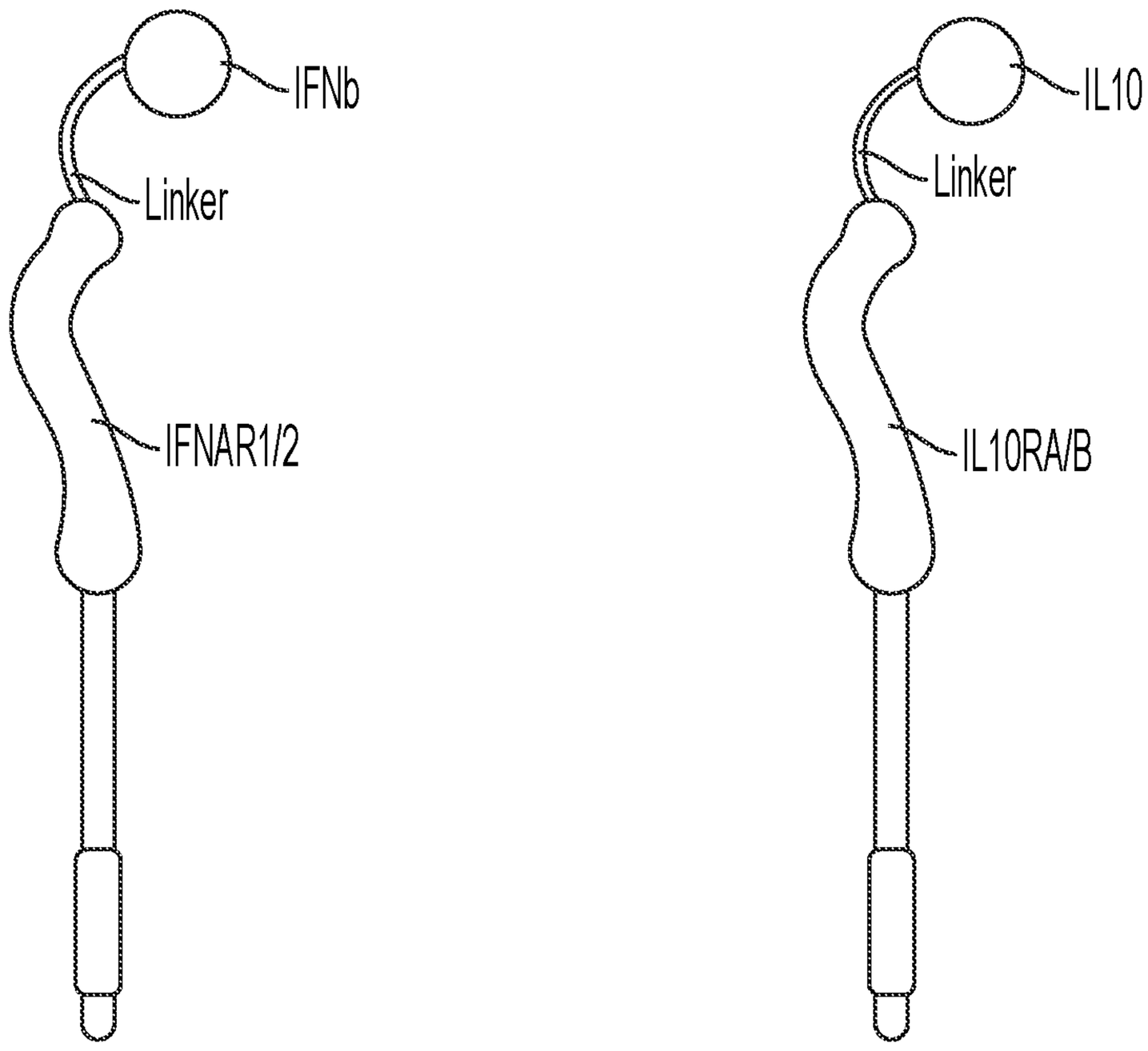


Figure 1

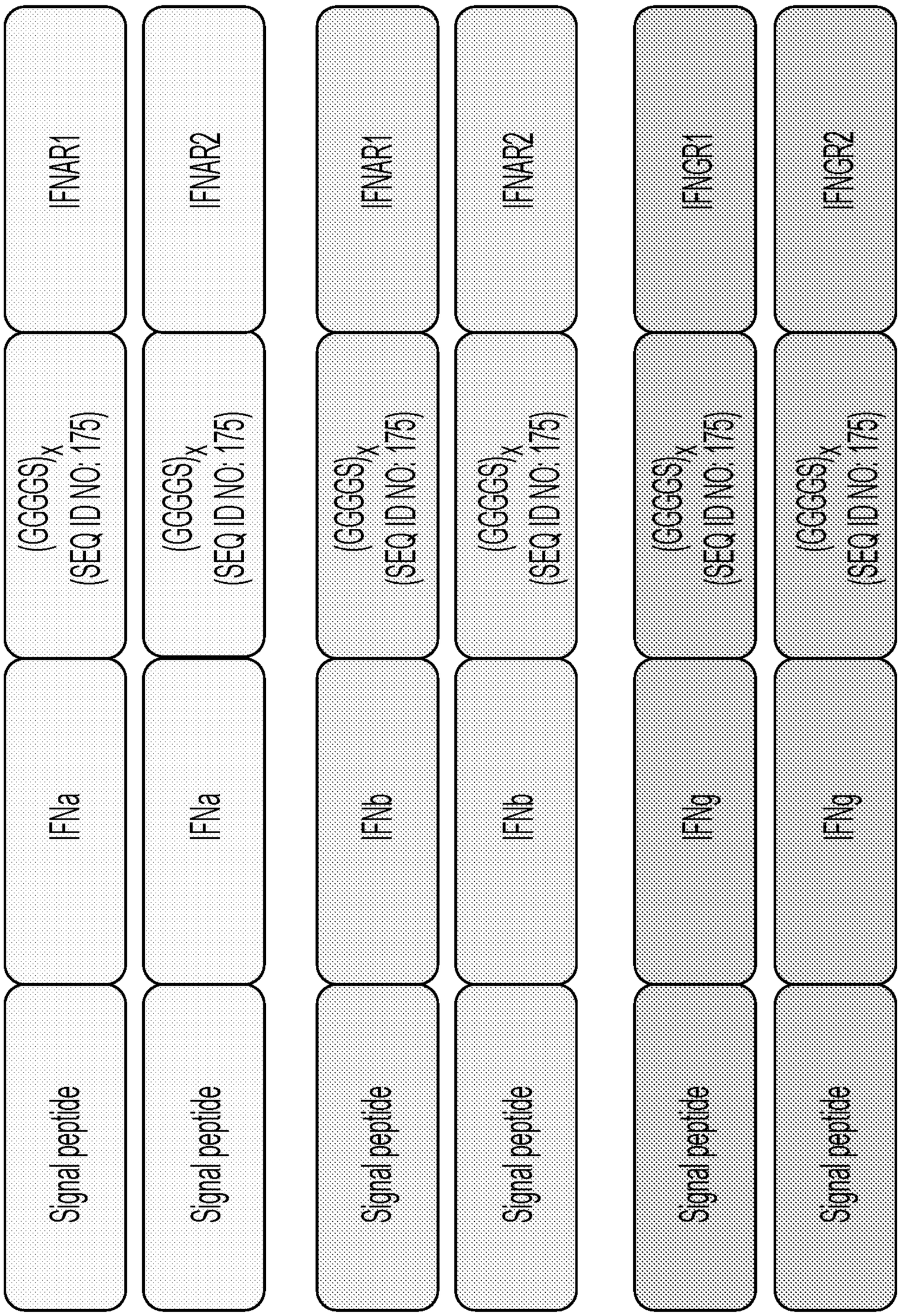

Signal peptide
IFNa
(GGGGS)x
(SEQ ID NO: 175)
IFNAR1
Signal peptide
IFNa
(GGGGS)x
(SEQ ID NO: 175)
IFNAR2
Signal peptide
IFNb
(GGGGS)x
(SEQ ID NO: 175)
IFNAR1
Signal peptide
IFNb
(GGGGS)x
(SEQ ID NO: 175)
IFNAR2
Signal peptide
IFNg
(GGGGS)x
(SEQ ID NO: 175)
IFNGR1
Signal peptide
IFNg
(GGGGS)x
(SEQ ID NO: 175)
IFNGR2

Figure 2

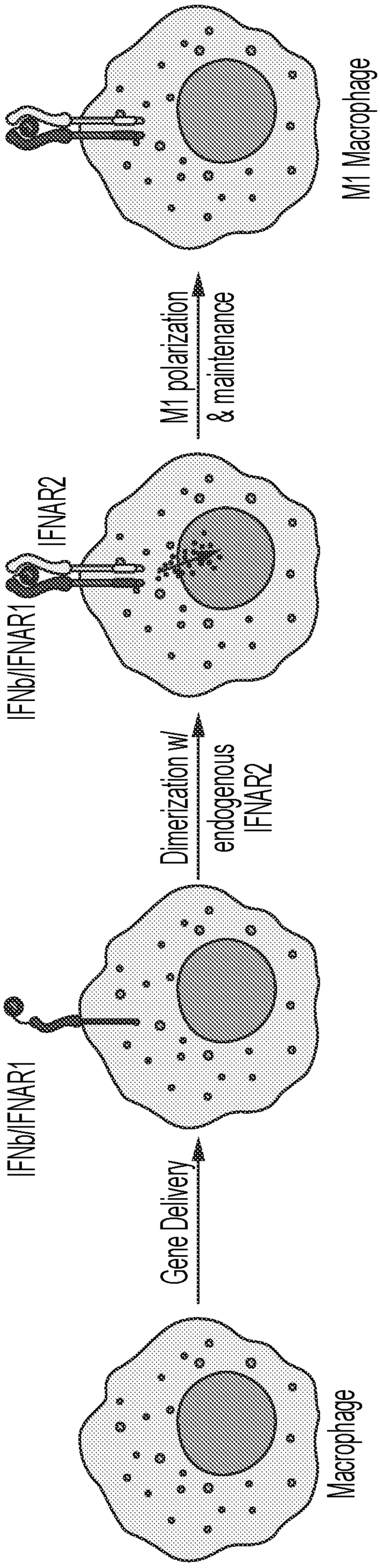

M1 Macrophage
M1 polarization & maintenance
IFNb/IFNAR1
IFNAR2
Dimerization w/ endogenous IFNAR2
IFNb/IFNAR1
Gene Delivery
Macrophage

Figure 3A

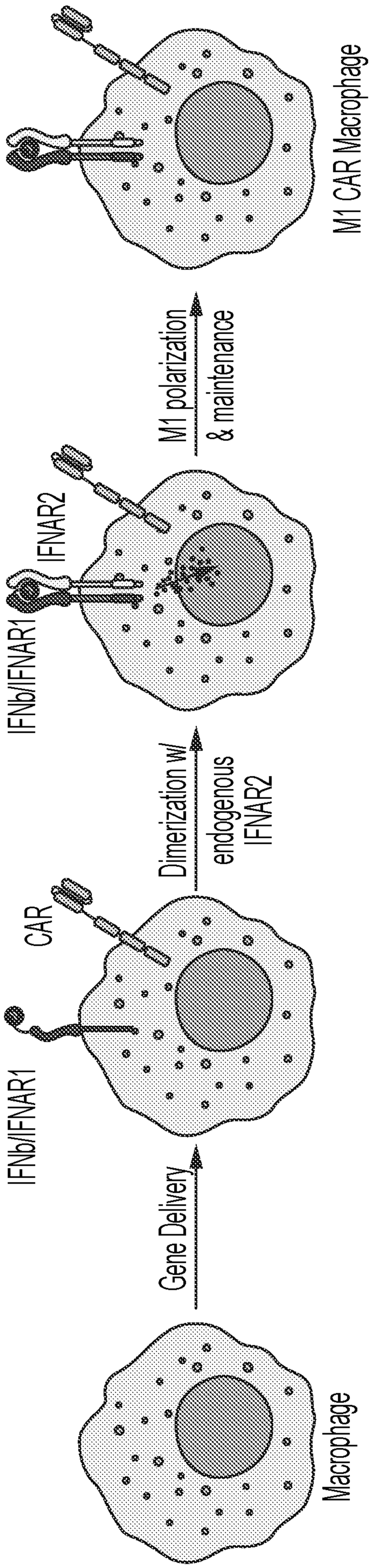

M1 CAR Macrophage
M1 polarization & maintenance
IFNb/IFNAR1 IFNAR2
Dimerization w/ endogenous IFNAR2
IFNb/IFNAR1 CAR
Gene Delivery
Macrophage

Figure 3B

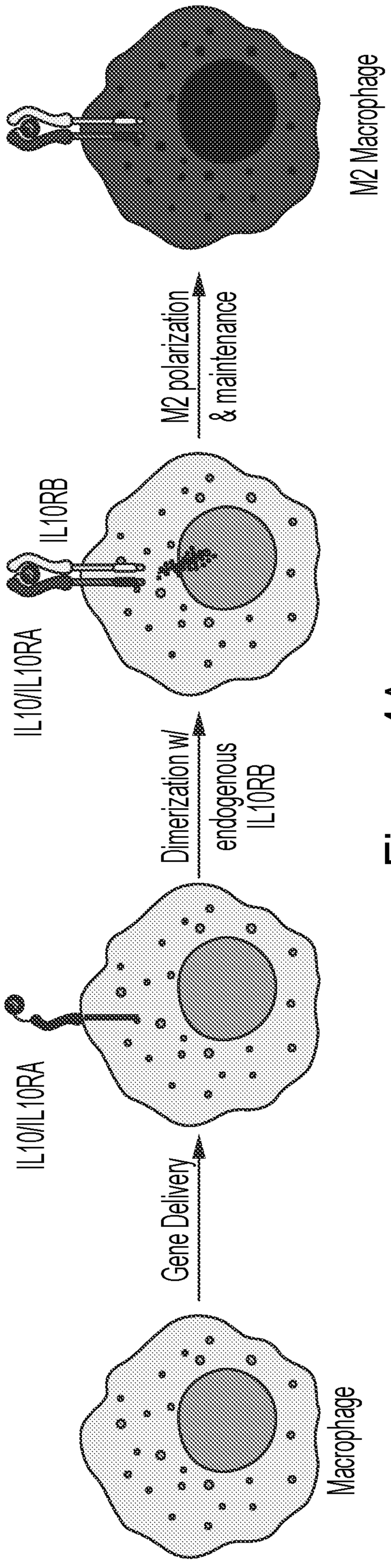

M2 Macrophage
M2 polarization
& maintenance
IL10RB
IL10/IL10RA
Dimerization w/
endogenous
IL10RB
IL10/IL10RA
Gene Delivery
Macrophage

Figure 4A

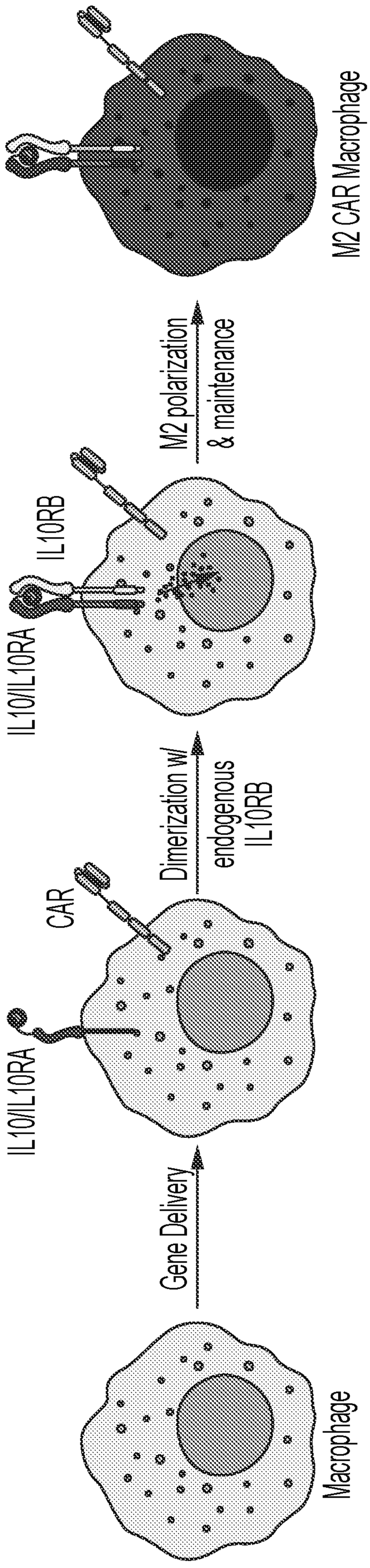

M2 CAR Macrophage
M2 polarization & maintenance
IL10/IL10RA
IL10RB
CAR
Dimerization w/ endogenous IL10RB
IL10/IL10RA
Gene Delivery
Macrophage

Figure 4B

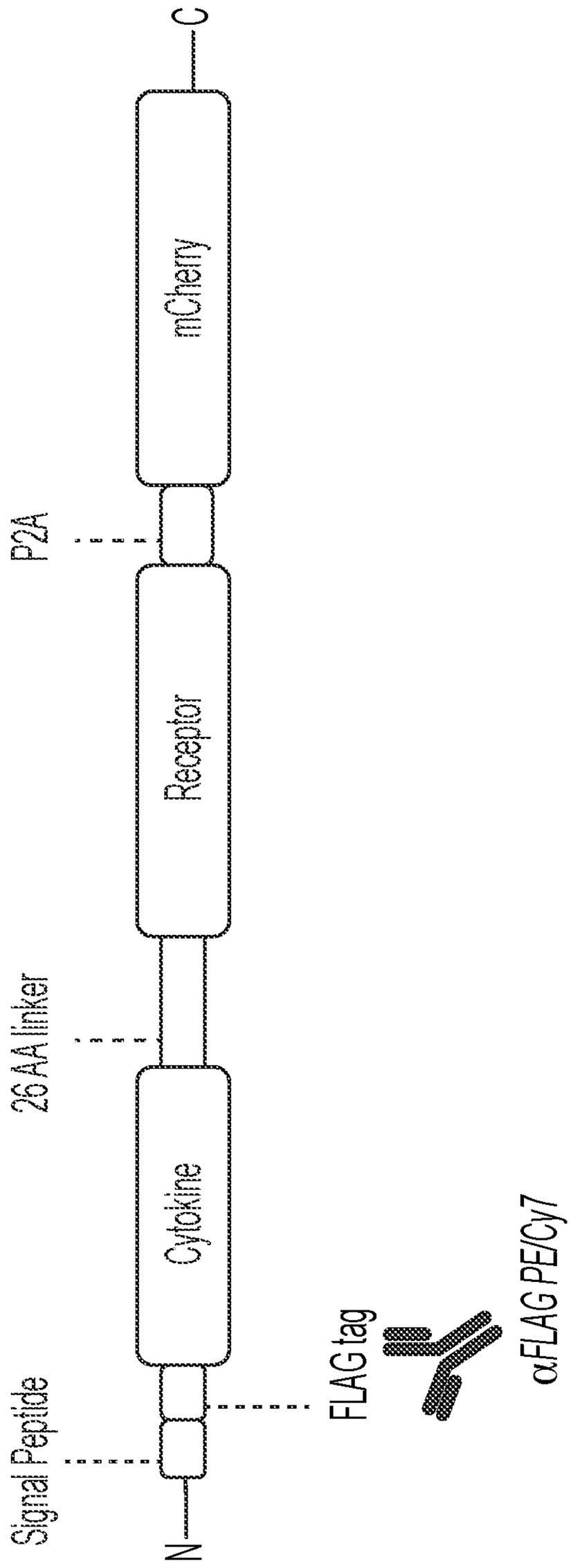

Signal Peptide
FLAG tag
αFLAG PE/Cy7
Cytokine
26 AA linker
Receptor
P2A
mCherry
N
C

Figure 5A

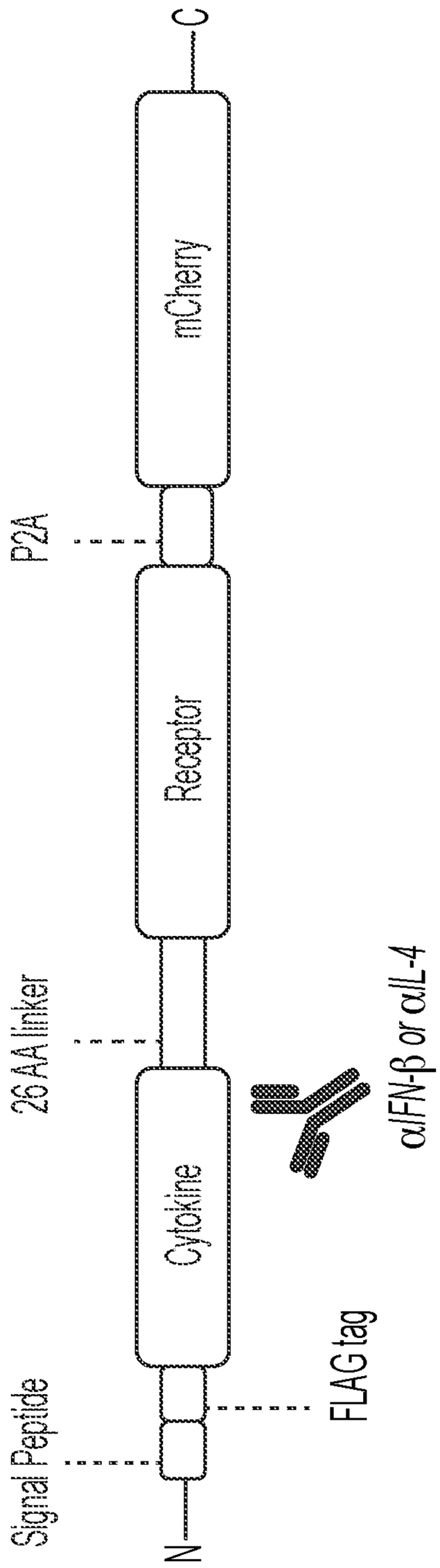

Signal Peptide
FLAG tag
Cytokine
26 AA linker
Receptor
P2A
mCherry
N
αIFN-β or αIL-4

Figure 5B

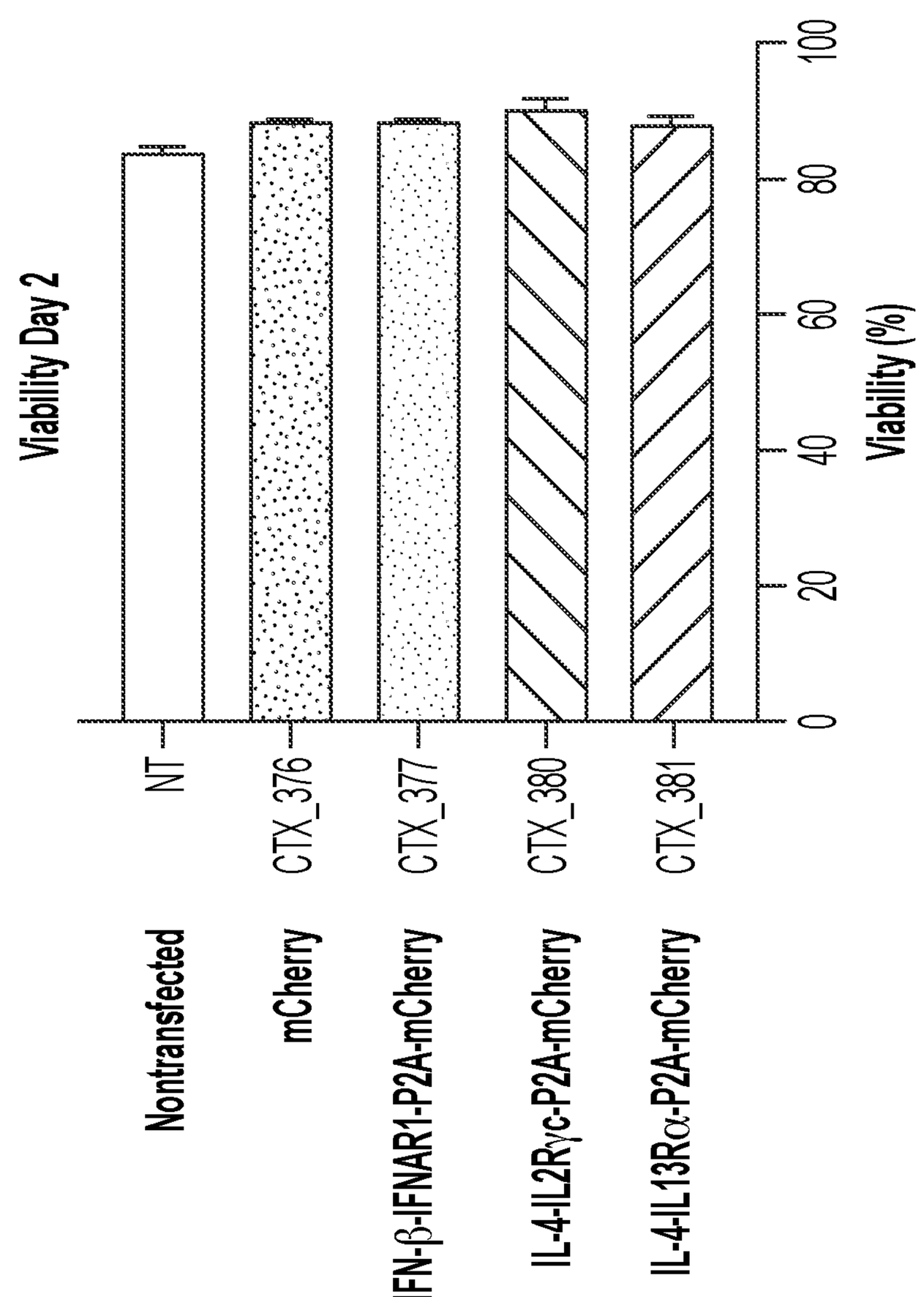

Viability Day 2
Viability (%)
0
20
40
60
80
100
NT
CTX_376
CTX_377
CTX_380
CTX_381
Nontransfected
mCherry
IFN-β-IFNAR1-P2A-mCherry
IL-4-IL2Rγc-P2A-mCherry
IL-4-IL13Rα-P2A-mCherry

Figure 6A

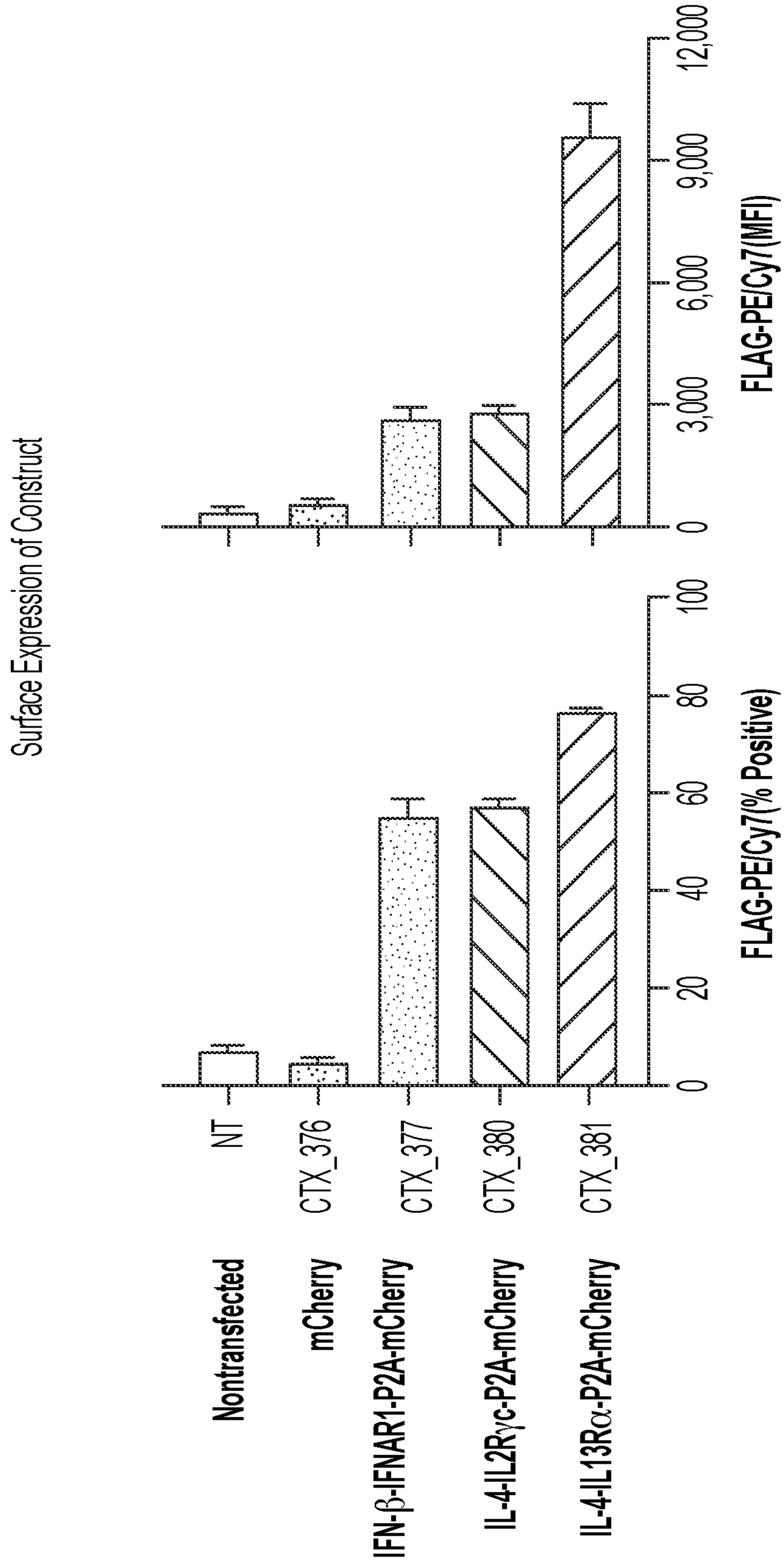

Surface Expression of Construct
Nontransfected
IFN-β-IFNAR1-P2A-mCherry
IL-4-IL2Rγc-P2A-mCherry
IL-4-IL13Rα-P2A-mCherry
NT
CTX_376
CTX_377
CTX_380
CTX_381
0
20
40
60
80
100
FLAG-PE/Cy7(% Positive)
0
3,000
6,000
9,000
12,000
FLAG-PE/Cy7(MFI)

Figure 6B

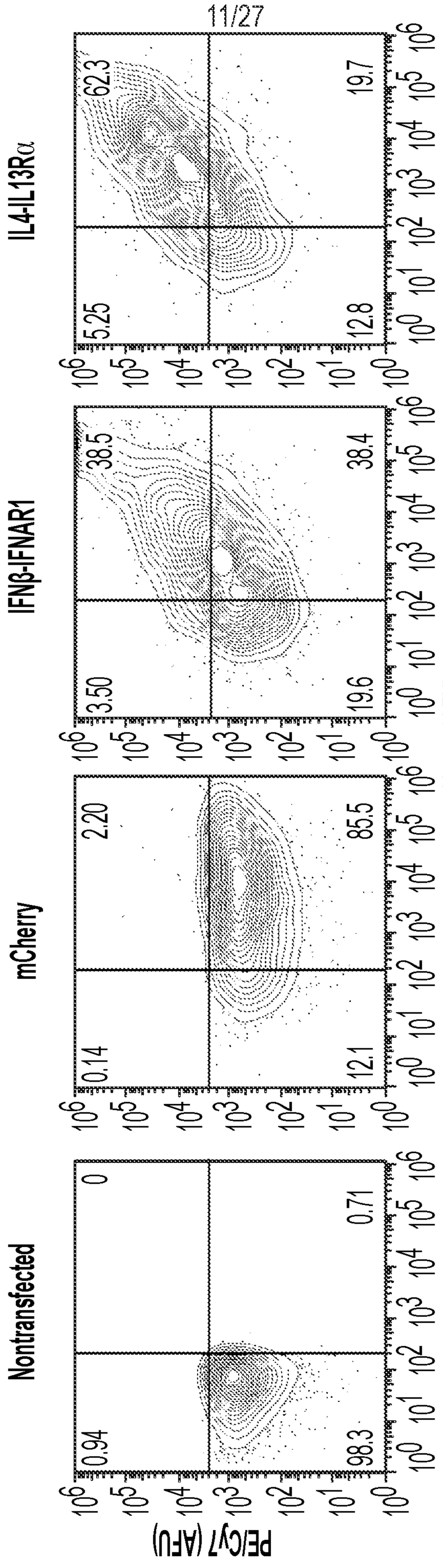

11/27
IL4-IL13Rα
62.3
19.7
5.25
12.8
IFNβ-IFNAR1
38.5
38.4
3.50
19.6
mCherry
2.20
85.5
0.14
12.1
Nontransfected
0
0.71
0.94
98.3
PE/Cy7 (AFU)
mCherry (AFU)

Figure 7

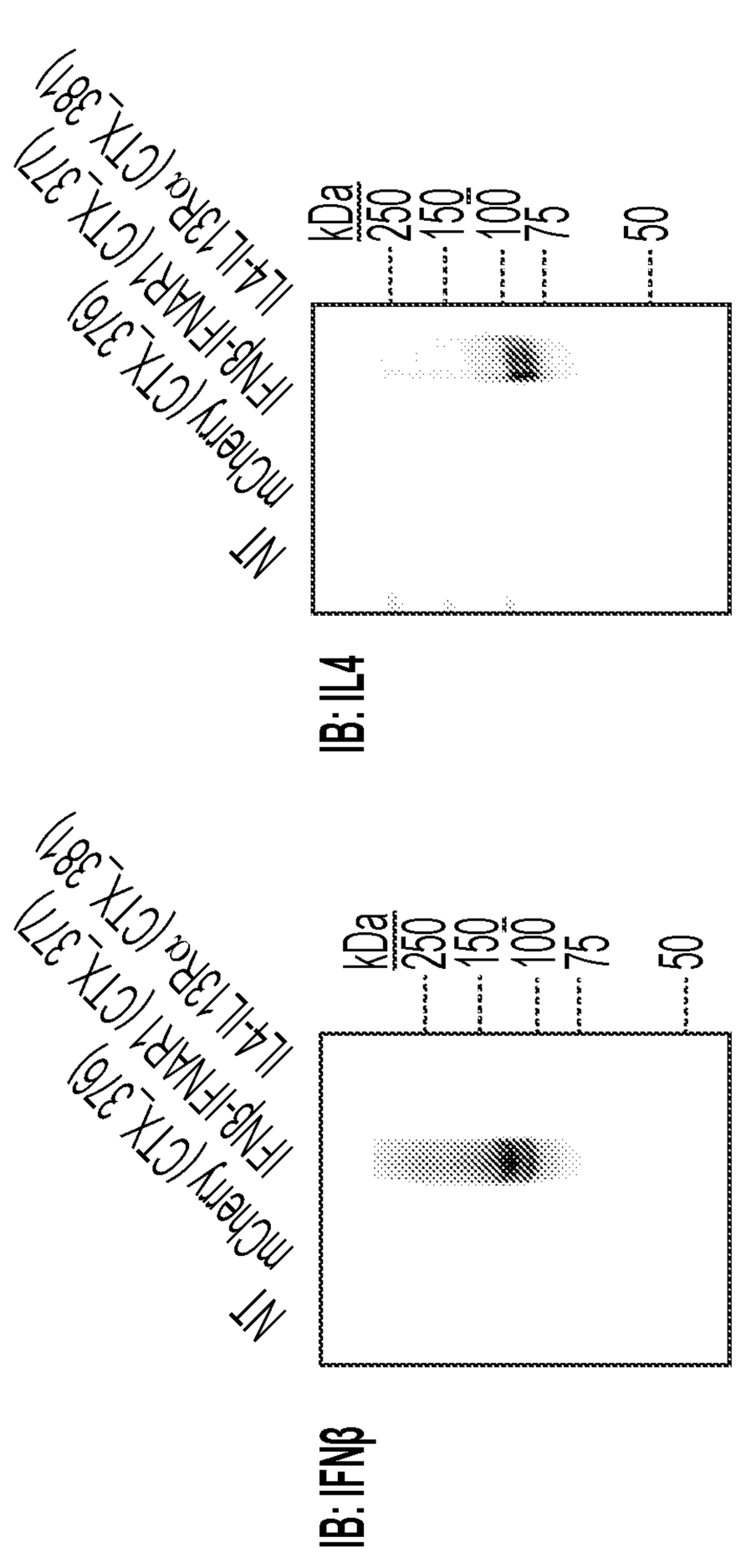

B: IL4
kDa
250
150
100
75
50
NT
mCherry (CTX_376)
IFNβ-IFNAR1 (CTX_377)
IL4-IL13Rα (CTX_381)
B: IFNβ
kDa
250
150
100
75
50
NT
mCherry (CTX_376)
IFNβ-IFNAR1 (CTX_377)
IL4-IL13Rα (CTX_381)

Figure 8

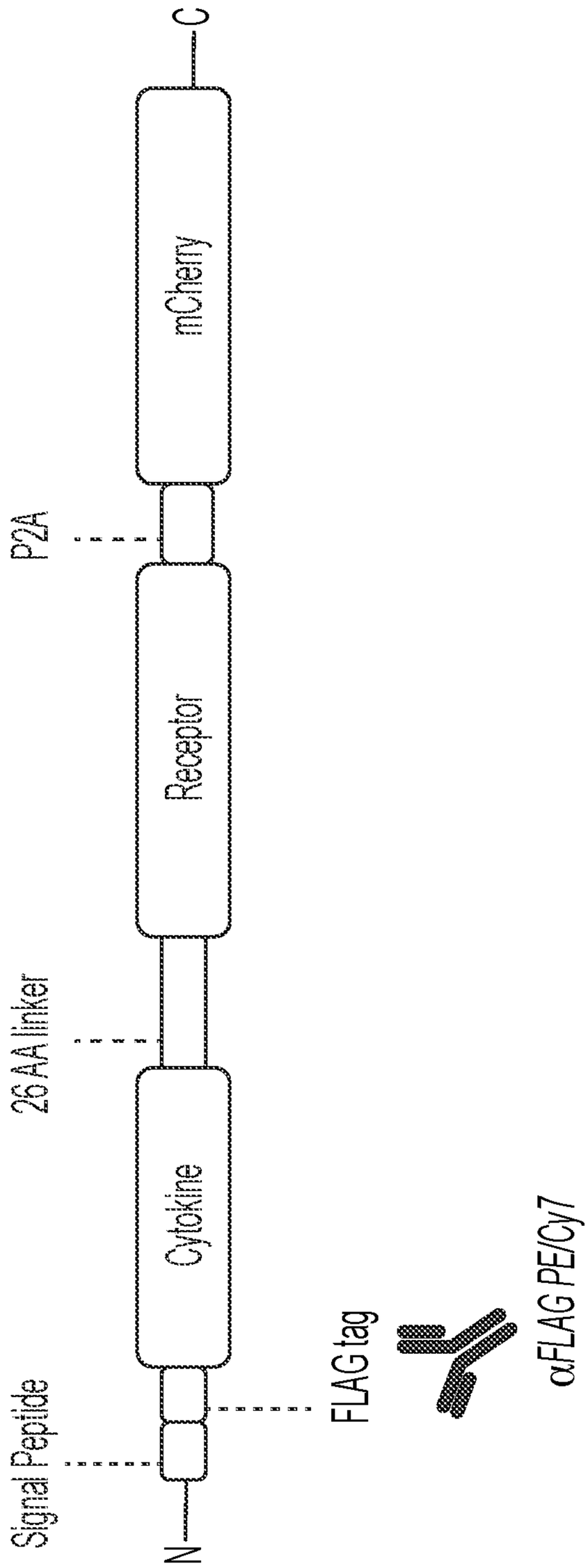
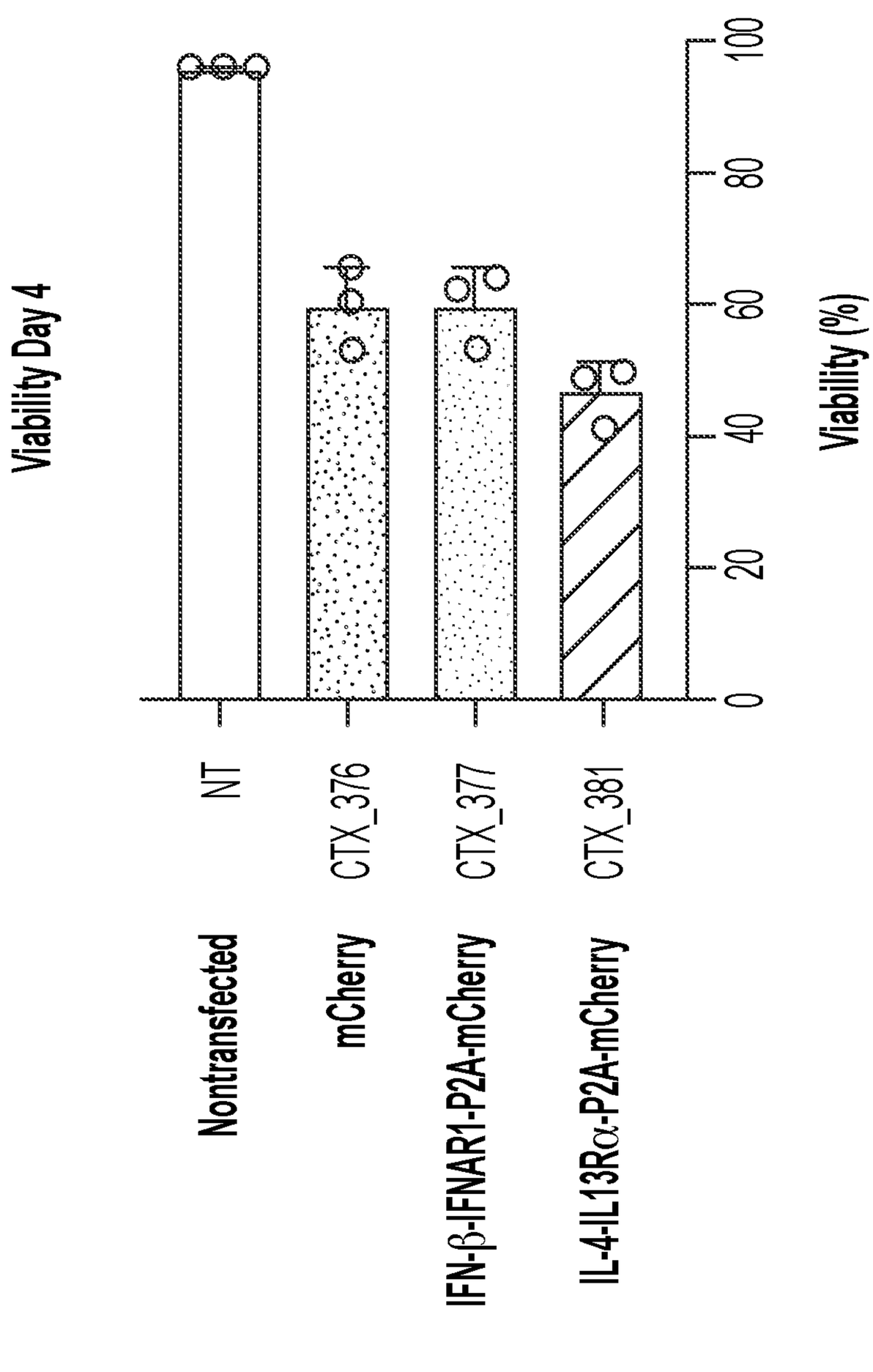

Signal Peptide
FLAG tag
Cytokine
26 AA linker
Receptor
P2A
mCherry
N
αFLAG PE/Cy7

Figure 9


Viability Day 4
Viability (%)
0
20
40
60
80
100
Nontransfected NT
mCherry CTX_376
IFN-β-IFNAR1-P2A-mCherry CTX_377
IL-4-IL13Rα-P2A-mCherry CTX_381

10A

Figure

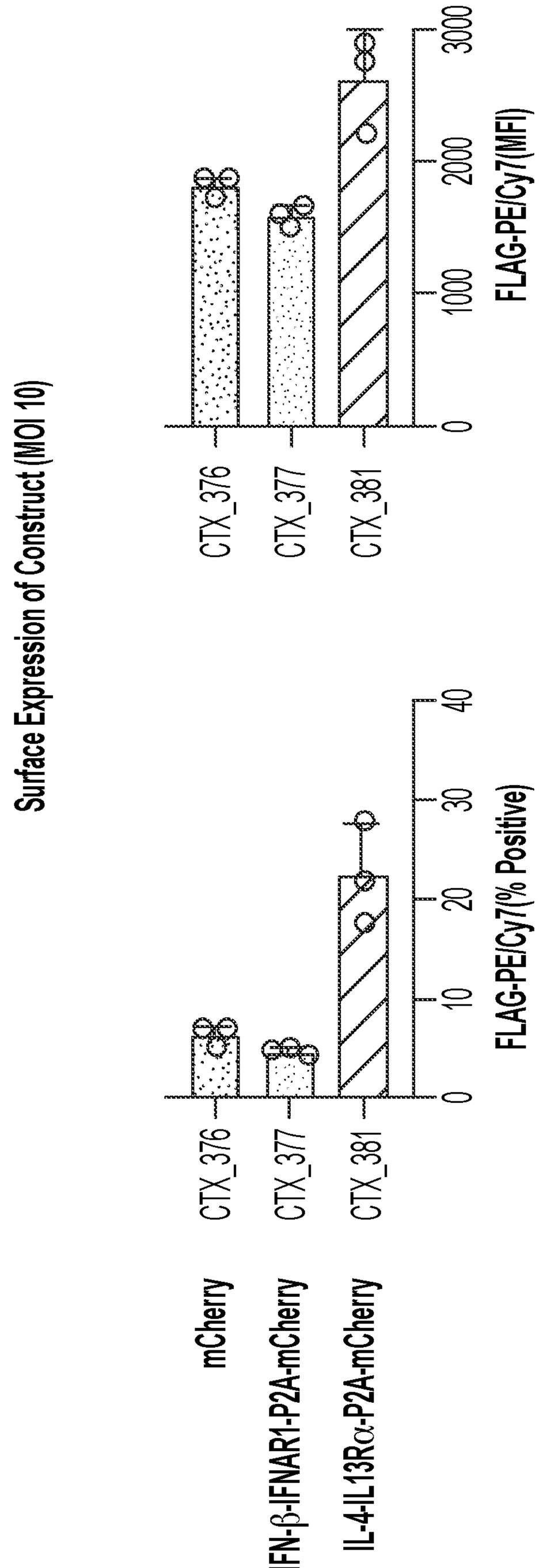

Surface Expression of Construct (MOI 10)
CTX_376
CTX_377
CTX_381
0
1000
2000
3000
FLAG-PE/Cy7(MFI)
CTX_376
CTX_377
CTX_381
0
10
20
30
40
FLAG-PE/Cy7(% Positive)
mCherry
IFN-β-IFNAR1-P2A-mCherry
IL-4-IL13Rα-P2A-mCherry

Figure 10B

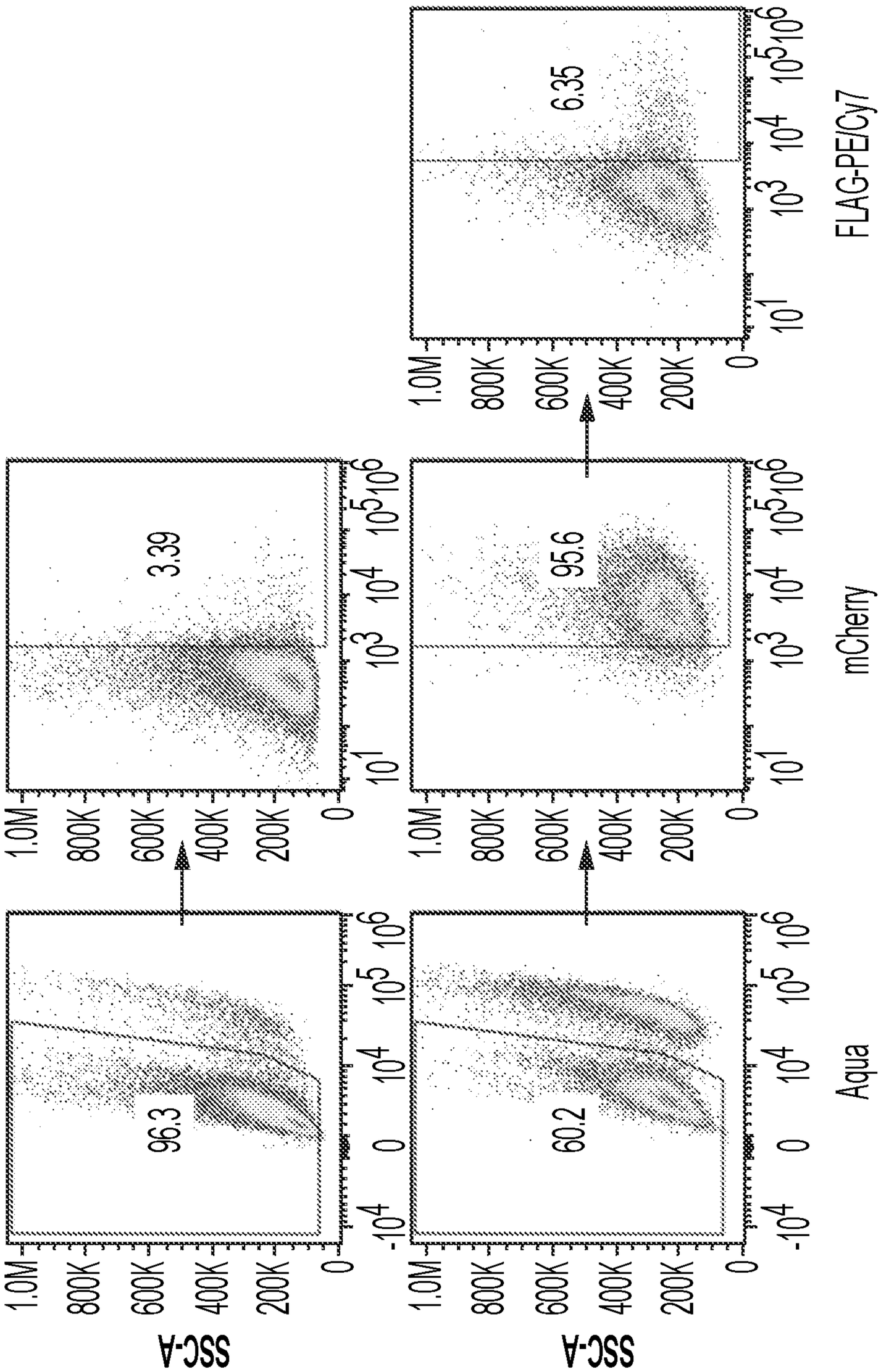

6.35
3.39
95.6
96.3
60.2
FLAG-PE/Cy7
mCherry
Aqua
SSC-A
UTD
(empty)-P2A-mCherry
CTX_376

Figure 11A

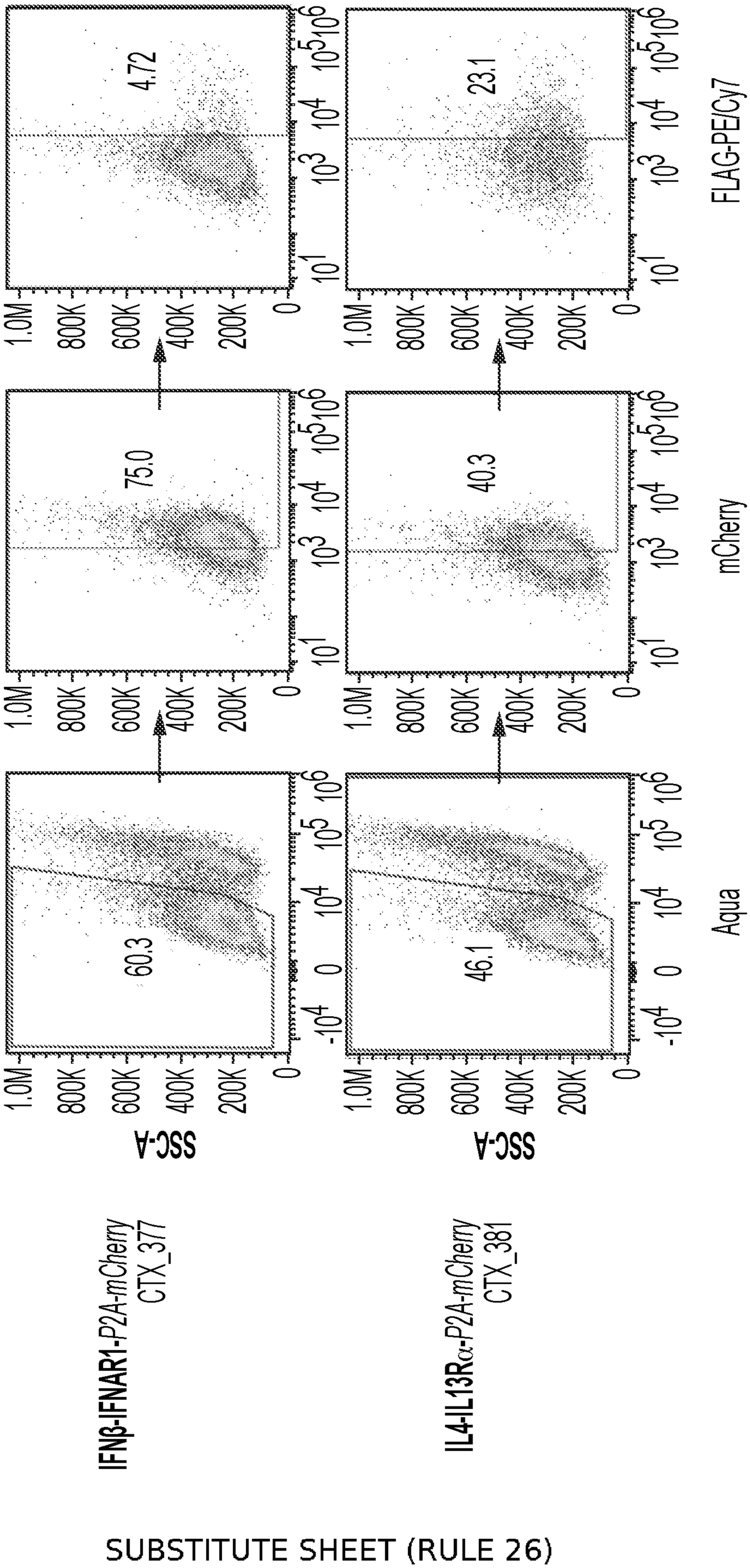

4.72
23.1
75.0
40.3
60.3
46.1
FLAG-PE/Cy7
mCherry
Aqua
SSC-A
SSC-A
IFNβ-IFNAR1-P2A-mCherry
CTX_377
IL4-IL13Rα-P2A-mCherry
CTX_381

Figure 11B

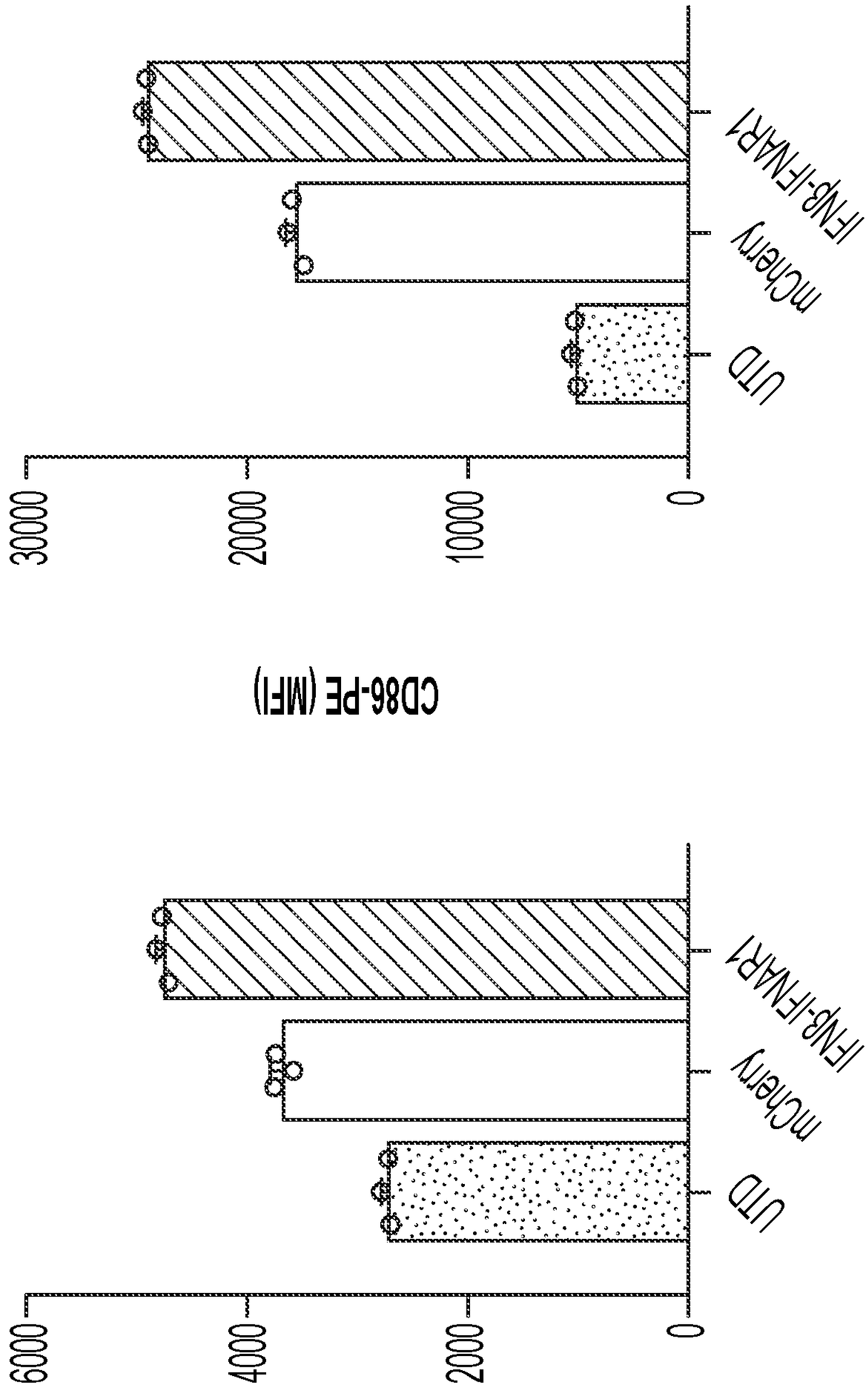

CD86
30000
20000
10000
0
UTD
mCherry
IFNβ-IFNAR1
CD86-PE (MFI)
CD80
6000
4000
2000
0
UTD
mCherry
IFNβ-IFNAR1
CD80-FITC (MFI)
M1 Markers

Figure 2A

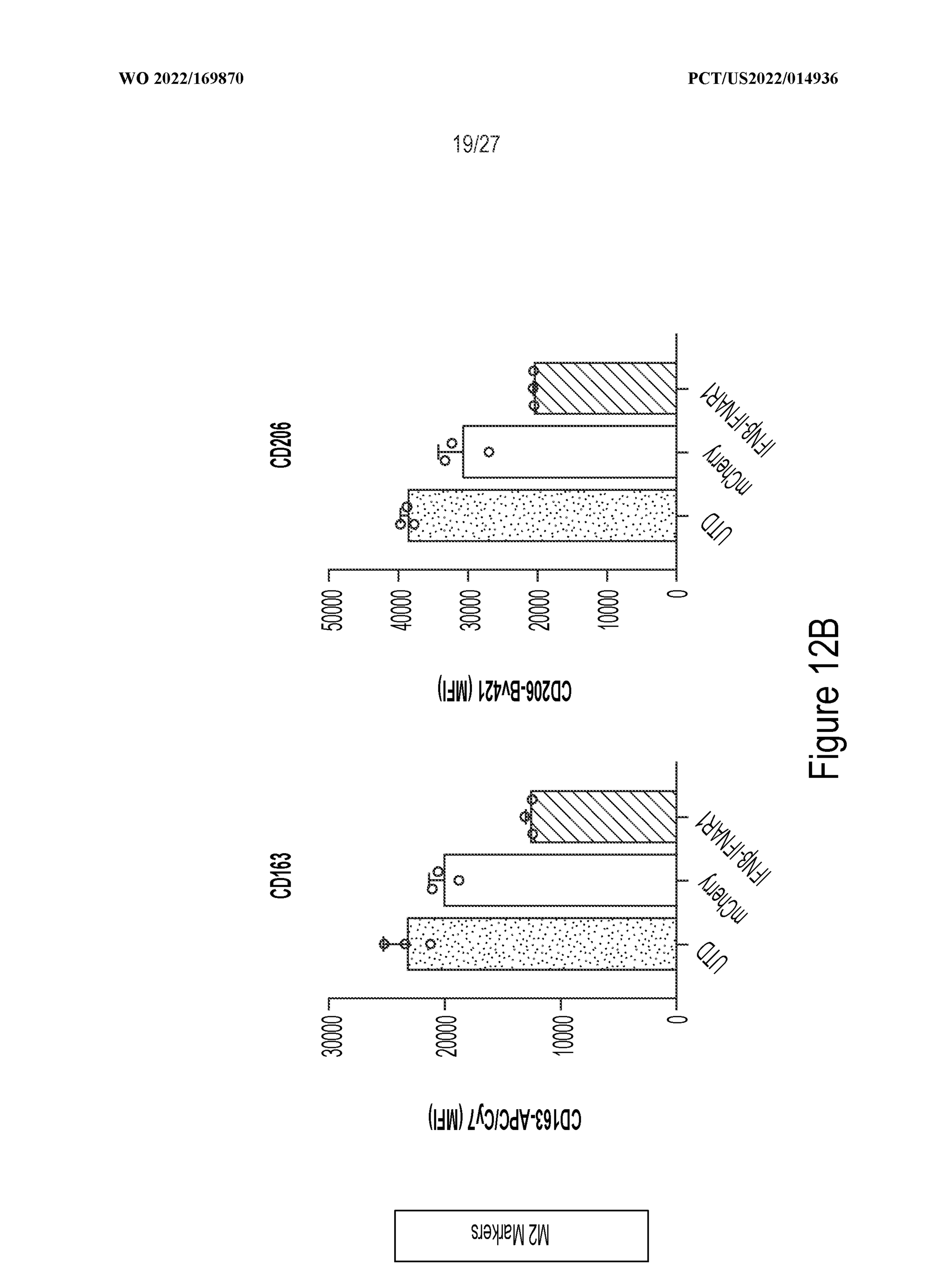

CD206
CD206-BV421 (MFI)
50000
40000
30000
20000
10000
0
UTD
mCherry
IFNβ-IFNAR1
CD163
CD163-APC/Cy7 (MFI)
30000
20000
10000
0
UTD
mCherry
IFNβ-IFNAR1
M2 Markers

Figure 12B

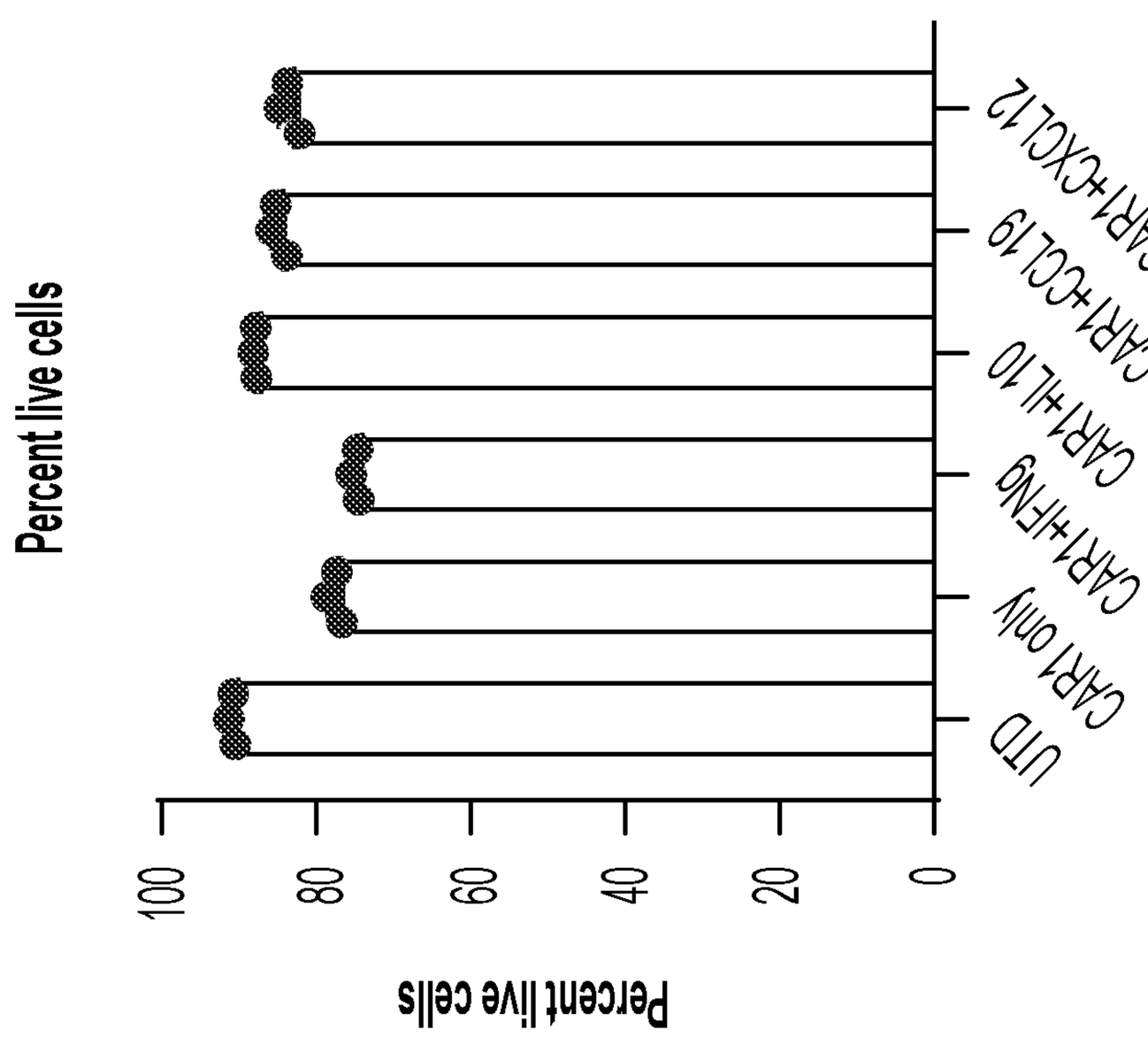

Percent live cells
100
80
60
40
20
0
UTD
CAR1 only
CAR1+IFNg
CAR1+IL10
CAR1+CCL19
CAR1+CXCL12

Figure 13

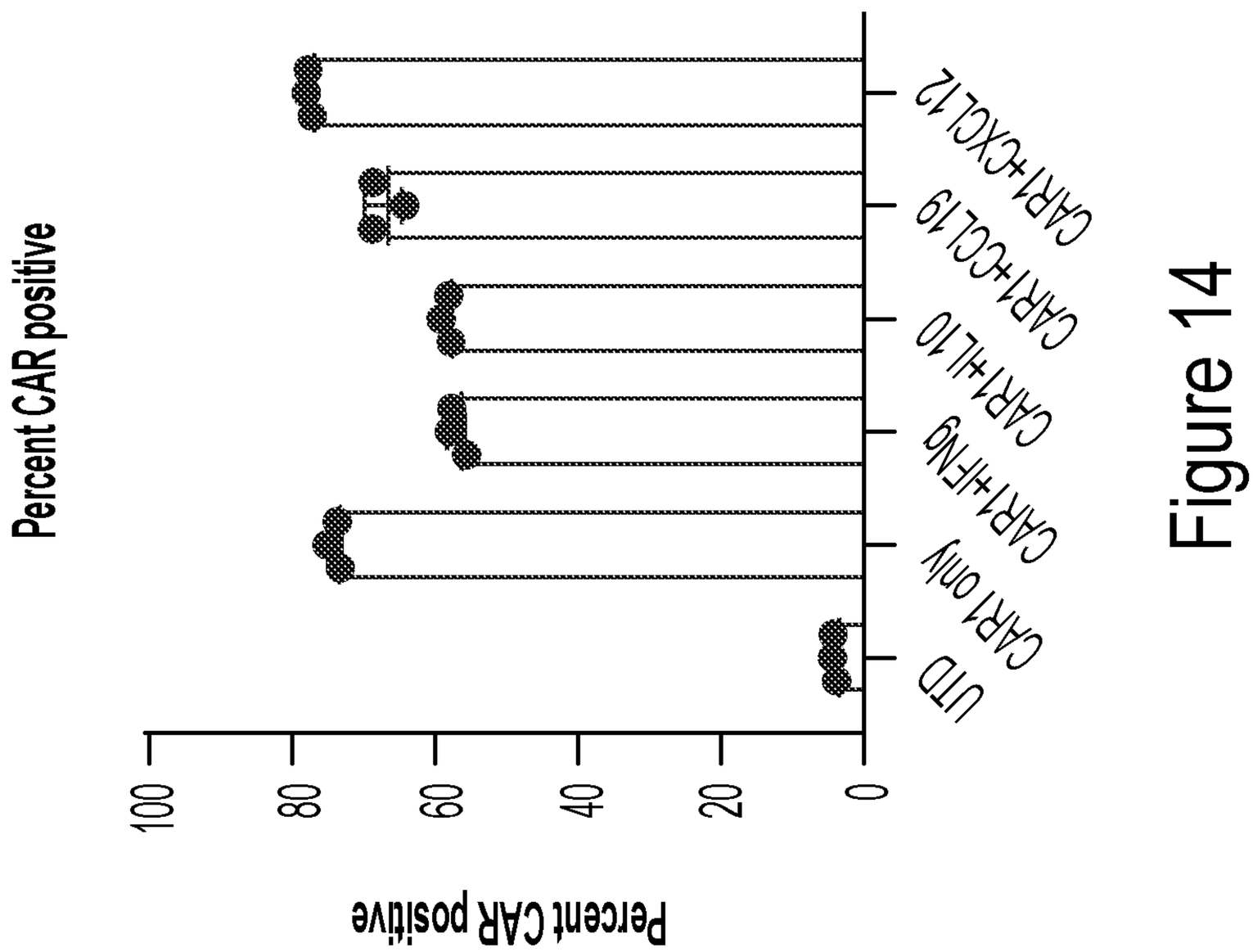

Percent CAR positive
Percent CAR positive
100
80
60
40
20
0
UTD
CAR1 only
CAR1+IFNg
CAR1+IL10
CAR1+CCL19
CAR1+CXCL12

Figure 14

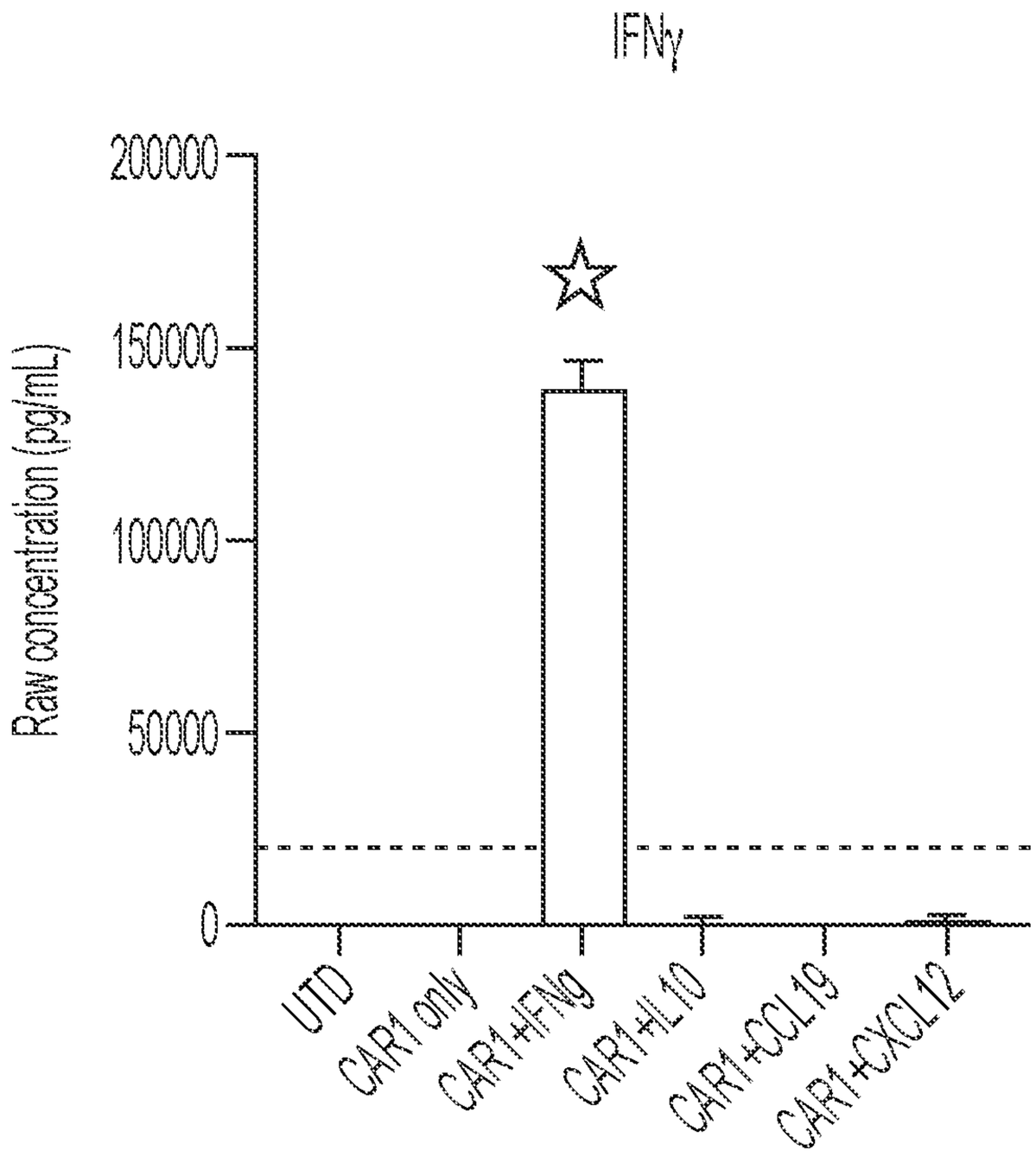

IFNγ
Raw concentration (pg/mL)
200000
150000
100000
50000
0
UTD
CAR1 only
CAR1+IFNg
CAR1+IL10
CAR1+CCL19
CAR1+CXCL12

Figure 15

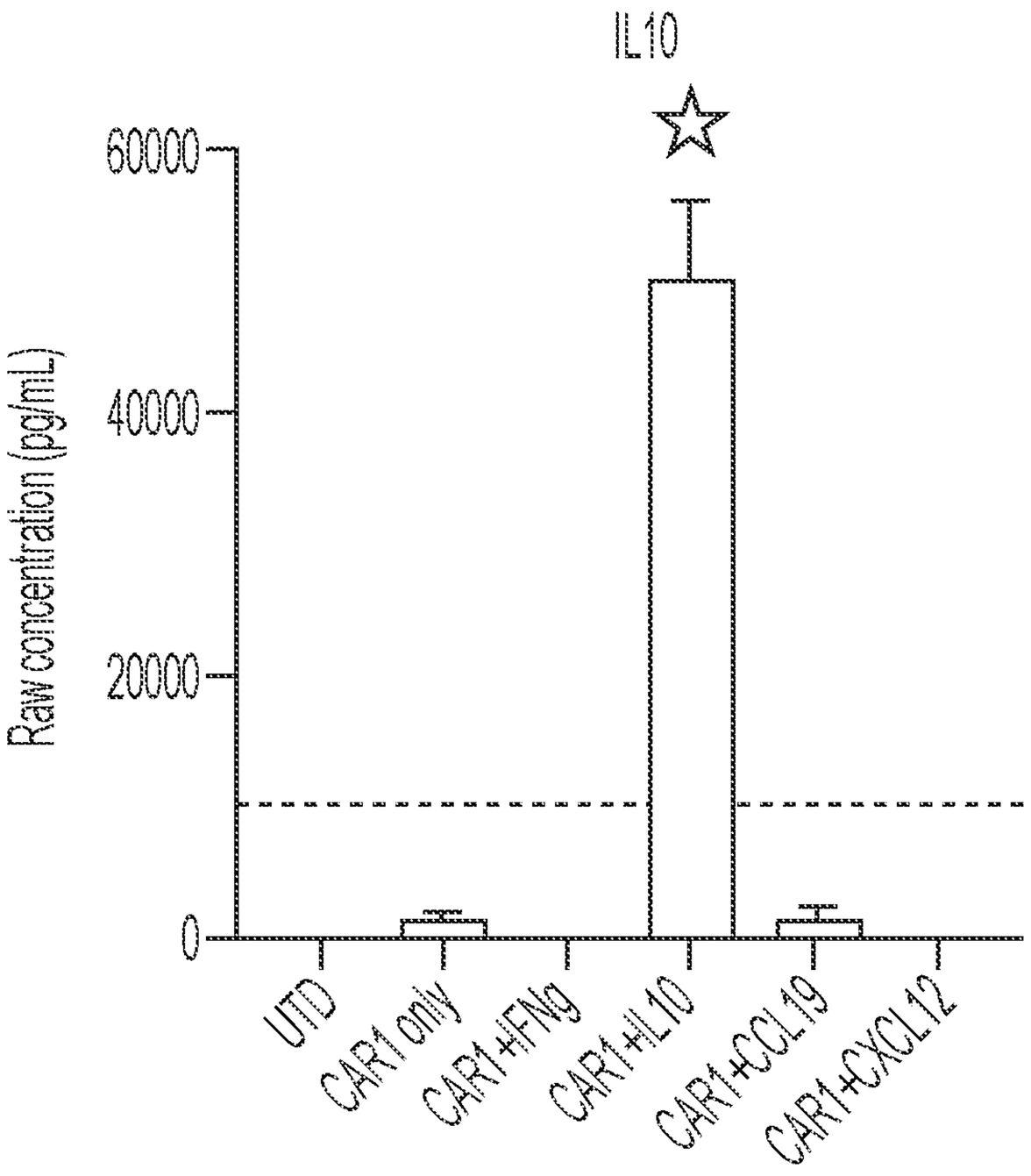

IL10
60000
40000
20000
0
Raw concentration (pg/mL)
UTD
CAR1 only
CAR1+IFNg
CAR1+IL10
CAR1+CCL19
CAR1+CXCL12

Figure 16

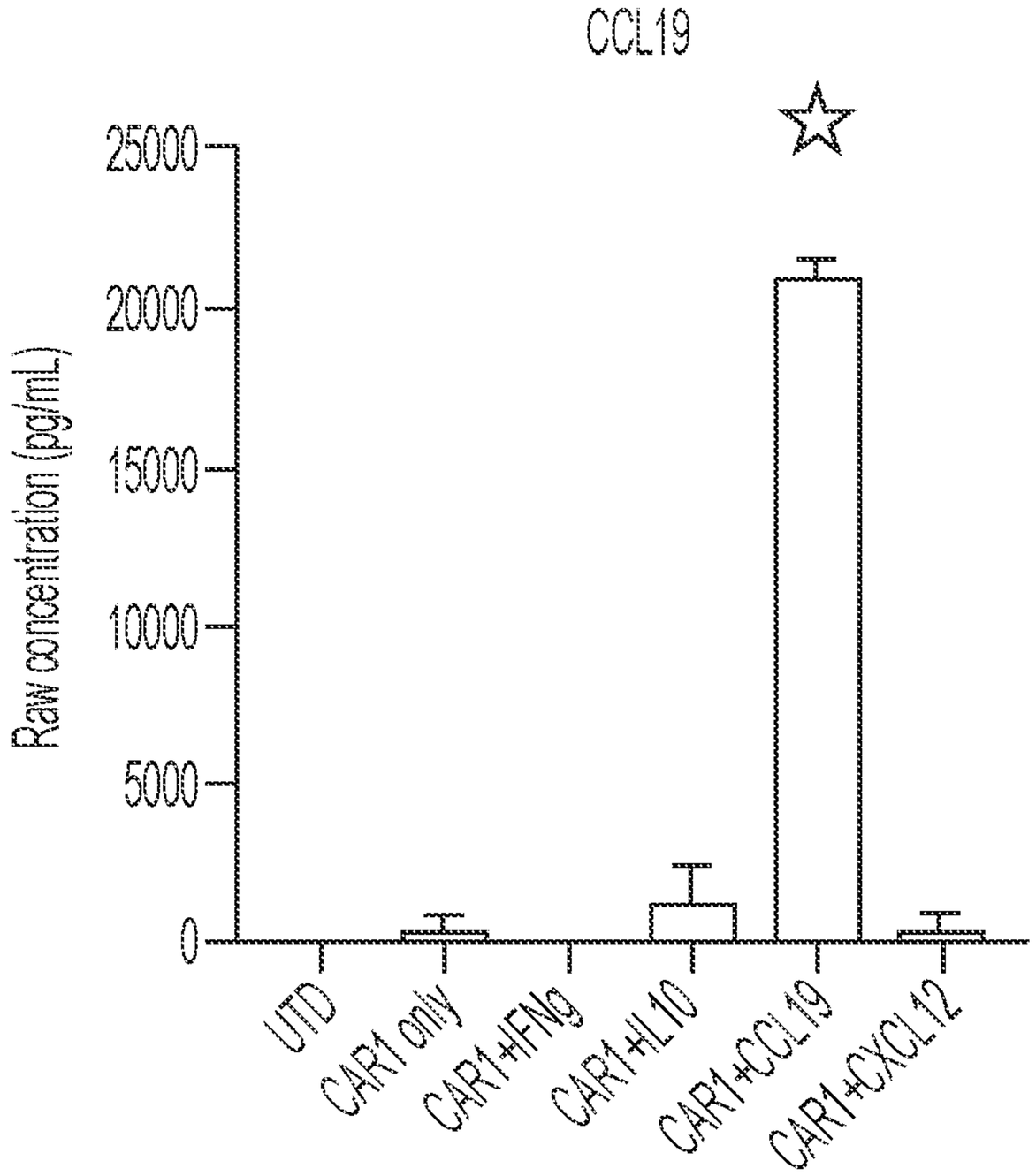

CCL19
Raw concentration (pg/mL)
25000
20000
15000
10000
5000
0
UTD
CAR1 only
CAR1+IFNg
CAR1+IL10
CAR1+CCL19
CAR1+CXCL12

Figure 17

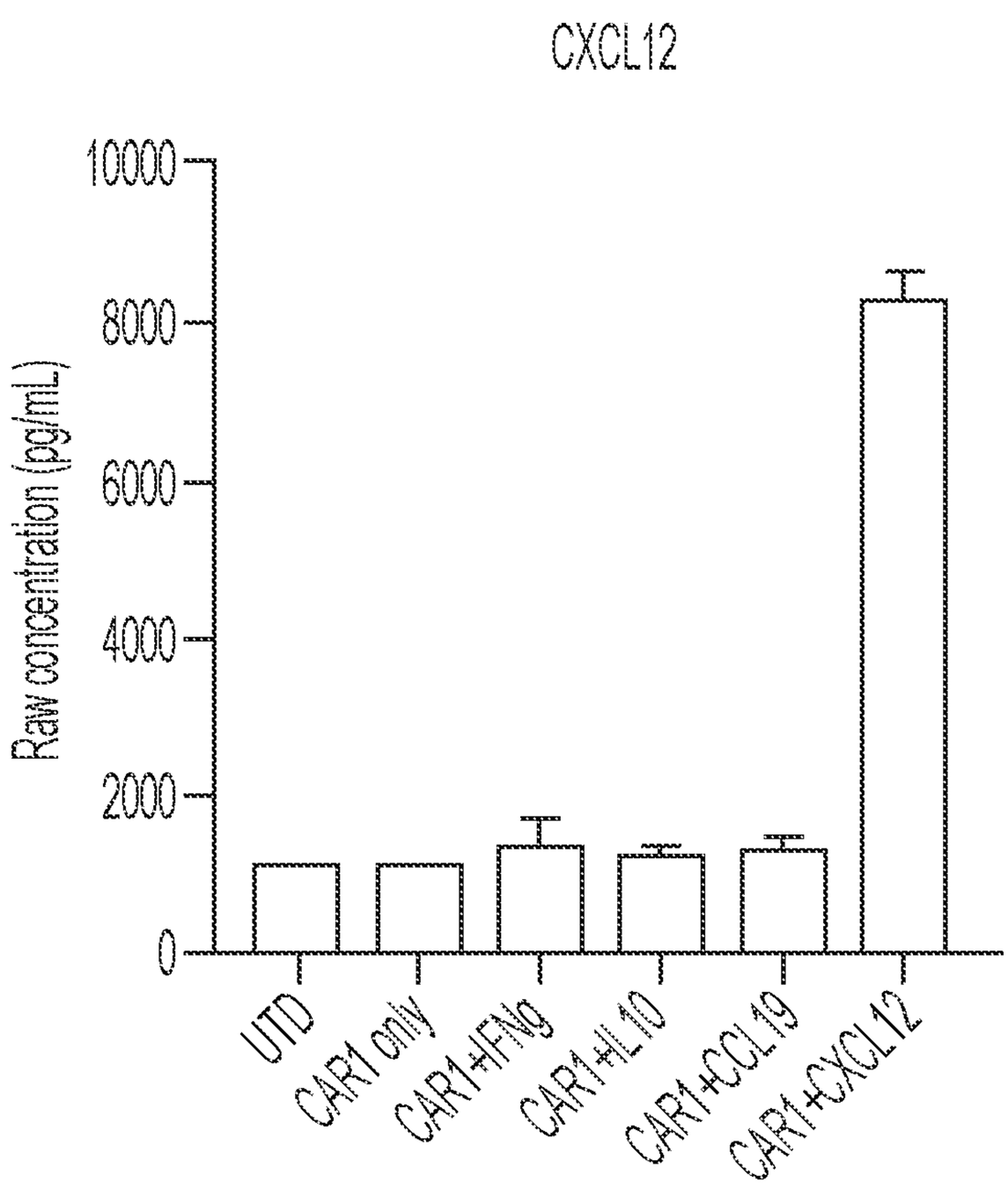

CXCL12
Raw concentration (pg/mL)
10000
8000
6000
4000
2000
0
UTD
CAR1 only
CAR1+IFNg
CAR1+IL10
CAR1+CCL19
CAR1+CXCL12

Figure 18

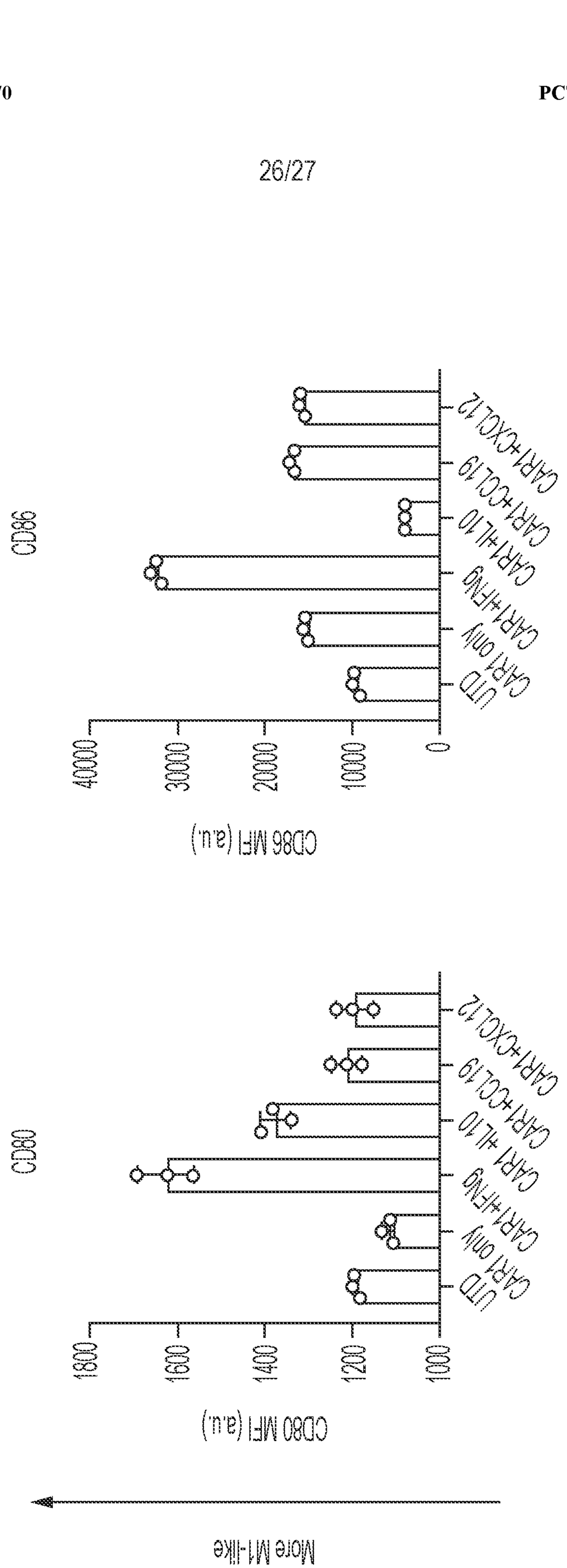

CD86
CD86 MFI (a.u.)
40000
30000
20000
10000
0
UTD
CAR1 only
CAR1+IFNg
CAR1+IL10
CAR1+CCL19
CAR1+CXCL12
CD80
CD80 MFI (a.u.)
1800
1600
1400
1200
1000
More M1-like

Figure 19

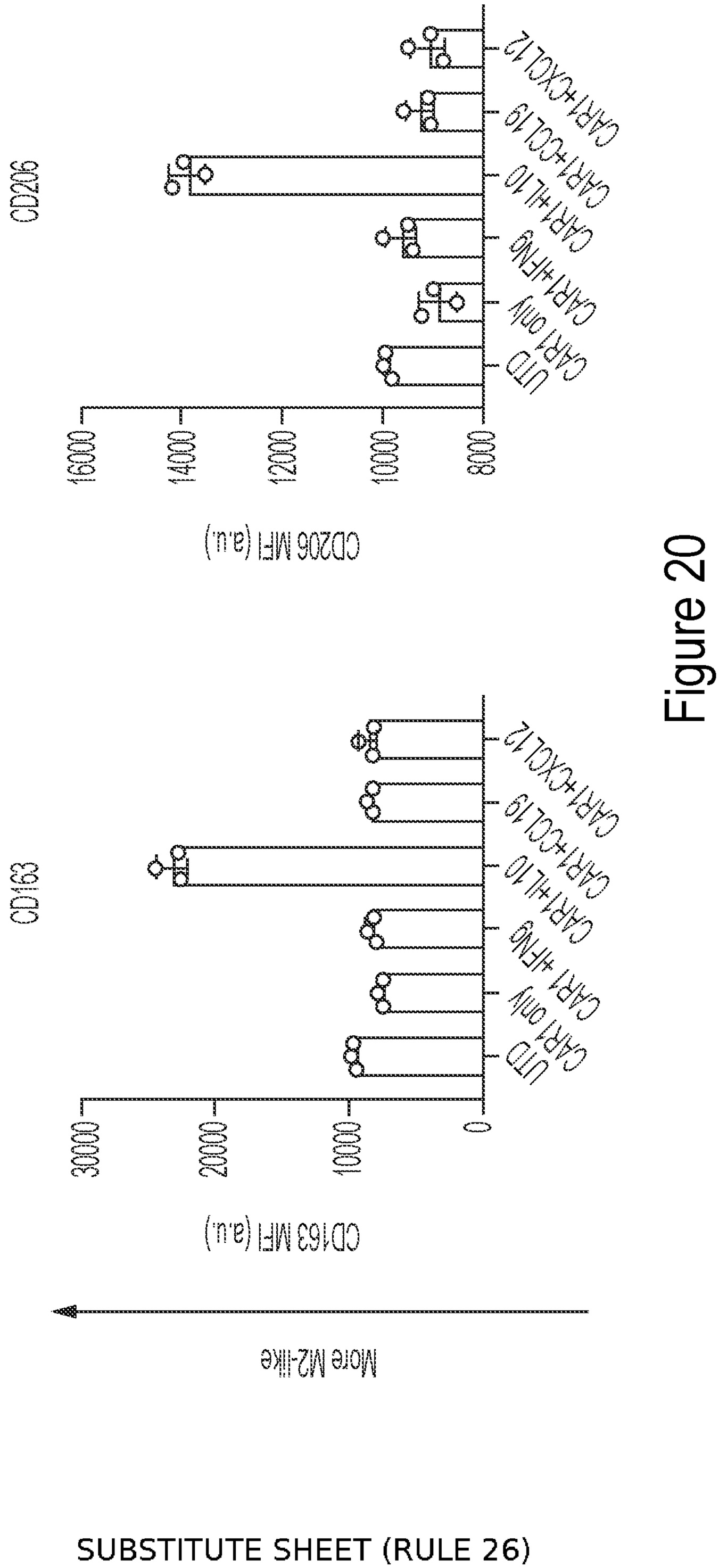

CD206
CD206 MFI (a.u.)
16000
14000
12000
10000
8000
UTD
CAR1 only
CAR1 +IFNg
CAR1+IL10
CAR1+CCL19
CAR1+CXCL12
CD163
CD163 MFI (a.u.)
30000
20000
10000
0
UTD
CAR1 only
CAR1 +IFNg
CAR1+IL10
CAR1+CCL19
CAR1+CXCL12
More M2-like

Figure 20

SEQUENCE LISTING

<110> CARISMA THERAPEUTICS INC.

<120> SELF-POLARIZING IMMUNE CELLS

<130> 2012851-0124

<140>
<141>

<150> 63/144,860
<151> 2021-02-02

<160> 177

<170> PatentIn version 3.5

<210> 1
<211> 165
<212> PRT
<213> Homo sapiens

<400> 1

```
Cys Asp Leu Pro Gln Thr His Ser Leu Gly Ser Arg Arg Thr Leu Met
1               5                  10                  15


Leu Leu Ala Gln Met Arg Lys Ile Ser Leu Phe Ser Cys Leu Lys Asp
            20                  25                  30


Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Gly Asn Gln Phe Gln
        35                  40                  45


Lys Ala Glu Thr Ile Pro Val Leu His Glu Met Ile Gln Gln Ile Phe
    50                  55                  60


Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr Leu
65                  70                  75                  80


Leu Asp Lys Phe Tyr Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu Glu
                85                  90                  95


Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met Lys
            100                 105                 110
```

Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr Leu
        115   120   125

Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val Arg
    130   135   140

Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu Ser
145   150   155   160

Leu Arg Ser Lys Glu
                165

<210> 2
<211> 166
<212> PRT
<213> Homo sapiens

<400> 2
Met Ser Tyr Asn Leu Leu Gly Phe Leu Gln Arg Ser Ser Asn Phe Gln
1   5   10   15

Cys Gln Lys Leu Leu Trp Gln Leu Asn Gly Arg Leu Glu Tyr Cys Leu
            20   25   30

Lys Asp Arg Met Asn Phe Asp Ile Pro Glu Glu Ile Lys Gln Leu Gln
        35   40   45

Gln Phe Gln Lys Glu Asp Ala Ala Leu Thr Ile Tyr Glu Met Leu Gln
    50   55   60

Asn Ile Phe Ala Ile Phe Arg Gln Asp Ser Ser Ser Thr Gly Trp Asn
65   70   75   80

Glu Thr Ile Val Glu Asn Leu Leu Ala Asn Val Tyr His Gln Ile Asn
                85   90   95

His Leu Lys Thr Val Leu Glu Glu Lys Leu Glu Lys Glu Asp Phe Thr
            100   105   110

Arg Gly Lys Leu Met Ser Ser Leu His Leu Lys Arg Tyr Tyr Gly Arg
115 120 125

Ile Leu His Tyr Leu Lys Ala Lys Glu Tyr Ser His Cys Ala Trp Thr
130 135 140

Ile Val Arg Val Glu Ile Leu Arg Asn Phe Tyr Phe Ile Asn Arg Leu
145 150 155 160

Thr Gly Tyr Leu Arg Asn
165

<210> 3
<211> 138
<212> PRT
<213> Homo sapiens

<400> 3
Gln Asp Pro Tyr Val Lys Glu Ala Glu Asn Leu Lys Lys Tyr Phe Asn
1 5 10 15

Ala Gly His Ser Asp Val Ala Asp Asn Gly Thr Leu Phe Leu Gly Ile
20 25 30

Leu Lys Asn Trp Lys Glu Glu Ser Asp Arg Lys Ile Met Gln Ser Gln
35 40 45

Ile Val Ser Phe Tyr Phe Lys Leu Phe Lys Asn Phe Lys Asp Asp Gln
50 55 60

Ser Ile Gln Lys Ser Val Glu Thr Ile Lys Glu Asp Met Asn Val Lys
65 70 75 80

Phe Phe Asn Ser Asn Lys Lys Lys Arg Asp Asp Phe Glu Lys Leu Thr
85 90 95

Asn Tyr Ser Val Thr Asp Leu Asn Val Gln Arg Lys Ala Ile His Glu
100 105 110

```
Leu Ile Gln Val Met Ala Glu Leu Ser Pro Ala Ala Lys Thr Gly Lys
        115                 120                 125


Arg Lys Arg Ser Gln Met Leu Phe Arg Gly
    130                 135


<210> 4
<211> 157
<212> PRT
<213> Homo sapiens

<400> 4
Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His Val
1               5                   10                  15


Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg
            20                  25                  30


Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu
        35                  40                  45


Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe
    50                  55                  60


Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile
65                  70                  75                  80


Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser Ala
                85                  90                  95


Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys
            100                 105                 110


Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Lys
        115                 120                 125


Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp Phe
    130                 135                 140
```

Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu
145 150 155

<210> 5
<211> 153
<212> PRT
<213> Homo sapiens

<400> 5
Ala Pro Val Arg Ser Leu Asn Cys Thr Leu Arg Asp Ser Gln Gln Lys
1 5 10 15

Ser Leu Val Met Ser Gly Pro Tyr Glu Leu Lys Ala Leu His Leu Gln
20 25 30

Gly Gln Asp Met Glu Gln Gln Val Val Phe Ser Met Ser Phe Val Gln
35 40 45

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

Lys Asn Leu Tyr Leu Ser Cys Val Leu Lys Asp Asp Lys Pro Thr Leu
65 70 75 80

Gln Leu Glu Ser Val Asp Pro Lys Asn Tyr Pro Lys Lys Lys Met Glu
85 90 95

Lys Arg Phe Val Phe Asn Lys Ile Glu Ile Asn Asn Lys Leu Glu Phe
100 105 110

Glu Ser Ala Gln Phe Pro Asn Trp Tyr Ile Ser Thr Ser Gln Ala Glu
115 120 125

Asn Met Pro Val Phe Leu Gly Gly Thr Lys Gly Gly Gln Asp Ile Thr
130 135 140

Asp Phe Thr Met Gln Phe Val Ser Ser
145 150

<210> 6
<211> 183
<212> PRT
<213> Homo sapiens

<400> 6
Val Pro Pro Gly Glu Asp Ser Lys Asp Val Ala Ala Pro His Arg Gln
1   5   10   15

Pro Leu Thr Ser Ser Glu Arg Ile Asp Lys Gln Ile Arg Tyr Ile Leu
            20   25   30

Asp Gly Ile Ser Ala Leu Arg Lys Glu Thr Cys Asn Lys Ser Asn Met
        35   40   45

Cys Glu Ser Ser Lys Glu Ala Leu Ala Glu Asn Asn Leu Asn Leu Pro
    50   55   60

Lys Met Ala Glu Lys Asp Gly Cys Phe Gln Ser Gly Phe Asn Glu Glu
65   70   75   80

Thr Cys Leu Val Lys Ile Ile Thr Gly Leu Leu Glu Phe Glu Val Tyr
                85   90   95

Leu Glu Tyr Leu Gln Asn Arg Phe Glu Ser Ser Glu Glu Gln Ala Arg
            100   105   110

Ala Val Gln Met Ser Thr Lys Val Leu Ile Gln Phe Leu Gln Lys Lys
        115   120   125

Ala Lys Asn Leu Asp Ala Ile Thr Thr Pro Asp Pro Thr Thr Asn Ala
    130   135   140

Ser Leu Leu Thr Lys Leu Gln Ala Gln Asn Gln Trp Leu Gln Asp Met
145   150   155   160

Thr Thr His Leu Ile Leu Arg Ser Phe Lys Glu Phe Leu Gln Ser Ser
                165   170   175

Leu Arg Ala Leu Arg Gln Met
            180

<210> 7
<211> 197
<212> PRT
<213> Homo sapiens

<400> 7
Arg Asn Leu Pro Val Ala Thr Pro Asp Pro Gly Met Phe Pro Cys Leu
1   5   10   15

His His Ser Gln Asn Leu Leu Arg Ala Val Ser Asn Met Leu Gln Lys
            20   25   30

Ala Arg Gln Thr Leu Glu Phe Tyr Pro Cys Thr Ser Glu Glu Ile Asp
        35   40   45

His Glu Asp Ile Thr Lys Asp Lys Thr Ser Thr Val Glu Ala Cys Leu
    50   55   60

Pro Leu Glu Leu Thr Lys Asn Glu Ser Cys Leu Asn Ser Arg Glu Thr
65   70   75   80

Ser Phe Ile Thr Asn Gly Ser Cys Leu Ala Ser Arg Lys Thr Ser Phe
                85   90   95

Met Met Ala Leu Cys Leu Ser Ser Ile Tyr Glu Asp Leu Lys Met Tyr
            100   105   110

Gln Val Glu Phe Lys Thr Met Asn Ala Lys Leu Leu Met Asp Pro Lys
        115   120   125

Arg Gln Ile Phe Leu Asp Gln Asn Met Leu Ala Val Ile Asp Glu Leu
    130   135   140

Met Gln Ala Leu Asn Phe Asn Ser Glu Thr Val Pro Gln Lys Ser Ser
145   150   155   160

```
Leu Glu Glu Pro Asp Phe Tyr Lys Thr Lys Ile Lys Leu Cys Ile Leu
                165                 170                 175


Leu His Ala Phe Arg Ile Arg Ala Val Thr Ile Asp Arg Val Met Ser
            180                 185                 190


Tyr Leu Asn Ala Ser
        195


<210> 8
<211> 306
<212> PRT
<213> Homo sapiens

<400> 8
Ile Trp Glu Leu Lys Lys Asp Val Tyr Val Val Glu Leu Asp Trp Tyr
1               5                   10                  15


Pro Asp Ala Pro Gly Glu Met Val Val Leu Thr Cys Asp Thr Pro Glu
            20                  25                  30


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


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


Gln Tyr Thr Cys His Lys Gly Gly Glu Val Leu Ser His Ser Leu Leu
65                  70                  75                  80


Leu Leu His Lys Lys Glu Asp Gly Ile Trp Ser Thr Asp Ile Leu Lys
                85                  90                  95


Asp Gln Lys Glu Pro Lys Asn Lys Thr Phe Leu Arg Cys Glu Ala Lys
            100                 105                 110


Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp Leu Thr Thr Ile Ser Thr
        115                 120                 125
```

```
Asp Leu Thr Phe Ser Val Lys Ser Ser Arg Gly Ser Ser Asp Pro Gln
    130                 135                 140

Gly Val Thr Cys Gly Ala Ala Thr Leu Ser Ala Glu Arg Val Arg Gly
145                 150                 155                 160

Asp Asn Lys Glu Tyr Glu Tyr Ser Val Glu Cys Gln Glu Asp Ser Ala
                165                 170                 175

Cys Pro Ala Ala Glu Glu Ser Leu Pro Ile Glu Val Met Val Asp Ala
            180                 185                 190

Val His Lys Leu Lys Tyr Glu Asn Tyr Thr Ser Ser Phe Phe Ile Arg
        195                 200                 205

Asp Ile Ile Lys Pro Asp Pro Pro Lys Asn Leu Gln Leu Lys Pro Leu
    210                 215                 220

Lys Asn Ser Arg Gln Val Glu Val Ser Trp Glu Tyr Pro Asp Thr Trp
225                 230                 235                 240

Ser Thr Pro His Ser Tyr Phe Ser Leu Thr Phe Cys Val Gln Val Gln
                245                 250                 255

Gly Lys Ser Lys Arg Glu Lys Lys Asp Arg Val Phe Thr Asp Lys Thr
            260                 265                 270

Ser Ala Thr Val Ile Cys Arg Lys Asn Ala Ser Ile Ser Val Arg Ala
        275                 280                 285

Gln Asp Arg Tyr Tyr Ser Ser Ser Trp Ser Glu Trp Ala Ser Val Pro
    290                 295                 300

Cys Ser
305
```

<210> 9
<211> 129
<212> PRT
<213> Homo sapiens

<400> 9
His Lys Cys Asp Ile Thr Leu Gln Glu Ile Ile Lys Thr Leu Asn Ser
1   5   10   15

Leu Thr Glu Gln Lys Thr Leu Cys Thr Glu Leu Thr Val Thr Asp Ile
            20   25   30

Phe Ala Ala Ser Lys Asn Thr Thr Glu Lys Glu Thr Phe Cys Arg Ala
        35   40   45

Ala Thr Val Leu Arg Gln Phe Tyr Ser His His Glu Lys Asp Thr Arg
    50   55   60

Cys Leu Gly Ala Thr Ala Gln Gln Phe His Arg His Lys Gln Leu Ile
65   70   75   80

Arg Phe Leu Lys Arg Leu Asp Arg Asn Leu Trp Gly Leu Ala Gly Leu
                85   90   95

Asn Ser Cys Pro Val Lys Glu Ala Asn Gln Ser Thr Leu Glu Asn Phe
            100   105   110

Leu Glu Arg Leu Lys Thr Ile Met Arg Glu Lys Tyr Ser Lys Cys Ser
        115   120   125

Ser

<210> 10
<211> 160
<212> PRT
<213> Homo sapiens

<400> 10
Ser Pro Gly Gln Gly Thr Gln Ser Glu Asn Ser Cys Thr His Phe Pro
1   5   10   15

```
Gly Asn Leu Pro Asn Met Leu Arg Asp Leu Arg Asp Ala Phe Ser Arg
            20                  25                  30

Val Lys Thr Phe Phe Gln Met Lys Asp Gln Leu Asp Asn Leu Leu Leu
        35                  40                  45

Lys Glu Ser Leu Leu Glu Asp Phe Lys Gly Tyr Leu Gly Cys Gln Ala
    50                  55                  60

Leu Ser Glu Met Ile Gln Phe Tyr Leu Glu Glu Val Met Pro Gln Ala
65                  70                  75                  80

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

Asn Leu Lys Thr Leu Arg Leu Arg Leu Arg Arg Cys His Arg Phe Leu
            100                 105                 110

Pro Cys Glu Asn Lys Ser Lys Ala Val Glu Gln Val Lys Asn Ala Phe
        115                 120                 125

Asn Lys Leu Gln Glu Lys Gly Ile Tyr Lys Ala Met Ser Glu Phe Asp
    130                 135                 140

Ile Phe Ile Asn Tyr Ile Glu Ala Tyr Met Thr Met Lys Ile Arg Asn
145                 150                 155                 160
```

<210> 11
<211> 122
<212> PRT
<213> Homo sapiens

<400> 11

```
Leu Thr Cys Leu Gly Gly Phe Ala Ser Pro Gly Pro Val Pro Pro Ser
1               5                   10                  15

Thr Ala Leu Arg Glu Leu Ile Glu Glu Leu Val Asn Ile Thr Gln Asn
            20                  25                  30
```

```
Gln Lys Ala Pro Leu Cys Asn Gly Ser Met Val Trp Ser Ile Asn Leu
        35                  40                  45

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

Gly Cys Ser Ala Ile Glu Lys Thr Gln Arg Met Leu Ser Gly Phe Cys
65                  70                  75                  80

Pro His Lys Val Ser Ala Gly Gln Phe Ser Ser Leu His Val Arg Asp
                85                  90                  95

Thr Lys Ile Glu Val Ala Gln Phe Val Lys Asp Leu Leu Leu His Leu
            100                 105                 110

Lys Lys Leu Phe Arg Glu Gly Arg Phe Asn
        115                 120
```

<210> 12
<211> 157
<212> PRT
<213> Homo sapiens

<400> 12

```
Tyr Phe Gly Lys Leu Glu Ser Lys Leu Ser Val Ile Arg Asn Leu Asn
1               5                   10                  15

Asp Gln Val Leu Phe Ile Asp Gln Gly Asn Arg Pro Leu Phe Glu Asp
            20                  25                  30

Met Thr Asp Ser Asp Cys Arg Asp Asn Ala Pro Arg Thr Ile Phe Ile
        35                  40                  45

Ile Ser Met Tyr Lys Asp Ser Gln Pro Arg Gly Met Ala Val Thr Ile
    50                  55                  60

Ser Val Lys Cys Glu Lys Ile Ser Thr Leu Ser Cys Glu Asn Lys Ile
65                  70                  75                  80
```

```
Ile Ser Phe Lys Glu Met Asn Pro Pro Asp Asn Ile Lys Asp Thr Lys
                85                  90                  95


Ser Asp Ile Ile Phe Phe Gln Arg Ser Val Pro Gly His Asp Asn Lys
            100                 105                 110


Met Gln Phe Glu Ser Ser Ser Tyr Glu Gly Tyr Phe Leu Ala Cys Glu
        115                 120                 125


Lys Glu Arg Asp Leu Phe Lys Leu Ile Leu Lys Lys Glu Asp Glu Leu
    130                 135                 140


Gly Asp Arg Ser Ile Met Phe Thr Val Gln Asn Glu Asp
145                 150                 155


<210> 13
<211> 530
<212> PRT
<213> Homo sapiens

<400> 13
Lys Asn Leu Lys Ser Pro Gln Lys Val Glu Val Asp Ile Ile Asp Asp
1               5                   10                  15


Asn Phe Ile Leu Arg Trp Asn Arg Ser Asp Glu Ser Val Gly Asn Val
            20                  25                  30


Thr Phe Ser Phe Asp Tyr Gln Lys Thr Gly Met Asp Asn Trp Ile Lys
        35                  40                  45


Leu Ser Gly Cys Gln Asn Ile Thr Ser Thr Lys Cys Asn Phe Ser Ser
    50                  55                  60


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


Lys Glu Asn Thr Ser Ser Trp Tyr Glu Val Asp Ser Phe Thr Pro Phe
                85                  90                  95
```

```
Arg Lys Ala Gln Ile Gly Pro Pro Glu Val His Leu Glu Ala Glu Asp
            100                 105                 110

Lys Ala Ile Val Ile His Ile Ser Pro Gly Thr Lys Asp Ser Val Met
        115                 120                 125

Trp Ala Leu Asp Gly Leu Ser Phe Thr Tyr Ser Leu Val Ile Trp Lys
    130                 135                 140

Asn Ser Ser Gly Val Glu Glu Arg Ile Glu Asn Ile Tyr Ser Arg His
145                 150                 155                 160

Lys Ile Tyr Lys Leu Ser Pro Glu Thr Thr Tyr Cys Leu Lys Val Lys
                165                 170                 175

Ala Ala Leu Leu Thr Ser Trp Lys Ile Gly Val Tyr Ser Pro Val His
            180                 185                 190

Cys Ile Lys Thr Thr Val Glu Asn Glu Leu Pro Pro Pro Glu Asn Ile
        195                 200                 205

Glu Val Ser Val Gln Asn Gln Asn Tyr Val Leu Lys Trp Asp Tyr Thr
    210                 215                 220

Tyr Ala Asn Met Thr Phe Gln Val Gln Trp Leu His Ala Phe Leu Lys
225                 230                 235                 240

Arg Asn Pro Gly Asn His Leu Tyr Lys Trp Lys Gln Ile Pro Asp Cys
                245                 250                 255

Glu Asn Val Lys Thr Thr Gln Cys Val Phe Pro Gln Asn Val Phe Gln
            260                 265                 270

Lys Gly Ile Tyr Leu Leu Arg Val Gln Ala Ser Asp Gly Asn Asn Thr
        275                 280                 285
```

```
Ser Phe Trp Ser Glu Glu Ile Lys Phe Asp Thr Glu Ile Gln Ala Phe
    290                 295                 300

Leu Leu Pro Pro Val Phe Asn Ile Arg Ser Leu Ser Asp Ser Phe His
305                 310                 315                 320

Ile Tyr Ile Gly Ala Pro Lys Gln Ser Gly Asn Thr Pro Val Ile Gln
                325                 330                 335

Asp Tyr Pro Leu Ile Tyr Glu Ile Ile Phe Trp Glu Asn Thr Ser Asn
            340                 345                 350

Ala Glu Arg Lys Ile Ile Glu Lys Lys Thr Asp Val Thr Val Pro Asn
        355                 360                 365

Leu Lys Pro Leu Thr Val Tyr Cys Val Lys Ala Arg Ala His Thr Met
    370                 375                 380

Asp Glu Lys Leu Asn Lys Ser Ser Val Phe Ser Asp Ala Val Cys Glu
385                 390                 395                 400

Lys Thr Lys Pro Gly Asn Thr Ser Lys Ile Trp Leu Ile Val Gly Ile
                405                 410                 415

Cys Ile Ala Leu Phe Ala Leu Pro Phe Val Ile Tyr Ala Ala Lys Val
            420                 425                 430

Phe Leu Arg Cys Ile Asn Tyr Val Phe Phe Pro Ser Leu Lys Pro Ser
        435                 440                 445

Ser Ser Ile Asp Glu Tyr Phe Ser Glu Gln Pro Leu Lys Asn Leu Leu
    450                 455                 460

Leu Ser Thr Ser Glu Glu Gln Ile Glu Lys Cys Phe Ile Ile Glu Asn
465                 470                 475                 480

Ile Ser Thr Ile Ala Thr Val Glu Glu Thr Asn Gln Thr Asp Glu Asp
                485                 490                 495
```

His Lys Lys Tyr Ser Ser Gln Thr Ser Gln Asp Ser Gly Asn Tyr Ser
500 505 510

Asn Glu Asp Glu Ser Glu Ser Lys Thr Ser Glu Glu Leu Gln Gln Asp
515 520 525

Phe Val
530

<210> 14
<211> 489
<212> PRT
<213> Homo sapiens

<400> 14
Ile Ser Tyr Asp Ser Pro Asp Tyr Thr Asp Glu Ser Cys Thr Phe Lys
1 5 10 15

Ile Ser Leu Arg Asn Phe Arg Ser Ile Leu Ser Trp Glu Leu Lys Asn
20 25 30

His Ser Ile Val Pro Thr His Tyr Thr Leu Leu Tyr Thr Ile Met Ser
35 40 45

Lys Pro Glu Asp Leu Lys Val Val Lys Asn Cys Ala Asn Thr Thr Arg
50 55 60

Ser Phe Cys Asp Leu Thr Asp Glu Trp Arg Ser Thr His Glu Ala Tyr
65 70 75 80

Val Thr Val Leu Glu Gly Phe Ser Gly Asn Thr Thr Leu Phe Ser Cys
85 90 95

Ser His Asn Phe Trp Leu Ala Ile Asp Met Ser Phe Glu Pro Pro Glu
100 105 110

Phe Glu Ile Val Gly Phe Thr Asn His Ile Asn Val Met Val Lys Phe
115 120 125

```
Pro Ser Ile Val Glu Glu Glu Leu Gln Phe Asp Leu Ser Leu Val Ile
    130                 135                 140

Glu Glu Gln Ser Glu Gly Ile Val Lys Lys His Lys Pro Glu Ile Lys
145                 150                 155                 160

Gly Asn Met Ser Gly Asn Phe Thr Tyr Ile Ile Asp Lys Leu Ile Pro
                165                 170                 175

Asn Thr Asn Tyr Cys Val Ser Val Tyr Leu Glu His Ser Asp Glu Gln
            180                 185                 190

Ala Val Ile Lys Ser Pro Leu Lys Cys Thr Leu Leu Pro Pro Gly Gln
        195                 200                 205

Glu Ser Glu Ser Ala Glu Ser Ala Lys Ile Gly Gly Ile Ile Thr Val
    210                 215                 220

Phe Leu Ile Ala Leu Val Leu Thr Ser Thr Ile Val Thr Leu Lys Trp
225                 230                 235                 240

Ile Gly Tyr Ile Cys Leu Arg Asn Ser Leu Pro Lys Val Leu Asn Phe
                245                 250                 255

His Asn Phe Leu Ala Trp Pro Phe Pro Asn Leu Pro Pro Leu Glu Ala
            260                 265                 270

Met Asp Met Val Glu Val Ile Tyr Ile Asn Arg Lys Lys Lys Val Trp
        275                 280                 285

Asp Tyr Asn Tyr Asp Asp Glu Ser Asp Ser Asp Thr Glu Ala Ala Pro
    290                 295                 300

Arg Thr Ser Gly Gly Gly Tyr Thr Met His Gly Leu Thr Val Arg Pro
305                 310                 315                 320
```

```
Leu Gly Gln Ala Ser Ala Thr Ser Thr Glu Ser Gln Leu Ile Asp Pro
                325                 330                 335

Glu Ser Glu Glu Glu Pro Asp Leu Pro Glu Val Asp Val Glu Leu Pro
            340                 345                 350

Thr Met Pro Lys Asp Ser Pro Gln Gln Leu Glu Leu Leu Ser Gly Pro
        355                 360                 365

Cys Glu Arg Arg Lys Ser Pro Leu Gln Asp Pro Phe Pro Glu Glu Asp
    370                 375                 380

Tyr Ser Ser Thr Glu Gly Ser Gly Gly Arg Ile Thr Phe Asn Val Asp
385                 390                 395                 400

Leu Asn Ser Val Phe Leu Arg Val Leu Asp Asp Glu Asp Ser Asp Asp
                405                 410                 415

Leu Glu Ala Pro Leu Met Leu Ser Ser His Leu Glu Glu Met Val Asp
            420                 425                 430

Pro Glu Asp Pro Asp Asn Val Gln Ser Asn His Leu Leu Ala Ser Gly
        435                 440                 445

Glu Gly Thr Gln Pro Thr Phe Pro Ser Pro Ser Ser Glu Gly Leu Trp
    450                 455                 460

Ser Glu Asp Ala Pro Ser Asp Gln Ser Asp Thr Ser Glu Ser Asp Val
465                 470                 475                 480

Asp Leu Gly Asp Gly Tyr Ile Met Arg
                485
```

<210> 15
<211> 472
<212> PRT
<213> Homo sapiens

<400> 15

```
Glu Met Gly Thr Ala Asp Leu Gly Pro Ser Ser Val Pro Thr Pro Thr
1               5                  10                  15

Asn Val Thr Ile Glu Ser Tyr Asn Met Asn Pro Ile Val Tyr Trp Glu
            20                  25                  30

Tyr Gln Ile Met Pro Gln Val Pro Val Phe Thr Val Glu Val Lys Asn
        35                  40                  45

Tyr Gly Val Lys Asn Ser Glu Trp Ile Asp Ala Cys Ile Asn Ile Ser
    50                  55                  60

His His Tyr Cys Asn Ile Ser Asp His Val Gly Asp Pro Ser Asn Ser
65                  70                  75                  80

Leu Trp Val Arg Val Lys Ala Arg Val Gly Gln Lys Glu Ser Ala Tyr
                85                  90                  95

Ala Lys Ser Glu Glu Phe Ala Val Cys Arg Asp Gly Lys Ile Gly Pro
            100                 105                 110

Pro Lys Leu Asp Ile Arg Lys Glu Glu Lys Gln Ile Met Ile Asp Ile
        115                 120                 125

Phe His Pro Ser Val Phe Val Asn Gly Asp Glu Gln Glu Val Asp Tyr
    130                 135                 140

Asp Pro Glu Thr Thr Cys Tyr Ile Arg Val Tyr Asn Val Tyr Val Arg
145                 150                 155                 160

Met Asn Gly Ser Glu Ile Gln Tyr Lys Ile Leu Thr Gln Lys Glu Asp
                165                 170                 175

Asp Cys Asp Glu Ile Gln Cys Gln Leu Ala Ile Pro Val Ser Ser Leu
            180                 185                 190

Asn Ser Gln Tyr Cys Val Ser Ala Glu Gly Val Leu His Val Trp Gly
        195                 200                 205
```

```
Val Thr Thr Glu Lys Ser Lys Glu Val Cys Ile Thr Ile Phe Asn Ser
    210                 215                 220

Ser Ile Lys Gly Ser Leu Trp Ile Pro Val Val Ala Ala Leu Leu Leu
225                 230                 235                 240

Phe Leu Val Leu Ser Leu Val Phe Ile Cys Phe Tyr Ile Lys Lys Ile
                245                 250                 255

Asn Pro Leu Lys Glu Lys Ser Ile Ile Leu Pro Lys Ser Leu Ile Ser
            260                 265                 270

Val Val Arg Ser Ala Thr Leu Glu Thr Lys Pro Glu Ser Lys Tyr Val
        275                 280                 285

Ser Leu Ile Thr Ser Tyr Gln Pro Phe Ser Leu Glu Lys Glu Val Val
    290                 295                 300

Cys Glu Glu Pro Leu Ser Pro Ala Thr Val Pro Gly Met His Thr Glu
305                 310                 315                 320

Asp Asn Pro Gly Lys Val Glu His Thr Glu Glu Leu Ser Ser Ile Thr
                325                 330                 335

Glu Val Val Thr Thr Glu Glu Asn Ile Pro Asp Val Val Pro Gly Ser
            340                 345                 350

His Leu Thr Pro Ile Glu Arg Glu Ser Ser Ser Pro Leu Ser Ser Asn
        355                 360                 365

Gln Ser Glu Pro Gly Ser Ile Ala Leu Asn Ser Tyr His Ser Arg Asn
    370                 375                 380

Cys Ser Glu Ser Asp His Ser Arg Asn Gly Phe Asp Thr Asp Ser Ser
385                 390                 395                 400
```

```
Cys Leu Glu Ser His Ser Ser Leu Ser Asp Ser Glu Phe Pro Pro Asn
                405                 410                 415


Asn Lys Gly Glu Ile Lys Thr Glu Gly Gln Glu Leu Ile Thr Val Ile
            420                 425                 430


Lys Ala Pro Thr Ser Phe Gly Tyr Asp Lys Pro His Val Leu Val Asp
        435                 440                 445


Leu Leu Val Asp Asp Ser Gly Lys Glu Ser Leu Ile Gly Tyr Arg Pro
    450                 455                 460


Thr Glu Asp Ser Lys Glu Phe Ser
465                 470


<210> 16
<211> 316
<212> PRT
<213> Homo sapiens

<400> 16
Ala Pro Pro Asp Pro Leu Ser Gln Leu Pro Ala Pro Gln His Pro Lys
1               5                   10                  15


Ile Arg Leu Tyr Asn Ala Glu Gln Val Leu Ser Trp Glu Pro Val Ala
            20                  25                  30


Leu Ser Asn Ser Thr Arg Pro Val Val Tyr Gln Val Gln Phe Lys Tyr
        35                  40                  45


Thr Asp Ser Lys Trp Phe Thr Ala Asp Ile Met Ser Ile Gly Val Asn
    50                  55                  60


Cys Thr Gln Ile Thr Ala Thr Glu Cys Asp Phe Thr Ala Ala Ser Pro
65                  70                  75                  80


Ser Ala Gly Phe Pro Met Asp Phe Asn Val Thr Leu Arg Leu Arg Ala
                85                  90                  95
```

```
Glu Leu Gly Ala Leu His Ser Ala Trp Val Thr Met Pro Trp Phe Gln
            100                 105                 110

His Tyr Arg Asn Val Thr Val Gly Pro Pro Glu Asn Ile Glu Val Thr
        115                 120                 125

Pro Gly Glu Gly Ser Leu Ile Ile Arg Phe Ser Ser Pro Phe Asp Ile
    130                 135                 140

Ala Asp Thr Ser Thr Ala Phe Phe Cys Tyr Tyr Val His Tyr Trp Glu
145                 150                 155                 160

Lys Gly Gly Ile Gln Gln Val Lys Gly Pro Phe Arg Ser Asn Ser Ile
                165                 170                 175

Ser Leu Asp Asn Leu Lys Pro Ser Arg Val Tyr Cys Leu Gln Val Gln
            180                 185                 190

Ala Gln Leu Leu Trp Asn Lys Ser Asn Ile Phe Arg Val Gly His Leu
        195                 200                 205

Ser Asn Ile Ser Cys Tyr Glu Thr Met Ala Asp Ala Ser Thr Glu Leu
    210                 215                 220

Gln Gln Val Ile Leu Ile Ser Val Gly Thr Phe Ser Leu Leu Ser Val
225                 230                 235                 240

Leu Ala Gly Ala Cys Phe Phe Leu Val Leu Lys Tyr Arg Gly Leu Ile
                245                 250                 255

Lys Tyr Trp Phe His Thr Pro Pro Ser Ile Pro Leu Gln Ile Glu Glu
            260                 265                 270

Tyr Leu Lys Asp Pro Thr Gln Pro Ile Leu Glu Ala Leu Asp Lys Asp
        275                 280                 285

Ser Ser Pro Lys Asp Asp Val Trp Asp Ser Val Ser Ile Ile Ser Phe
    290                 295                 300
```

Pro Glu Lys Glu Gln Glu Asp Val Leu Gln Thr Leu
305 310 315

<210> 17
<211> 426
<212> PRT
<213> Homo sapiens

<400> 17
Leu Val Pro His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro
1 5 10 15

Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys
20 25 30

Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln
35 40 45

Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu
50 55 60

Asn His Leu Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met
65 70 75 80

Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys
85 90 95

Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe
100 105 110

Gln Cys Phe Asn Cys Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser
115 120 125

Cys Gln Glu Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe
130 135 140

Leu Arg Glu Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys Ser Leu
145 150 155 160

```
Glu Cys Thr Lys Leu Cys Leu Pro Gln Ile Glu Asn Val Lys Gly Thr
                165                 170                 175

Glu Asp Ser Gly Thr Thr Val Leu Leu Pro Leu Val Ile Phe Phe Gly
            180                 185                 190

Leu Cys Leu Leu Ser Leu Leu Phe Ile Gly Leu Met Tyr Arg Tyr Gln
        195                 200                 205

Arg Trp Lys Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys Ser Thr Pro
    210                 215                 220

Glu Lys Glu Gly Glu Leu Glu Gly Thr Thr Thr Lys Pro Leu Ala Pro
225                 230                 235                 240

Asn Pro Ser Phe Ser Pro Thr Pro Gly Phe Thr Pro Thr Leu Gly Phe
                245                 250                 255

Ser Pro Val Pro Ser Ser Thr Phe Thr Ser Ser Ser Thr Tyr Thr Pro
            260                 265                 270

Gly Asp Cys Pro Asn Phe Ala Ala Pro Arg Arg Glu Val Ala Pro Pro
        275                 280                 285

Tyr Gln Gly Ala Asp Pro Ile Leu Ala Thr Ala Leu Ala Ser Asp Pro
    290                 295                 300

Ile Pro Asn Pro Leu Gln Lys Trp Glu Asp Ser Ala His Lys Pro Gln
305                 310                 315                 320

Ser Leu Asp Thr Asp Asp Pro Ala Thr Leu Tyr Ala Val Val Glu Asn
                325                 330                 335

Val Pro Pro Leu Arg Trp Lys Glu Phe Val Arg Arg Leu Gly Leu Ser
            340                 345                 350
```

```
Asp His Glu Ile Asp Arg Leu Glu Leu Gln Asn Gly Arg Cys Leu Arg
        355                 360                 365

Glu Ala Gln Tyr Ser Met Leu Ala Thr Trp Arg Arg Arg Thr Pro Arg
    370                 375                 380

Arg Glu Ala Thr Leu Glu Leu Leu Gly Arg Val Leu Arg Asp Met Asp
385                 390                 395                 400

Leu Leu Gly Cys Leu Glu Asp Ile Glu Glu Ala Leu Cys Gly Pro Ala
                405                 410                 415

Ala Leu Pro Pro Ala Pro Ser Leu Leu Arg
            420                 425
```

<210> 18
<211> 439
<212> PRT
<213> Homo sapiens

<400> 18

```
Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr Ala Pro Glu Pro Gly Ser
1               5                   10                  15

Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln Thr Ala Gln Met Cys Cys
            20                  25                  30

Ser Lys Cys Ser Pro Gly Gln His Ala Lys Val Phe Cys Thr Lys Thr
        35                  40                  45

Ser Asp Thr Val Cys Asp Ser Cys Glu Asp Ser Thr Tyr Thr Gln Leu
    50                  55                  60

Trp Asn Trp Val Pro Glu Cys Leu Ser Cys Gly Ser Arg Cys Ser Ser
65                  70                  75                  80

Asp Gln Val Glu Thr Gln Ala Cys Thr Arg Glu Gln Asn Arg Ile Cys
                85                  90                  95
```

```
Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu Ser Lys Gln Glu Gly Cys
            100                 105                 110

Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg Pro Gly Phe Gly Val Ala
        115                 120                 125

Arg Pro Gly Thr Glu Thr Ser Asp Val Val Cys Lys Pro Cys Ala Pro
    130                 135                 140

Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr Asp Ile Cys Arg Pro His
145                 150                 155                 160

Gln Ile Cys Asn Val Val Ala Ile Pro Gly Asn Ala Ser Met Asp Ala
                165                 170                 175

Val Cys Thr Ser Thr Ser Pro Thr Arg Ser Met Ala Pro Gly Ala Val
            180                 185                 190

His Leu Pro Gln Pro Val Ser Thr Arg Ser Gln His Thr Gln Pro Thr
        195                 200                 205

Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser Phe Leu Leu Pro Met Gly
    210                 215                 220

Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly Asp Phe Ala Leu Pro Val
225                 230                 235                 240

Gly Leu Ile Val Gly Val Thr Ala Leu Gly Leu Leu Ile Ile Gly Val
                245                 250                 255

Val Asn Cys Val Ile Met Thr Gln Val Lys Lys Lys Pro Leu Cys Leu
            260                 265                 270

Gln Arg Glu Ala Lys Val Pro His Leu Pro Ala Asp Lys Ala Arg Gly
        275                 280                 285

Thr Gln Gly Pro Glu Gln Gln His Leu Leu Ile Thr Ala Pro Ser Ser
    290                 295                 300
```

```
Ser Ser Ser Ser Leu Glu Ser Ser Ala Ser Ala Leu Asp Arg Arg Ala
305                 310                 315                 320


Pro Thr Arg Asn Gln Pro Gln Ala Pro Gly Val Glu Ala Ser Gly Ala
                325                 330                 335


Gly Glu Ala Arg Ala Ser Thr Gly Ser Ser Asp Ser Ser Pro Gly Gly
            340                 345                 350


His Gly Thr Gln Val Asn Val Thr Cys Ile Val Asn Val Cys Ser Ser
        355                 360                 365


Ser Asp His Ser Ser Gln Cys Ser Ser Gln Ala Ser Ser Thr Met Gly
    370                 375                 380


Asp Thr Asp Ser Ser Pro Ser Glu Ser Pro Lys Asp Glu Gln Val Pro
385                 390                 395                 400


Phe Ser Lys Glu Glu Cys Ala Phe Arg Ser Gln Leu Glu Thr Pro Glu
                405                 410                 415


Thr Leu Leu Gly Ser Thr Glu Glu Lys Pro Leu Pro Leu Gly Val Pro
            420                 425                 430


Asp Ala Gly Met Lys Pro Ser
        435


<210> 19
<211> 552
<212> PRT
<213> Homo sapiens

<400> 19
Leu Glu Ala Asp Lys Cys Lys Glu Arg Glu Glu Lys Ile Ile Leu Val
1               5                   10                  15


Ser Ser Ala Asn Glu Ile Asp Val Arg Pro Cys Pro Leu Asn Pro Asn
            20                  25                  30
```

```
Glu His Lys Gly Thr Ile Thr Trp Tyr Lys Asp Asp Ser Lys Thr Pro
        35                  40                  45

Val Ser Thr Glu Gln Ala Ser Arg Ile His Gln His Lys Glu Lys Leu
    50                  55                  60

Trp Phe Val Pro Ala Lys Val Glu Asp Ser Gly His Tyr Tyr Cys Val
65                  70                  75                  80

Val Arg Asn Ser Ser Tyr Cys Leu Arg Ile Lys Ile Ser Ala Lys Phe
                85                  90                  95

Val Glu Asn Glu Pro Asn Leu Cys Tyr Asn Ala Gln Ala Ile Phe Lys
            100                 105                 110

Gln Lys Leu Pro Val Ala Gly Asp Gly Gly Leu Val Cys Pro Tyr Met
        115                 120                 125

Glu Phe Phe Lys Asn Glu Asn Asn Glu Leu Pro Lys Leu Gln Trp Tyr
    130                 135                 140

Lys Asp Cys Lys Pro Leu Leu Leu Asp Asn Ile His Phe Ser Gly Val
145                 150                 155                 160

Lys Asp Arg Leu Ile Val Met Asn Val Ala Glu Lys His Arg Gly Asn
                165                 170                 175

Tyr Thr Cys His Ala Ser Tyr Thr Tyr Leu Gly Lys Gln Tyr Pro Ile
            180                 185                 190

Thr Arg Val Ile Glu Phe Ile Thr Leu Glu Glu Asn Lys Pro Thr Arg
        195                 200                 205

Pro Val Ile Val Ser Pro Ala Asn Glu Thr Met Glu Val Asp Leu Gly
    210                 215                 220
```

```
Ser Gln Ile Gln Leu Ile Cys Asn Val Thr Gly Gln Leu Ser Asp Ile
225                 230                 235                 240

Ala Tyr Trp Lys Trp Asn Gly Ser Val Ile Asp Glu Asp Asp Pro Val
                245                 250                 255

Leu Gly Glu Asp Tyr Tyr Ser Val Glu Asn Pro Ala Asn Lys Arg Arg
            260                 265                 270

Ser Thr Leu Ile Thr Val Leu Asn Ile Ser Glu Ile Glu Ser Arg Phe
        275                 280                 285

Tyr Lys His Pro Phe Thr Cys Phe Ala Lys Asn Thr His Gly Ile Asp
    290                 295                 300

Ala Ala Tyr Ile Gln Leu Ile Tyr Pro Val Thr Asn Phe Gln Lys His
305                 310                 315                 320

Met Ile Gly Ile Cys Val Thr Leu Thr Val Ile Ile Val Cys Ser Val
                325                 330                 335

Phe Ile Tyr Lys Ile Phe Lys Ile Asp Ile Val Leu Trp Tyr Arg Asp
            340                 345                 350

Ser Cys Tyr Asp Phe Leu Pro Ile Lys Ala Ser Asp Gly Lys Thr Tyr
        355                 360                 365

Asp Ala Tyr Ile Leu Tyr Pro Lys Thr Val Gly Glu Gly Ser Thr Ser
    370                 375                 380

Asp Cys Asp Ile Phe Val Phe Lys Val Leu Pro Glu Val Leu Glu Lys
385                 390                 395                 400

Gln Cys Gly Tyr Lys Leu Phe Ile Tyr Gly Arg Asp Asp Tyr Val Gly
                405                 410                 415

Glu Asp Ile Val Glu Val Ile Asn Glu Asn Val Lys Lys Ser Arg Arg
            420                 425                 430
```

```
Leu Ile Ile Ile Leu Val Arg Glu Thr Ser Gly Phe Ser Trp Leu Gly
        435                 440                 445

Gly Ser Ser Glu Glu Gln Ile Ala Met Tyr Asn Ala Leu Val Gln Asp
    450                 455                 460

Gly Ile Lys Val Val Leu Leu Glu Leu Glu Lys Ile Gln Asp Tyr Glu
465                 470                 475                 480

Lys Met Pro Glu Ser Ile Lys Phe Ile Lys Gln Lys His Gly Ala Ile
                485                 490                 495

Arg Trp Ser Gly Asp Phe Thr Gln Gly Pro Gln Ser Ala Lys Thr Arg
            500                 505                 510

Phe Trp Lys Asn Val Arg Tyr His Met Pro Val Gln Arg Arg Ser Pro
        515                 520                 525

Ser Ser Lys His Gln Leu Leu Ser Pro Ala Thr Lys Glu Lys Leu Gln
    530                 535                 540

Arg Glu Ala His Val Pro Leu Gly
545                 550


<210> 20
<211> 550
<212> PRT
<213> Homo sapiens

<400> 20
Ser Glu Arg Cys Asp Asp Trp Gly Leu Asp Thr Met Arg Gln Ile Gln
1               5                   10                  15

Val Phe Glu Asp Glu Pro Ala Arg Ile Lys Cys Pro Leu Phe Glu His
            20                  25                  30

Phe Leu Lys Phe Asn Tyr Ser Thr Ala His Ser Ala Gly Leu Thr Leu
        35                  40                  45
```

```
Ile Trp Tyr Trp Thr Arg Gln Asp Arg Asp Leu Glu Glu Pro Ile Asn
    50                  55                  60

Phe Arg Leu Pro Glu Asn Arg Ile Ser Lys Glu Lys Asp Val Leu Trp
65                  70                  75                  80

Phe Arg Pro Thr Leu Leu Asn Asp Thr Gly Asn Tyr Thr Cys Met Leu
                85                  90                  95

Arg Asn Thr Thr Tyr Cys Ser Lys Val Ala Phe Pro Leu Glu Val Val
            100                 105                 110

Gln Lys Asp Ser Cys Phe Asn Ser Pro Met Lys Leu Pro Val His Lys
        115                 120                 125

Leu Tyr Ile Glu Tyr Gly Ile Gln Arg Ile Thr Cys Pro Asn Val Asp
    130                 135                 140

Gly Tyr Phe Pro Ser Ser Val Lys Pro Thr Ile Thr Trp Tyr Met Gly
145                 150                 155                 160

Cys Tyr Lys Ile Gln Asn Phe Asn Asn Val Ile Pro Glu Gly Met Asn
                165                 170                 175

Leu Ser Phe Leu Ile Ala Leu Ile Ser Asn Asn Gly Asn Tyr Thr Cys
            180                 185                 190

Val Val Thr Tyr Pro Glu Asn Gly Arg Thr Phe His Leu Thr Arg Thr
        195                 200                 205

Leu Thr Val Lys Val Val Gly Ser Pro Lys Asn Ala Val Pro Pro Val
    210                 215                 220

Ile His Ser Pro Asn Asp His Val Val Tyr Glu Lys Glu Pro Gly Glu
225                 230                 235                 240
```

```
Glu Leu Leu Ile Pro Cys Thr Val Tyr Phe Ser Phe Leu Met Asp Ser
                245                 250                 255

Arg Asn Glu Val Trp Trp Thr Ile Asp Gly Lys Lys Pro Asp Asp Ile
            260                 265                 270

Thr Ile Asp Val Thr Ile Asn Glu Ser Ile Ser His Ser Arg Thr Glu
        275                 280                 285

Asp Glu Thr Arg Thr Gln Ile Leu Ser Ile Lys Lys Val Thr Ser Glu
    290                 295                 300

Asp Leu Lys Arg Ser Tyr Val Cys His Ala Arg Ser Ala Lys Gly Glu
305                 310                 315                 320

Val Ala Lys Ala Ala Lys Val Lys Gln Lys Val Pro Ala Pro Arg Tyr
                325                 330                 335

Thr Val Glu Leu Ala Cys Gly Phe Gly Ala Thr Val Leu Leu Val Val
            340                 345                 350

Ile Leu Ile Val Val Tyr His Val Tyr Trp Leu Glu Met Val Leu Phe
        355                 360                 365

Tyr Arg Ala His Phe Gly Thr Asp Glu Thr Ile Leu Asp Gly Lys Glu
    370                 375                 380

Tyr Asp Ile Tyr Val Ser Tyr Ala Arg Asn Ala Glu Glu Glu Glu Phe
385                 390                 395                 400

Val Leu Leu Thr Leu Arg Gly Val Leu Glu Asn Glu Phe Gly Tyr Lys
                405                 410                 415

Leu Cys Ile Phe Asp Arg Asp Ser Leu Pro Gly Gly Ile Val Thr Asp
            420                 425                 430

Glu Thr Leu Ser Phe Ile Gln Lys Ser Arg Arg Leu Leu Val Val Leu
        435                 440                 445
```

```
Ser Pro Asn Tyr Val Leu Gln Gly Thr Gln Ala Leu Leu Glu Leu Lys
    450                 455                 460


Ala Gly Leu Glu Asn Met Ala Ser Arg Gly Asn Ile Asn Val Ile Leu
465                 470                 475                 480


Val Gln Tyr Lys Ala Val Lys Glu Thr Lys Val Lys Glu Leu Lys Arg
                485                 490                 495


Ala Lys Thr Val Leu Thr Val Ile Lys Trp Lys Gly Glu Lys Ser Lys
            500                 505                 510


Tyr Pro Gln Gly Arg Phe Trp Lys Gln Leu Gln Val Ala Met Pro Val
        515                 520                 525


Lys Lys Ser Pro Arg Arg Ser Ser Ser Asp Glu Gln Gly Leu Ser Tyr
    530                 535                 540


Ser Ser Leu Lys Asn Val
545                 550
```

<210> 21
<211> 449
<212> PRT
<213> Homo sapiens

<400> 21

```
Leu Ala Pro Arg Arg Cys Pro Ala Gln Glu Val Ala Arg Gly Val Leu
1               5                   10                  15


Thr Ser Leu Pro Gly Asp Ser Val Thr Leu Thr Cys Pro Gly Val Glu
            20                  25                  30


Pro Glu Asp Asn Ala Thr Val His Trp Val Leu Arg Lys Pro Ala Ala
        35                  40                  45


Gly Ser His Pro Ser Arg Trp Ala Gly Met Gly Arg Arg Leu Leu Leu
    50                  55                  60
```

```
Arg Ser Val Gln Leu His Asp Ser Gly Asn Tyr Ser Cys Tyr Arg Ala
65                  70                  75                  80

Gly Arg Pro Ala Gly Thr Val His Leu Leu Val Asp Val Pro Pro Glu
                85                  90                  95

Glu Pro Gln Leu Ser Cys Phe Arg Lys Ser Pro Leu Ser Asn Val Val
            100                 105                 110

Cys Glu Trp Gly Pro Arg Ser Thr Pro Ser Leu Thr Thr Lys Ala Val
        115                 120                 125

Leu Leu Val Arg Lys Phe Gln Asn Ser Pro Ala Glu Asp Phe Gln Glu
    130                 135                 140

Pro Cys Gln Tyr Ser Gln Glu Ser Gln Lys Phe Ser Cys Gln Leu Ala
145                 150                 155                 160

Val Pro Glu Gly Asp Ser Ser Phe Tyr Ile Val Ser Met Cys Val Ala
                165                 170                 175

Ser Ser Val Gly Ser Lys Phe Ser Lys Thr Gln Thr Phe Gln Gly Cys
            180                 185                 190

Gly Ile Leu Gln Pro Asp Pro Pro Ala Asn Ile Thr Val Thr Ala Val
        195                 200                 205

Ala Arg Asn Pro Arg Trp Leu Ser Val Thr Trp Gln Asp Pro His Ser
    210                 215                 220

Trp Asn Ser Ser Phe Tyr Arg Leu Arg Phe Glu Leu Arg Tyr Arg Ala
225                 230                 235                 240

Glu Arg Ser Lys Thr Phe Thr Thr Trp Met Val Lys Asp Leu Gln His
                245                 250                 255
```

```
His Cys Val Ile His Asp Ala Trp Ser Gly Leu Arg His Val Val Gln
            260                 265                 270

Leu Arg Ala Gln Glu Glu Phe Gly Gln Gly Glu Trp Ser Glu Trp Ser
        275                 280                 285

Pro Glu Ala Met Gly Thr Pro Trp Thr Glu Ser Arg Ser Pro Pro Ala
    290                 295                 300

Glu Asn Glu Val Ser Thr Pro Met Gln Ala Leu Thr Thr Asn Lys Asp
305                 310                 315                 320

Asp Asp Asn Ile Leu Phe Arg Asp Ser Ala Asn Ala Thr Ser Leu Pro
                325                 330                 335

Val Gln Asp Ser Ser Ser Val Pro Leu Pro Thr Phe Leu Val Ala Gly
            340                 345                 350

Gly Ser Leu Ala Phe Gly Thr Leu Leu Cys Ile Ala Ile Val Leu Arg
        355                 360                 365

Phe Lys Lys Thr Trp Lys Leu Arg Ala Leu Lys Glu Gly Lys Thr Ser
    370                 375                 380

Met His Pro Pro Tyr Ser Leu Gly Gln Leu Val Pro Glu Arg Pro Arg
385                 390                 395                 400

Pro Thr Pro Val Leu Val Pro Leu Ile Ser Pro Pro Val Ser Pro Ser
                405                 410                 415

Ser Leu Gly Ser Asp Asn Thr Ser Ser His Asn Arg Pro Asp Ala Arg
            420                 425                 430

Asp Pro Arg Ser Pro Tyr Asp Ile Ser Asn Thr Asp Tyr Phe Phe Pro
        435                 440                 445

Arg
```

<210> 22
<211> 896
<212> PRT
<213> Homo sapiens

<400> 22
Glu Leu Leu Asp Pro Cys Gly Tyr Ile Ser Pro Glu Ser Pro Val Val
1   5   10   15

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

Met Asp Tyr Phe His Val Asn Ala Asn Tyr Ile Val Trp Lys Thr Asn
        35   40   45

His Phe Thr Ile Pro Lys Glu Gln Tyr Thr Ile Ile Asn Arg Thr Ala
    50   55   60

Ser Ser Val Thr Phe Thr Asp Ile Ala Ser Leu Asn Ile Gln Leu Thr
65   70   75   80

Cys Asn Ile Leu Thr Phe Gly Gln Leu Glu Gln Asn Val Tyr Gly Ile
                85   90   95

Thr Ile Ile Ser Gly Leu Pro Pro Glu Lys Pro Lys Asn Leu Ser Cys
            100   105   110

Ile Val Asn Glu Gly Lys Lys Met Arg Cys Glu Trp Asp Gly Gly Arg
        115   120   125

Glu Thr His Leu Glu Thr Asn Phe Thr Leu Lys Ser Glu Trp Ala Thr
    130   135   140

His Lys Phe Ala Asp Cys Lys Ala Lys Arg Asp Thr Pro Thr Ser Cys
145   150   155   160

Thr Val Asp Tyr Ser Thr Val Tyr Phe Val Asn Ile Glu Val Trp Val
                165   170   175

```
Glu Ala Glu Asn Ala Leu Gly Lys Val Thr Ser Asp His Ile Asn Phe
            180                 185                 190

Asp Pro Val Tyr Lys Val Lys Pro Asn Pro Pro His Asn Leu Ser Val
        195                 200                 205

Ile Asn Ser Glu Glu Leu Ser Ser Ile Leu Lys Leu Thr Trp Thr Asn
    210                 215                 220

Pro Ser Ile Lys Ser Val Ile Ile Leu Lys Tyr Asn Ile Gln Tyr Arg
225                 230                 235                 240

Thr Lys Asp Ala Ser Thr Trp Ser Gln Ile Pro Pro Glu Asp Thr Ala
                245                 250                 255

Ser Thr Arg Ser Ser Phe Thr Val Gln Asp Leu Lys Pro Phe Thr Glu
            260                 265                 270

Tyr Val Phe Arg Ile Arg Cys Met Lys Glu Asp Gly Lys Gly Tyr Trp
        275                 280                 285

Ser Asp Trp Ser Glu Glu Ala Ser Gly Ile Thr Tyr Glu Asp Arg Pro
    290                 295                 300

Ser Lys Ala Pro Ser Phe Trp Tyr Lys Ile Asp Pro Ser His Thr Gln
305                 310                 315                 320

Gly Tyr Arg Thr Val Gln Leu Val Trp Lys Thr Leu Pro Pro Phe Glu
                325                 330                 335

Ala Asn Gly Lys Ile Leu Asp Tyr Glu Val Thr Leu Thr Arg Trp Lys
            340                 345                 350

Ser His Leu Gln Asn Tyr Thr Val Asn Ala Thr Lys Leu Thr Val Asn
        355                 360                 365
```

```
Leu Thr Asn Asp Arg Tyr Leu Ala Thr Leu Thr Val Arg Asn Leu Val
    370                 375                 380

Gly Lys Ser Asp Ala Ala Val Leu Thr Ile Pro Ala Cys Asp Phe Gln
385                 390                 395                 400

Ala Thr His Pro Val Met Asp Leu Lys Ala Phe Pro Lys Asp Asn Met
                405                 410                 415

Leu Trp Val Glu Trp Thr Thr Pro Arg Glu Ser Val Lys Lys Tyr Ile
            420                 425                 430

Leu Glu Trp Cys Val Leu Ser Asp Lys Ala Pro Cys Ile Thr Asp Trp
        435                 440                 445

Gln Gln Glu Asp Gly Thr Val His Arg Thr Tyr Leu Arg Gly Asn Leu
    450                 455                 460

Ala Glu Ser Lys Cys Tyr Leu Ile Thr Val Thr Pro Val Tyr Ala Asp
465                 470                 475                 480

Gly Pro Gly Ser Pro Glu Ser Ile Lys Ala Tyr Leu Lys Gln Ala Pro
                485                 490                 495

Pro Ser Lys Gly Pro Thr Val Arg Thr Lys Lys Val Gly Lys Asn Glu
            500                 505                 510

Ala Val Leu Glu Trp Asp Gln Leu Pro Val Asp Val Gln Asn Gly Phe
        515                 520                 525

Ile Arg Asn Tyr Thr Ile Phe Tyr Arg Thr Ile Ile Gly Asn Glu Thr
    530                 535                 540

Ala Val Asn Val Asp Ser Ser His Thr Glu Tyr Thr Leu Ser Ser Leu
545                 550                 555                 560

Thr Ser Asp Thr Leu Tyr Met Val Arg Met Ala Ala Tyr Thr Asp Glu
                565                 570                 575
```

```
Gly Gly Lys Asp Gly Pro Glu Phe Thr Phe Thr Thr Pro Lys Phe Ala
            580                 585                 590

Gln Gly Glu Ile Glu Ala Ile Val Val Pro Val Cys Leu Ala Phe Leu
        595                 600                 605

Leu Thr Thr Leu Leu Gly Val Leu Phe Cys Phe Asn Lys Arg Asp Leu
    610                 615                 620

Ile Lys Lys His Ile Trp Pro Asn Val Pro Asp Pro Ser Lys Ser His
625                 630                 635                 640

Ile Ala Gln Trp Ser Pro His Thr Pro Pro Arg His Asn Phe Asn Ser
                645                 650                 655

Lys Asp Gln Met Tyr Ser Asp Gly Asn Phe Thr Asp Val Ser Val Val
            660                 665                 670

Glu Ile Glu Ala Asn Asp Lys Lys Pro Phe Pro Glu Asp Leu Lys Ser
        675                 680                 685

Leu Asp Leu Phe Lys Lys Glu Lys Ile Asn Thr Glu Gly His Ser Ser
    690                 695                 700

Gly Ile Gly Gly Ser Ser Cys Met Ser Ser Ser Arg Pro Ser Ile Ser
705                 710                 715                 720

Ser Ser Asp Glu Asn Glu Ser Ser Gln Asn Thr Ser Ser Thr Val Gln
                725                 730                 735

Tyr Ser Thr Val Val His Ser Gly Tyr Arg His Gln Val Pro Ser Val
            740                 745                 750

Gln Val Phe Ser Arg Ser Glu Ser Thr Gln Pro Leu Leu Asp Ser Glu
        755                 760                 765
```

```
Glu Arg Pro Glu Asp Leu Gln Leu Val Asp His Val Asp Gly Gly Asp
    770                 775                 780

Gly Ile Leu Pro Arg Gln Gln Tyr Phe Lys Gln Asn Cys Ser Gln His
785                 790                 795                 800

Glu Ser Ser Pro Asp Ile Ser His Phe Glu Arg Ser Lys Gln Val Ser
                805                 810                 815

Ser Val Asn Glu Glu Asp Phe Val Arg Leu Lys Gln Gln Ile Ser Asp
            820                 825                 830

His Ile Ser Gln Ser Cys Gly Ser Gly Gln Met Lys Met Phe Gln Glu
        835                 840                 845

Val Ser Ala Ala Asp Ala Phe Gly Pro Gly Thr Glu Gly Gln Val Glu
    850                 855                 860

Arg Phe Glu Thr Val Gly Met Glu Ala Ala Thr Asp Glu Gly Met Pro
865                 870                 875                 880

Lys Ser Tyr Leu Pro Gln Thr Val Arg Gln Gly Gly Tyr Met Pro Gln
                885                 890                 895
```

<210> 23
<211> 639
<212> PRT
<213> Homo sapiens

<400> 23

```
Cys Arg Thr Ser Glu Cys Cys Phe Gln Asp Pro Pro Tyr Pro Asp Ala
1               5                   10                  15

Asp Ser Gly Ser Ala Ser Gly Pro Arg Asp Leu Arg Cys Tyr Arg Ile
            20                  25                  30

Ser Ser Asp Arg Tyr Glu Cys Ser Trp Gln Tyr Glu Gly Pro Thr Ala
        35                  40                  45
```

```
Gly Val Ser His Phe Leu Arg Cys Cys Leu Ser Ser Gly Arg Cys Cys
    50                  55                  60

Tyr Phe Ala Ala Gly Ser Ala Thr Arg Leu Gln Phe Ser Asp Gln Ala
65                  70                  75                  80

Gly Val Ser Val Leu Tyr Thr Val Thr Leu Trp Val Glu Ser Trp Ala
                85                  90                  95

Arg Asn Gln Thr Glu Lys Ser Pro Glu Val Thr Leu Gln Leu Tyr Asn
            100                 105                 110

Ser Val Lys Tyr Glu Pro Pro Leu Gly Asp Ile Lys Val Ser Lys Leu
        115                 120                 125

Ala Gly Gln Leu Arg Met Glu Trp Glu Thr Pro Asp Asn Gln Val Gly
    130                 135                 140

Ala Glu Val Gln Phe Arg His Arg Thr Pro Ser Ser Pro Trp Lys Leu
145                 150                 155                 160

Gly Asp Cys Gly Pro Gln Asp Asp Asp Thr Glu Ser Cys Leu Cys Pro
                165                 170                 175

Leu Glu Met Asn Val Ala Gln Glu Phe Gln Leu Arg Arg Arg Gln Leu
            180                 185                 190

Gly Ser Gln Gly Ser Ser Trp Ser Lys Trp Ser Ser Pro Val Cys Val
        195                 200                 205

Pro Pro Glu Asn Pro Pro Gln Pro Gln Val Arg Phe Ser Val Glu Gln
    210                 215                 220

Leu Gly Gln Asp Gly Arg Arg Arg Leu Thr Leu Lys Glu Gln Pro Thr
225                 230                 235                 240

Gln Leu Glu Leu Pro Glu Gly Cys Gln Gly Leu Ala Pro Gly Thr Glu
                245                 250                 255
```

```
Val Thr Tyr Arg Leu Gln Leu His Met Leu Ser Cys Pro Cys Lys Ala
            260                 265                 270

Lys Ala Thr Arg Thr Leu His Leu Gly Lys Met Pro Tyr Leu Ser Gly
        275                 280                 285

Ala Ala Tyr Asn Val Ala Val Ile Ser Ser Asn Gln Phe Gly Pro Gly
    290                 295                 300

Leu Asn Gln Thr Trp His Ile Pro Ala Asp Thr His Thr Glu Pro Val
305                 310                 315                 320

Ala Leu Asn Ile Ser Val Gly Thr Asn Gly Thr Thr Met Tyr Trp Pro
                325                 330                 335

Ala Arg Ala Gln Ser Met Thr Tyr Cys Ile Glu Trp Gln Pro Val Gly
            340                 345                 350

Gln Asp Gly Gly Leu Ala Thr Cys Ser Leu Thr Ala Pro Gln Asp Pro
        355                 360                 365

Asp Pro Ala Gly Met Ala Thr Tyr Ser Trp Ser Arg Glu Ser Gly Ala
    370                 375                 380

Met Gly Gln Glu Lys Cys Tyr Tyr Ile Thr Ile Phe Ala Ser Ala His
385                 390                 395                 400

Pro Glu Lys Leu Thr Leu Trp Ser Thr Val Leu Ser Thr Tyr His Phe
                405                 410                 415

Gly Gly Asn Ala Ser Ala Ala Gly Thr Pro His His Val Ser Val Lys
            420                 425                 430

Asn His Ser Leu Asp Ser Val Ser Val Asp Trp Ala Pro Ser Leu Leu
        435                 440                 445
```

```
Ser Thr Cys Pro Gly Val Leu Lys Glu Tyr Val Val Arg Cys Arg Asp
    450                 455                 460

Glu Asp Ser Lys Gln Val Ser Glu His Pro Val Gln Pro Thr Glu Thr
465                 470                 475                 480

Gln Val Thr Leu Ser Gly Leu Arg Ala Gly Val Ala Tyr Thr Val Gln
                485                 490                 495

Val Arg Ala Asp Thr Ala Trp Leu Arg Gly Val Trp Ser Gln Pro Gln
            500                 505                 510

Arg Phe Ser Ile Glu Val Gln Val Ser Asp Trp Leu Ile Phe Phe Ala
        515                 520                 525

Ser Leu Gly Ser Phe Leu Ser Ile Leu Leu Val Gly Val Leu Gly Tyr
    530                 535                 540

Leu Gly Leu Asn Arg Ala Ala Arg His Leu Cys Pro Pro Leu Pro Thr
545                 550                 555                 560

Pro Cys Ala Ser Ser Ala Ile Glu Phe Pro Gly Gly Lys Glu Thr Trp
                565                 570                 575

Gln Trp Ile Asn Pro Val Asp Phe Gln Glu Glu Ala Ser Leu Gln Glu
            580                 585                 590

Ala Leu Val Val Glu Met Ser Trp Asp Lys Gly Glu Arg Thr Glu Pro
        595                 600                 605

Leu Glu Lys Thr Glu Leu Pro Glu Gly Ala Pro Glu Leu Ala Leu Asp
    610                 615                 620

Thr Glu Leu Ser Leu Glu Asp Gly Asp Arg Cys Lys Ala Lys Met
625                 630                 635
```

<210> 24
<211> 839

<212> PRT
<213> Homo sapiens

<400> 24
Lys Ile Asp Ala Cys Lys Arg Gly Asp Val Thr Val Lys Pro Ser His
1   5   10   15

Val Ile Leu Leu Gly Ser Thr Val Asn Ile Thr Cys Ser Leu Lys Pro
            20   25   30

Arg Gln Gly Cys Phe His Tyr Ser Arg Arg Asn Lys Leu Ile Leu Tyr
        35   40   45

Lys Phe Asp Arg Arg Ile Asn Phe His His Gly His Ser Leu Asn Ser
    50   55   60

Gln Val Thr Gly Leu Pro Leu Gly Thr Thr Leu Phe Val Cys Lys Leu
65   70   75   80

Ala Cys Ile Asn Ser Asp Glu Ile Gln Ile Cys Gly Ala Glu Ile Phe
                85   90   95

Val Gly Val Ala Pro Glu Gln Pro Gln Asn Leu Ser Cys Ile Gln Lys
            100   105   110

Gly Glu Gln Gly Thr Val Ala Cys Thr Trp Glu Arg Gly Arg Asp Thr
        115   120   125

His Leu Tyr Thr Glu Tyr Thr Leu Gln Leu Ser Gly Pro Lys Asn Leu
    130   135   140

Thr Trp Gln Lys Gln Cys Lys Asp Ile Tyr Cys Asp Tyr Leu Asp Phe
145   150   155   160

Gly Ile Asn Leu Thr Pro Glu Ser Pro Glu Ser Asn Phe Thr Ala Lys
                165   170   175

Val Thr Ala Val Asn Ser Leu Gly Ser Ser Ser Ser Leu Pro Ser Thr
            180   185   190

```
Phe Thr Phe Leu Asp Ile Val Arg Pro Leu Pro Pro Trp Asp Ile Arg
        195                 200                 205

Ile Lys Phe Gln Lys Ala Ser Val Ser Arg Cys Thr Leu Tyr Trp Arg
    210                 215                 220

Asp Glu Gly Leu Val Leu Leu Asn Arg Leu Arg Tyr Arg Pro Ser Asn
225                 230                 235                 240

Ser Arg Leu Trp Asn Met Val Asn Val Thr Lys Ala Lys Gly Arg His
                245                 250                 255

Asp Leu Leu Asp Leu Lys Pro Phe Thr Glu Tyr Glu Phe Gln Ile Ser
            260                 265                 270

Ser Lys Leu His Leu Tyr Lys Gly Ser Trp Ser Asp Trp Ser Glu Ser
        275                 280                 285

Leu Arg Ala Gln Thr Pro Glu Glu Glu Pro Thr Gly Met Leu Asp Val
    290                 295                 300

Trp Tyr Met Lys Arg His Ile Asp Tyr Ser Arg Gln Gln Ile Ser Leu
305                 310                 315                 320

Phe Trp Lys Asn Leu Ser Val Ser Glu Ala Arg Gly Lys Ile Leu His
                325                 330                 335

Tyr Gln Val Thr Leu Gln Glu Leu Thr Gly Gly Lys Ala Met Thr Gln
            340                 345                 350

Asn Ile Thr Gly His Thr Ser Trp Thr Thr Val Ile Pro Arg Thr Gly
        355                 360                 365

Asn Trp Ala Val Ala Val Ser Ala Ala Asn Ser Lys Gly Ser Ser Leu
    370                 375                 380
```

```
Pro Thr Arg Ile Asn Ile Met Asn Leu Cys Glu Ala Gly Leu Leu Ala
385                 390                 395                 400

Pro Arg Gln Val Ser Ala Asn Ser Glu Gly Met Asp Asn Ile Leu Val
                405                 410                 415

Thr Trp Gln Pro Pro Arg Lys Asp Pro Ser Ala Val Gln Glu Tyr Val
            420                 425                 430

Val Glu Trp Arg Glu Leu His Pro Gly Gly Asp Thr Gln Val Pro Leu
        435                 440                 445

Asn Trp Leu Arg Ser Arg Pro Tyr Asn Val Ser Ala Leu Ile Ser Glu
    450                 455                 460

Asn Ile Lys Ser Tyr Ile Cys Tyr Glu Ile Arg Val Tyr Ala Leu Ser
465                 470                 475                 480

Gly Asp Gln Gly Gly Cys Ser Ser Ile Leu Gly Asn Ser Lys His Lys
                485                 490                 495

Ala Pro Leu Ser Gly Pro His Ile Asn Ala Ile Thr Glu Glu Lys Gly
            500                 505                 510

Ser Ile Leu Ile Ser Trp Asn Ser Ile Pro Val Gln Glu Gln Met Gly
        515                 520                 525

Cys Leu Leu His Tyr Arg Ile Tyr Trp Lys Glu Arg Asp Ser Asn Ser
    530                 535                 540

Gln Pro Gln Leu Cys Glu Ile Pro Tyr Arg Val Ser Gln Asn Ser His
545                 550                 555                 560

Pro Ile Asn Ser Leu Gln Pro Arg Val Thr Tyr Val Leu Trp Met Thr
                565                 570                 575

Ala Leu Thr Ala Ala Gly Glu Ser Ser His Gly Asn Glu Arg Glu Phe
            580                 585                 590
```

```
Cys Leu Gln Gly Lys Ala Asn Trp Met Ala Phe Val Ala Pro Ser Ile
        595                 600                 605

Cys Ile Ala Ile Ile Met Val Gly Ile Phe Ser Thr His Tyr Phe Gln
    610                 615                 620

Gln Lys Val Phe Val Leu Leu Ala Ala Leu Arg Pro Gln Trp Cys Ser
625                 630                 635                 640

Arg Glu Ile Pro Asp Pro Ala Asn Ser Thr Cys Ala Lys Lys Tyr Pro
                645                 650                 655

Ile Ala Glu Glu Lys Thr Gln Leu Pro Leu Asp Arg Leu Leu Ile Asp
            660                 665                 670

Trp Pro Thr Pro Glu Asp Pro Glu Pro Leu Val Ile Ser Glu Val Leu
        675                 680                 685

His Gln Val Thr Pro Val Phe Arg His Pro Pro Cys Ser Asn Trp Pro
    690                 695                 700

Gln Arg Glu Lys Gly Ile Gln Gly His Gln Ala Ser Glu Lys Asp Met
705                 710                 715                 720

Met His Ser Ala Ser Ser Pro Pro Pro Pro Arg Ala Leu Gln Ala Glu
                725                 730                 735

Ser Arg Gln Leu Val Asp Leu Tyr Lys Val Leu Glu Ser Arg Gly Ser
            740                 745                 750

Asp Pro Lys Pro Glu Asn Pro Ala Cys Pro Trp Thr Val Leu Pro Ala
        755                 760                 765

Gly Asp Leu Pro Thr His Asp Gly Tyr Leu Pro Ser Asn Ile Asp Asp
    770                 775                 780
```

```
Leu Pro Ser His Glu Ala Pro Leu Ala Asp Ser Leu Glu Glu Leu Glu
785                 790                 795                 800


Pro Gln His Ile Ser Leu Ser Val Phe Pro Ser Ser Ser Leu His Pro
                805                 810                 815


Leu Thr Phe Ser Cys Gly Asp Lys Leu Thr Leu Asp Gln Leu Lys Met
            820                 825                 830


Arg Cys Asp Ser Leu Met Leu
        835
```

<210> 25
<211> 800
<212> PRT
<213> Homo sapiens

<400> 25

```
Met Lys Val Leu Gln Glu Pro Thr Cys Val Ser Asp Tyr Met Ser Ile
1               5                   10                  15


Ser Thr Cys Glu Trp Lys Met Asn Gly Pro Thr Asn Cys Ser Thr Glu
            20                  25                  30


Leu Arg Leu Leu Tyr Gln Leu Val Phe Leu Leu Ser Glu Ala His Thr
        35                  40                  45


Cys Ile Pro Glu Asn Asn Gly Gly Ala Gly Cys Val Cys His Leu Leu
    50                  55                  60


Met Asp Asp Val Val Ser Ala Asp Asn Tyr Thr Leu Asp Leu Trp Ala
65                  70                  75                  80


Gly Gln Gln Leu Leu Trp Lys Gly Ser Phe Lys Pro Ser Glu His Val
                85                  90                  95


Lys Pro Arg Ala Pro Gly Asn Leu Thr Val His Thr Asn Val Ser Asp
            100                 105                 110
```

```
Thr Leu Leu Leu Thr Trp Ser Asn Pro Tyr Pro Pro Asp Asn Tyr Leu
        115                 120                 125

Tyr Asn His Leu Thr Tyr Ala Val Asn Ile Trp Ser Glu Asn Asp Pro
    130                 135                 140

Ala Asp Phe Arg Ile Tyr Asn Val Thr Tyr Leu Glu Pro Ser Leu Arg
145                 150                 155                 160

Ile Ala Ala Ser Thr Leu Lys Ser Gly Ile Ser Tyr Arg Ala Arg Val
                165                 170                 175

Arg Ala Trp Ala Gln Cys Tyr Asn Thr Thr Trp Ser Glu Trp Ser Pro
            180                 185                 190

Ser Thr Lys Trp His Asn Ser Tyr Arg Glu Pro Phe Glu Gln His Leu
        195                 200                 205

Leu Leu Gly Val Ser Val Ser Cys Ile Val Ile Leu Ala Val Cys Leu
    210                 215                 220

Leu Cys Tyr Val Ser Ile Thr Lys Ile Lys Lys Glu Trp Trp Asp Gln
225                 230                 235                 240

Ile Pro Asn Pro Ala Arg Ser Arg Leu Val Ala Ile Ile Ile Gln Asp
                245                 250                 255

Ala Gln Gly Ser Gln Trp Glu Lys Arg Ser Arg Gly Gln Glu Pro Ala
            260                 265                 270

Lys Cys Pro His Trp Lys Asn Cys Leu Thr Lys Leu Leu Pro Cys Phe
        275                 280                 285

Leu Glu His Asn Met Lys Arg Asp Glu Asp Pro His Lys Ala Ala Lys
    290                 295                 300

Glu Met Pro Phe Gln Gly Ser Gly Lys Ser Ala Trp Cys Pro Val Glu
305                 310                 315                 320
```

```
Ile Ser Lys Thr Val Leu Trp Pro Glu Ser Ile Ser Val Val Arg Cys
                325                 330                 335

Val Glu Leu Phe Glu Ala Pro Val Glu Cys Glu Glu Glu Glu Glu Val
            340                 345                 350

Glu Glu Glu Lys Gly Ser Phe Cys Ala Ser Pro Glu Ser Ser Arg Asp
        355                 360                 365

Asp Phe Gln Glu Gly Arg Glu Gly Ile Val Ala Arg Leu Thr Glu Ser
    370                 375                 380

Leu Phe Leu Asp Leu Leu Gly Glu Glu Asn Gly Gly Phe Cys Gln Gln
385                 390                 395                 400

Asp Met Gly Glu Ser Cys Leu Leu Pro Pro Ser Gly Ser Thr Ser Ala
                405                 410                 415

His Met Pro Trp Asp Glu Phe Pro Ser Ala Gly Pro Lys Glu Ala Pro
            420                 425                 430

Pro Trp Gly Lys Glu Gln Pro Leu His Leu Glu Pro Ser Pro Pro Ala
        435                 440                 445

Ser Pro Thr Gln Ser Pro Asp Asn Leu Thr Cys Thr Glu Thr Pro Leu
    450                 455                 460

Val Ile Ala Gly Asn Pro Ala Tyr Arg Ser Phe Ser Asn Ser Leu Ser
465                 470                 475                 480

Gln Ser Pro Cys Pro Arg Glu Leu Gly Pro Asp Pro Leu Leu Ala Arg
                485                 490                 495

His Leu Glu Glu Val Glu Pro Glu Met Pro Cys Val Pro Gln Leu Ser
            500                 505                 510
```

```
Glu Pro Thr Thr Val Pro Gln Pro Glu Pro Glu Thr Trp Glu Gln Ile
        515                 520                 525

Leu Arg Arg Asn Val Leu Gln His Gly Ala Ala Ala Ala Pro Val Ser
    530                 535                 540

Ala Pro Thr Ser Gly Tyr Gln Glu Phe Val His Ala Val Glu Gln Gly
545                 550                 555                 560

Gly Thr Gln Ala Ser Ala Val Val Gly Leu Gly Pro Pro Gly Glu Ala
                565                 570                 575

Gly Tyr Lys Ala Phe Ser Ser Leu Leu Ala Ser Ser Ala Val Ser Pro
            580                 585                 590

Glu Lys Cys Gly Phe Gly Ala Ser Ser Gly Glu Glu Gly Tyr Lys Pro
        595                 600                 605

Phe Gln Asp Leu Ile Pro Gly Cys Pro Gly Asp Pro Ala Pro Val Pro
    610                 615                 620

Val Pro Leu Phe Thr Phe Gly Leu Asp Arg Glu Pro Pro Arg Ser Pro
625                 630                 635                 640

Gln Ser Ser His Leu Pro Ser Ser Ser Pro Glu His Leu Gly Leu Glu
                645                 650                 655

Pro Gly Glu Lys Val Glu Asp Met Pro Lys Pro Pro Leu Pro Gln Glu
            660                 665                 670

Gln Ala Thr Asp Pro Leu Val Asp Ser Leu Gly Ser Gly Ile Val Tyr
        675                 680                 685

Ser Ala Leu Thr Cys His Leu Cys Gly His Leu Lys Gln Cys His Gly
    690                 695                 700

Gln Glu Asp Gly Gly Gln Thr Pro Val Met Ala Ser Pro Cys Cys Gly
705                 710                 715                 720
```

```
Cys Cys Cys Gly Asp Arg Ser Ser Pro Pro Thr Thr Pro Leu Arg Ala
                725                 730                 735


Pro Asp Pro Ser Pro Gly Gly Val Pro Leu Glu Ala Ser Leu Cys Pro
            740                 745                 750


Ala Ser Leu Ala Pro Ser Gly Ile Ser Glu Lys Ser Lys Ser Ser Ser
        755                 760                 765


Ser Phe His Pro Ala Pro Gly Asn Ala Gln Ser Ser Ser Gln Thr Pro
    770                 775                 780


Lys Ile Val Asn Phe Val Ser Val Gly Pro Thr Tyr Met Arg Val Ser
785                 790                 795                 800


<210> 26
<211> 347
<212> PRT
<213> Homo sapiens

<400> 26
Leu Asn Thr Thr Ile Leu Thr Pro Asn Gly Asn Glu Asp Thr Thr Ala
1               5                   10                  15


Asp Phe Phe Leu Thr Thr Met Pro Thr Asp Ser Leu Ser Val Ser Thr
            20                  25                  30


Leu Pro Leu Pro Glu Val Gln Cys Phe Val Phe Asn Val Glu Tyr Met
        35                  40                  45


Asn Cys Thr Trp Asn Ser Ser Ser Glu Pro Gln Pro Thr Asn Leu Thr
    50                  55                  60


Leu His Tyr Trp Tyr Lys Asn Ser Asp Asn Asp Lys Val Gln Lys Cys
65                  70                  75                  80


Ser His Tyr Leu Phe Ser Glu Glu Ile Thr Ser Gly Cys Gln Leu Gln
                85                  90                  95
```

```
Lys Lys Glu Ile His Leu Tyr Gln Thr Phe Val Val Gln Leu Gln Asp
            100                 105                 110

Pro Arg Glu Pro Arg Arg Gln Ala Thr Gln Met Leu Lys Leu Gln Asn
        115                 120                 125

Leu Val Ile Pro Trp Ala Pro Glu Asn Leu Thr Leu His Lys Leu Ser
    130                 135                 140

Glu Ser Gln Leu Glu Leu Asn Trp Asn Asn Arg Phe Leu Asn His Cys
145                 150                 155                 160

Leu Glu His Leu Val Gln Tyr Arg Thr Asp Trp Asp His Ser Trp Thr
                165                 170                 175

Glu Gln Ser Val Asp Tyr Arg His Lys Phe Ser Leu Pro Ser Val Asp
            180                 185                 190

Gly Gln Lys Arg Tyr Thr Phe Arg Val Arg Ser Arg Phe Asn Pro Leu
        195                 200                 205

Cys Gly Ser Ala Gln His Trp Ser Glu Trp Ser His Pro Ile His Trp
    210                 215                 220

Gly Ser Asn Thr Ser Lys Glu Asn Pro Phe Leu Phe Ala Leu Glu Ala
225                 230                 235                 240

Val Val Ile Ser Val Gly Ser Met Gly Leu Ile Ile Ser Leu Leu Cys
                245                 250                 255

Val Tyr Phe Trp Leu Glu Arg Thr Met Pro Arg Ile Pro Thr Leu Lys
            260                 265                 270

Asn Leu Glu Asp Leu Val Thr Glu Tyr His Gly Asn Phe Ser Ala Trp
        275                 280                 285
```

```
Ser Gly Val Ser Lys Gly Leu Ala Glu Ser Leu Gln Pro Asp Tyr Ser
    290                 295                 300

Glu Arg Leu Cys Leu Val Ser Glu Ile Pro Pro Lys Gly Gly Ala Leu
305                 310                 315                 320

Gly Glu Gly Pro Gly Ala Ser Pro Cys Asn Gln His Ser Pro Tyr Trp
                325                 330                 335

Ala Pro Pro Cys Tyr Thr Leu Lys Pro Glu Thr
            340                 345
```

<210> 27
<211> 406
<212> PRT
<213> Homo sapiens

<400> 27

```
Gly Gly Gly Gly Ala Ala Pro Thr Glu Thr Gln Pro Pro Val Thr Asn
1               5                   10                  15

Leu Ser Val Ser Val Glu Asn Leu Cys Thr Val Ile Trp Thr Trp Asn
            20                  25                  30

Pro Pro Glu Gly Ala Ser Ser Asn Cys Ser Leu Trp Tyr Phe Ser His
        35                  40                  45

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

Ile Glu Val Pro Leu Asn Glu Arg Ile Cys Leu Gln Val Gly Ser Gln
65                  70                  75                  80

Cys Ser Thr Asn Glu Ser Glu Lys Pro Ser Ile Leu Val Glu Lys Cys
                85                  90                  95

Ile Ser Pro Pro Glu Gly Asp Pro Glu Ser Ala Val Thr Glu Leu Gln
            100                 105                 110
```

```
Cys Ile Trp His Asn Leu Ser Tyr Met Lys Cys Ser Trp Leu Pro Gly
        115                 120                 125

Arg Asn Thr Ser Pro Asp Thr Asn Tyr Thr Leu Tyr Tyr Trp His Arg
    130                 135                 140

Ser Leu Glu Lys Ile His Gln Cys Glu Asn Ile Phe Arg Glu Gly Gln
145                 150                 155                 160

Tyr Phe Gly Cys Ser Phe Asp Leu Thr Lys Val Lys Asp Ser Ser Phe
                165                 170                 175

Glu Gln His Ser Val Gln Ile Met Val Lys Asp Asn Ala Gly Lys Ile
            180                 185                 190

Lys Pro Ser Phe Asn Ile Val Pro Leu Thr Ser Arg Val Lys Pro Asp
        195                 200                 205

Pro Pro His Ile Lys Asn Leu Ser Phe His Asn Asp Asp Leu Tyr Val
    210                 215                 220

Gln Trp Glu Asn Pro Gln Asn Phe Ile Ser Arg Cys Leu Phe Tyr Glu
225                 230                 235                 240

Val Glu Val Asn Asn Ser Gln Thr Glu Thr His Asn Val Phe Tyr Val
                245                 250                 255

Gln Glu Ala Lys Cys Glu Asn Pro Glu Phe Glu Arg Asn Val Glu Asn
            260                 265                 270

Thr Ser Cys Phe Met Val Pro Gly Val Leu Pro Asp Thr Leu Asn Thr
        275                 280                 285

Val Arg Ile Arg Val Lys Thr Asn Lys Leu Cys Tyr Glu Asp Asp Lys
    290                 295                 300

Leu Trp Ser Asn Trp Ser Gln Glu Met Ser Ile Gly Lys Lys Arg Asn
305                 310                 315                 320
```

```
Ser Thr Leu Tyr Ile Thr Met Leu Leu Ile Val Pro Val Ile Val Ala
                325                 330                 335

Gly Ala Ile Ile Val Leu Leu Leu Tyr Leu Lys Arg Leu Lys Ile Ile
            340                 345                 350

Ile Phe Pro Pro Ile Pro Asp Pro Gly Lys Ile Phe Lys Glu Met Phe
        355                 360                 365

Gly Asp Gln Asn Asp Asp Thr Leu His Trp Lys Lys Tyr Asp Ile Tyr
    370                 375                 380

Glu Lys Gln Thr Lys Glu Glu Thr Asp Ser Val Val Leu Ile Glu Asn
385                 390                 395                 400

Leu Lys Lys Ala Ser Gln
                405
```

<210> 28
<211> 557
<212> PRT
<213> Homo sapiens

<400> 28

```
His Gly Thr Glu Leu Pro Ser Pro Pro Ser Val Trp Phe Glu Ala Glu
1               5                   10                  15

Phe Phe His His Ile Leu His Trp Thr Pro Ile Pro Asn Gln Ser Glu
            20                  25                  30

Ser Thr Cys Tyr Glu Val Ala Leu Leu Arg Tyr Gly Ile Glu Ser Trp
        35                  40                  45

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

Val Thr Leu Asp Leu Tyr His Ser Asn Gly Tyr Arg Ala Arg Val Arg
65                  70                  75                  80
```

```
Ala Val Asp Gly Ser Arg His Ser Asn Trp Thr Val Thr Asn Thr Arg
                85                  90                  95

Phe Ser Val Asp Glu Val Thr Leu Thr Val Gly Ser Val Asn Leu Glu
            100                 105                 110

Ile His Asn Gly Phe Ile Leu Gly Lys Ile Gln Leu Pro Arg Pro Lys
        115                 120                 125

Met Ala Pro Ala Asn Asp Thr Tyr Glu Ser Ile Phe Ser His Phe Arg
    130                 135                 140

Glu Tyr Glu Ile Ala Ile Arg Lys Val Pro Gly Asn Phe Thr Phe Thr
145                 150                 155                 160

His Lys Lys Val Lys His Glu Asn Phe Ser Leu Leu Thr Ser Gly Glu
                165                 170                 175

Val Gly Glu Phe Cys Val Gln Val Lys Pro Ser Val Ala Ser Arg Ser
            180                 185                 190

Asn Lys Gly Met Trp Ser Lys Glu Glu Cys Ile Ser Leu Thr Arg Gln
        195                 200                 205

Tyr Phe Thr Val Thr Asn Val Ile Ile Phe Phe Ala Phe Val Leu Leu
    210                 215                 220

Leu Ser Gly Ala Leu Ala Tyr Cys Leu Ala Leu Gln Leu Tyr Val Arg
225                 230                 235                 240

Arg Arg Lys Lys Leu Pro Ser Val Leu Leu Phe Lys Lys Pro Ser Pro
                245                 250                 255

Phe Ile Phe Ile Ser Gln Arg Pro Ser Pro Glu Thr Gln Asp Thr Ile
            260                 265                 270
```

```
His Pro Leu Asp Glu Glu Ala Phe Leu Lys Val Ser Pro Glu Leu Lys
        275                 280                 285

Asn Leu Asp Leu His Gly Ser Thr Asp Ser Gly Phe Gly Ser Thr Lys
    290                 295                 300

Pro Ser Leu Gln Thr Glu Glu Pro Gln Phe Leu Leu Pro Asp Pro His
305                 310                 315                 320

Pro Gln Ala Asp Arg Thr Leu Gly Asn Arg Glu Pro Pro Val Leu Gly
                325                 330                 335

Asp Ser Cys Ser Ser Gly Ser Ser Asn Ser Thr Asp Ser Gly Ile Cys
            340                 345                 350

Leu Gln Glu Pro Ser Leu Ser Pro Ser Thr Gly Pro Thr Trp Glu Gln
        355                 360                 365

Gln Val Gly Ser Asn Ser Arg Gly Gln Asp Asp Ser Gly Ile Asp Leu
    370                 375                 380

Val Gln Asn Ser Glu Gly Arg Ala Gly Asp Thr Gln Gly Gly Ser Ala
385                 390                 395                 400

Leu Gly His His Ser Pro Pro Glu Pro Glu Val Pro Gly Glu Glu Asp
                405                 410                 415

Pro Ala Ala Val Ala Phe Gln Gly Tyr Leu Arg Gln Thr Arg Cys Ala
            420                 425                 430

Glu Glu Lys Ala Thr Lys Thr Gly Cys Leu Glu Glu Glu Ser Pro Leu
        435                 440                 445

Thr Asp Gly Leu Gly Pro Lys Phe Gly Arg Cys Leu Val Asp Glu Ala
    450                 455                 460

Gly Leu His Pro Pro Ala Leu Ala Lys Gly Tyr Leu Lys Gln Asp Pro
465                 470                 475                 480
```

Leu Glu Met Thr Leu Ala Ser Ser Gly Ala Pro Thr Gly Gln Trp Asn
485 490 495

Gln Pro Thr Glu Glu Trp Ser Leu Leu Ala Leu Ser Ser Cys Ser Asp
500 505 510

Leu Gly Ile Ser Asp Trp Ser Phe Ala His Asp Leu Ala Pro Leu Gly
515 520 525

Cys Val Ala Ala Pro Gly Gly Leu Leu Gly Ser Phe Asn Ser Asp Leu
530 535 540

Val Thr Leu Pro Leu Ile Ser Ser Leu Gln Ser Ser Glu
545 550 555

<210> 29
<211> 306
<212> PRT
<213> Homo sapiens

<400> 29
Met Val Pro Pro Pro Glu Asn Val Arg Met Asn Ser Val Asn Phe Lys
1 5 10 15

Asn Ile Leu Gln Trp Glu Ser Pro Ala Phe Ala Lys Gly Asn Leu Thr
20 25 30

Phe Thr Ala Gln Tyr Leu Ser Tyr Arg Ile Phe Gln Asp Lys Cys Met
35 40 45

Asn Thr Thr Leu Thr Glu Cys Asp Phe Ser Ser Leu Ser Lys Tyr Gly
50 55 60

Asp His Thr Leu Arg Val Arg Ala Glu Phe Ala Asp Glu His Ser Asp
65 70 75 80

Trp Val Asn Ile Thr Phe Cys Pro Val Asp Asp Thr Ile Ile Gly Pro
85 90 95

```
Pro Gly Met Gln Val Glu Val Leu Ala Asp Ser Leu His Met Arg Phe
            100                 105                 110

Leu Ala Pro Lys Ile Glu Asn Glu Tyr Glu Thr Trp Thr Met Lys Asn
        115                 120                 125

Val Tyr Asn Ser Trp Thr Tyr Asn Val Gln Tyr Trp Lys Asn Gly Thr
    130                 135                 140

Asp Glu Lys Phe Gln Ile Thr Pro Gln Tyr Asp Phe Glu Val Leu Arg
145                 150                 155                 160

Asn Leu Glu Pro Trp Thr Thr Tyr Cys Val Gln Val Arg Gly Phe Leu
                165                 170                 175

Pro Asp Arg Asn Lys Ala Gly Glu Trp Ser Glu Pro Val Cys Glu Gln
            180                 185                 190

Thr Thr His Asp Glu Thr Val Pro Ser Trp Met Val Ala Val Ile Leu
        195                 200                 205

Met Ala Ser Val Phe Met Val Cys Leu Ala Leu Leu Gly Cys Phe Ala
    210                 215                 220

Leu Leu Trp Cys Val Tyr Lys Lys Thr Lys Tyr Ala Phe Ser Pro Arg
225                 230                 235                 240

Asn Ser Leu Pro Gln His Leu Lys Glu Phe Leu Gly His Pro His His
                245                 250                 255

Asn Thr Leu Leu Phe Phe Ser Phe Pro Leu Ser Asp Glu Asn Asp Val
            260                 265                 270

Phe Asp Lys Leu Ser Val Ile Ala Glu Asp Ser Glu Ser Gly Lys Gln
        275                 280                 285
```

```
Asn Pro Gly Asp Ser Cys Ser Leu Gly Thr Pro Pro Gly Gln Gly Pro
    290                 295                 300


Gln Ser
305


<210> 30
<211> 523
<212> PRT
<213> Homo sapiens

<400> 30
Ala Glu Ser Cys Thr Ser Arg Pro His Ile Thr Val Val Glu Gly Glu
1               5                   10                  15


Pro Phe Tyr Leu Lys His Cys Ser Cys Ser Leu Ala His Glu Ile Glu
            20                  25                  30


Thr Thr Thr Lys Ser Trp Tyr Lys Ser Ser Gly Ser Gln Glu His Val
        35                  40                  45


Glu Leu Asn Pro Arg Ser Ser Ser Arg Ile Ala Leu His Asp Cys Val
    50                  55                  60


Leu Glu Phe Trp Pro Val Glu Leu Asn Asp Thr Gly Ser Tyr Phe Phe
65                  70                  75                  80


Gln Met Lys Asn Tyr Thr Gln Lys Trp Lys Leu Asn Val Ile Arg Arg
                85                  90                  95


Asn Lys His Ser Cys Phe Thr Glu Arg Gln Val Thr Ser Lys Ile Val
            100                 105                 110


Glu Val Lys Lys Phe Phe Gln Ile Thr Cys Glu Asn Ser Tyr Tyr Gln
        115                 120                 125


Thr Leu Val Asn Ser Thr Ser Leu Tyr Lys Asn Cys Lys Lys Leu Leu
    130                 135                 140
```

```
Leu Glu Asn Asn Lys Asn Pro Thr Ile Lys Lys Asn Ala Glu Phe Glu
145                 150                 155                 160

Asp Gln Gly Tyr Tyr Ser Cys Val His Phe Leu His His Asn Gly Lys
                165                 170                 175

Leu Phe Asn Ile Thr Lys Thr Phe Asn Ile Thr Ile Val Glu Asp Arg
            180                 185                 190

Ser Asn Ile Val Pro Val Leu Leu Gly Pro Lys Leu Asn His Val Ala
        195                 200                 205

Val Glu Leu Gly Lys Asn Val Arg Leu Asn Cys Ser Ala Leu Leu Asn
    210                 215                 220

Glu Glu Asp Val Ile Tyr Trp Met Phe Gly Glu Glu Asn Gly Ser Asp
225                 230                 235                 240

Pro Asn Ile His Glu Glu Lys Glu Met Arg Ile Met Thr Pro Glu Gly
                245                 250                 255

Lys Trp His Ala Ser Lys Val Leu Arg Ile Glu Asn Ile Gly Glu Ser
            260                 265                 270

Asn Leu Asn Val Leu Tyr Asn Cys Thr Val Ala Ser Thr Gly Gly Thr
        275                 280                 285

Asp Thr Lys Ser Phe Ile Leu Val Arg Lys Ala Asp Met Ala Asp Ile
    290                 295                 300

Pro Gly His Val Phe Thr Arg Gly Met Ile Ile Ala Val Leu Ile Leu
305                 310                 315                 320

Val Ala Val Val Cys Leu Val Thr Val Cys Val Ile Tyr Arg Val Asp
                325                 330                 335

Leu Val Leu Phe Tyr Arg His Leu Thr Arg Arg Asp Glu Thr Leu Thr
            340                 345                 350
```

```
Asp Gly Lys Thr Tyr Asp Ala Phe Val Ser Tyr Leu Lys Glu Cys Arg
        355                 360                 365

Pro Glu Asn Gly Glu Glu His Thr Phe Ala Val Glu Ile Leu Pro Arg
    370                 375                 380

Val Leu Glu Lys His Phe Gly Tyr Lys Leu Cys Ile Phe Glu Arg Asp
385                 390                 395                 400

Val Val Pro Gly Gly Ala Val Val Asp Glu Ile His Ser Leu Ile Glu
                405                 410                 415

Lys Ser Arg Arg Leu Ile Ile Val Leu Ser Lys Ser Tyr Met Ser Asn
            420                 425                 430

Glu Val Arg Tyr Glu Leu Glu Ser Gly Leu His Glu Ala Leu Val Glu
        435                 440                 445

Arg Lys Ile Lys Ile Ile Leu Ile Glu Phe Thr Pro Val Thr Asp Phe
    450                 455                 460

Thr Phe Leu Pro Gln Ser Leu Lys Leu Leu Lys Ser His Arg Val Leu
465                 470                 475                 480

Lys Trp Lys Ala Asp Lys Ser Leu Ser Tyr Asn Ser Arg Phe Trp Lys
                485                 490                 495

Asn Leu Leu Tyr Leu Met Pro Ala Lys Thr Val Lys Pro Gly Arg Asp
            500                 505                 510

Glu Pro Glu Val Leu Pro Val Leu Ser Glu Ser
        515                 520
```

<210> 31
<211> 580
<212> PRT
<213> Homo sapiens

<400> 31
Phe Asn Ile Ser Gly Cys Ser Thr Lys Lys Leu Leu Trp Thr Tyr Ser
1   5   10   15

Thr Arg Ser Glu Glu Glu Phe Val Leu Phe Cys Asp Leu Pro Glu Pro
            20   25   30

Gln Lys Ser His Phe Cys His Arg Asn Arg Leu Ser Pro Lys Gln Val
        35   40   45

Pro Glu His Leu Pro Phe Met Gly Ser Asn Asp Leu Ser Asp Val Gln
    50   55   60

Trp Tyr Gln Gln Pro Ser Asn Gly Asp Pro Leu Glu Asp Ile Arg Lys
65   70   75   80

Ser Tyr Pro His Ile Ile Gln Asp Lys Cys Thr Leu His Phe Leu Thr
                85   90   95

Pro Gly Val Asn Asn Ser Gly Ser Tyr Ile Cys Arg Pro Lys Met Ile
            100   105   110

Lys Ser Pro Tyr Asp Val Ala Cys Cys Val Lys Met Ile Leu Glu Val
        115   120   125

Lys Pro Gln Thr Asn Ala Ser Cys Glu Tyr Ser Ala Ser His Lys Gln
    130   135   140

Asp Leu Leu Leu Gly Ser Thr Gly Ser Ile Ser Cys Pro Ser Leu Ser
145   150   155   160

Cys Gln Ser Asp Ala Gln Ser Pro Ala Val Thr Trp Tyr Lys Asn Gly
                165   170   175

Lys Leu Leu Ser Val Glu Arg Ser Asn Arg Ile Val Val Asp Glu Val
            180   185   190

```
Tyr Asp Tyr His Gln Gly Thr Tyr Val Cys Asp Tyr Thr Gln Ser Asp
        195                 200                 205

Thr Val Ser Ser Trp Thr Val Arg Ala Val Val Gln Val Arg Thr Ile
    210                 215                 220

Val Gly Asp Thr Lys Leu Lys Pro Asp Ile Leu Asp Pro Val Glu Asp
225                 230                 235                 240

Thr Leu Glu Val Glu Leu Gly Lys Pro Leu Thr Ile Ser Cys Lys Ala
                245                 250                 255

Arg Phe Gly Phe Glu Arg Val Phe Asn Pro Val Ile Lys Trp Tyr Ile
            260                 265                 270

Lys Asp Ser Asp Leu Glu Trp Glu Val Ser Val Pro Glu Ala Lys Ser
        275                 280                 285

Ile Lys Ser Thr Leu Lys Asp Glu Ile Ile Glu Arg Asn Ile Ile Leu
    290                 295                 300

Glu Lys Val Thr Gln Arg Asp Leu Arg Arg Lys Phe Val Cys Phe Val
305                 310                 315                 320

Gln Asn Ser Ile Gly Asn Thr Thr Gln Ser Val Gln Leu Lys Glu Lys
                325                 330                 335

Arg Gly Val Val Leu Leu Tyr Ile Leu Leu Gly Thr Ile Gly Thr Leu
            340                 345                 350

Val Ala Val Leu Ala Ala Ser Ala Leu Leu Tyr Arg His Trp Ile Glu
        355                 360                 365

Ile Val Leu Leu Tyr Arg Thr Tyr Gln Ser Lys Asp Gln Thr Leu Gly
    370                 375                 380

Asp Lys Lys Asp Phe Asp Ala Phe Val Ser Tyr Ala Lys Trp Ser Ser
385                 390                 395                 400
```

```
Phe Pro Ser Glu Ala Thr Ser Ser Leu Ser Glu Glu His Leu Ala Leu
                405                 410                 415

Ser Leu Phe Pro Asp Val Leu Glu Asn Lys Tyr Gly Tyr Ser Leu Cys
            420                 425                 430

Leu Leu Glu Arg Asp Val Ala Pro Gly Gly Val Tyr Ala Glu Asp Ile
        435                 440                 445

Val Ser Ile Ile Lys Arg Ser Arg Arg Gly Ile Phe Ile Leu Ser Pro
    450                 455                 460

Asn Tyr Val Asn Gly Pro Ser Ile Phe Glu Leu Gln Ala Ala Val Asn
465                 470                 475                 480

Leu Ala Leu Asp Asp Gln Thr Leu Lys Leu Ile Leu Ile Lys Phe Cys
                485                 490                 495

Tyr Phe Gln Glu Pro Glu Ser Leu Pro His Leu Val Lys Lys Ala Leu
            500                 505                 510

Arg Val Leu Pro Thr Val Thr Trp Arg Gly Leu Lys Ser Val Pro Pro
        515                 520                 525

Asn Ser Arg Phe Trp Ala Lys Met Arg Tyr His Met Pro Val Lys Asn
    530                 535                 540

Ser Gln Gly Phe Thr Trp Asn Gln Leu Arg Ile Thr Ser Arg Ile Phe
545                 550                 555                 560

Gln Trp Lys Gly Leu Ser Arg Thr Glu Thr Thr Gly Arg Ser Ser Gln
                565                 570                 575

Pro Lys Glu Trp
            580
```

<210> 32
<211> 495
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 32
tgcgaccttc cacagaccca ttccctcggc tctcgaagaa ctctgatgtt gctggcccag 60

atgcggaaga tttctctttt ctcatgtctg aaagacaggc acgactttgg ttttccccag 120

gaggagttcg gaaaccagtt ccagaaagcg gaaaccattc ctgtgctgca cgaaatgatc 180

caacaaattt tcaacctgtt ttcaactaaa gatagctccg ctgcatggga cgagacactc 240

ctcgataagt tttatacaga gctttaccag cagttaaatg atctggaagc ttgtgtcatc 300

caaggggtcg gcgtaaccga gacgcccctg atgaaggagg atagcatact ggcagtgcgg 360

aagtacttcc agaggatcac cctctatcta aaggaaaaaa agtacagtcc gtgcgcctgg 420

gaagtggtta gagccgaaat catgcgtagc ttttccttat ctacaaattt gcaggagtcg 480

ttgcgcagta aagag 495

<210> 33
<211> 498
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 33
atgagttata atttactcgg atttctacag cggtctagca acttccaatg tcagaagctg 60

ctgtggcaac tcaacggcag gctggagtac tgcctcaaag atagaatgaa ctttgatatt 120

cccgaagaaa tcaagcagct tcagcagttc cagaaagagg acgccgcact aaccatatac 180

gagatgctgc agaacatttt cgctatattc agacaggact cgtcctctac tggatggaat 240

gagaccatcg tcgagaattt gctggccaat gtgtatcatc aaattaacca cctcaagacg 300

gtgcttgaag aaaagttgga aaaagaggac ttcactagag gcaaactgat gtcatccctt 360

cacctcaaac gctactatgg gaggatcctg cactacttaa aggcgaagga gtatagccat 420

tgcgcttgga caatcgttcg cgtagagatt ctgcggaatt tttactttat caatcgtttg 480

acaggttacc tgcgaaac 498

<210> 34
<211> 414
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 34
caggatccct acgtgaagga agcagaaaat ctcaaaaagt atttcaatgc gggccatagc 60

gatgtggccg ataacggcac cctgtttctg gggattctta agaattggaa agaggagtct 120

gataggaaga ttatgcagtc ccagatcgtg agcttctatt tcaagctgtt caaaaacttc 180

aaagacgacc agtcgatcca aaaatctgtt gagacaataa aagaggacat gaatgtgaag 240

ttttttaatt caaacaaaaa gaagcgcgac gattttgaga aattaacgaa ctactccgtc 300

accgacttga acgtacaacg aaaggctatt cacgaactaa tccaggtcat ggctgaactg 360

agtcctgccg ccaagactgg taagcgtaaa cggagtcaga tgctctttag agga 414

<210> 35
<211> 471
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 35
gtgcgatctt caagccggac accctcagac aagccagtgg cacacgtggt agcgaaccca 60

caagctgagg ggcagctcca gtggctcaat cggcgtgcca acgccctgtt agccaatggg 120

gtcgagctta gggacaacca acttgtggta ccctcggaag gattatactt gatttacagt 180

caggtgctgt tcaaaggaca gggctgccct tccacacatg ttctgctcac tcacacgatc 240

tcccgcattg cagtgtctta tcagaccaag gtcaacttgc taagcgctat caaaagtcca 300

tgtcagagag agaccccgga gggtgctgag gctaagcctt ggtacgaacc tatttatctg 360

ggcggagtct ttcaactgga aaaaggtgat agactgagcg cagagatcaa taggcccgat 420

tacctggact tcgccgaatc cggccaggtt tattttggga taatcgccct c 471

<210> 36
<211> 459
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 36
gcgcctgtca gaagcctcaa ctgcacgctg agggactcac agcaaaagag cctggtcatg 60

agtggcccct acgagctgaa agcactccac cttcaggggc aggacatgga acaacaggtg 120

gttttctcca tgtctttcgt acagggagag gagtctaacg ataagatccc cgtggctttg 180

ggcttaaaag agaaaaacct gtatctgagc tgtgtgctaa aggacgataa gcccacactt 240

cagctcgagt ccgttgatcc aaaaaattat ccaaagaaga aaatggaaaa gcggtttgtg 300

tttaacaaga ttgagattaa taacaaattg gaattcgaat cagcccagtt ccctaattgg 360

tacatcagta cctctcaagc cgaaaatatg ccggtgtttc tgggagggac caagggtggc 420

caggatataa cagacttcac tatgcagttt gtctcgtcc 459

<210> 37
<211> 549
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 37
gtgccgcccg gggaagatag caaggatgtg gctgctcctc acaggcagcc actgacaagc 60

agcgagagaa tcgacaagca aataaggtat attcttgatg gaatcagcgc gctgcgaaag 120

gagacatgta acaagtcgaa tatgtgcgag tcttccaaag aagcacttgc tgaaaataat 180

ctgaacctcc caaaaatggc cgagaaagac ggctgctttc agtccggttt taacgaggag 240

acttgtttag taaagattat aacgggcttg ttggaattcg aagtctacct agaatacctc 300

caaaatagat tcgagagtag tgaggaacag gcccgcgctg ttcagatgtc aacaaaagtg 360

ttgatccaat tcctgcagaa aaaagccaag aacttagatg caatcaccac acctgacccc 420

actaccaatg cctctctgct caccaagctg caagcccaga accagtggct gcaggacatg 480

actacccatc taattctgcg gtcttttaag gagttcctcc agtcatccct gcgtgcactt 540

cggcagatg 549

<210> 38
<211> 591
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 38
cgaaatctgc cagtggctac ccccgacccg ggcatgtttc cctgcctcca tcatagccag 60

aatctgctca gagcggtcag caacatgcta cagaaggccc gccagacctt agagttttac 120

ccttgcacct ctgaggaaat cgatcacgaa gacatcacca aagataagac tagcaccgtt 180

gaagcctgtc tcccattgga acttacaaaa aatgaatctt gtctgaattc cagagagaca 240

tcttttatca ctaatggaag ttgcctcgcc agtcggaaaa cttccttcat gatggccctg 300

tgtctgagtt caatctacga ggatcttaag atgtatcaag tggaattcaa aacgatgaac 360

gcaaaactgt tgatggatcc taagaggcag atatttttgg atcagaacat gttagctgtg 420

atcgacgagc tgatgcaagc actcaacttc aactcagaga cagtccccca gaagtcctcc 480

ctggaggagc ctgacttcta caagacgaaa attaagctat gcattctgct tcacgcattc 540

aggatacggg ccgtaacaat tgaccgtgtg atgagctatc tgaacgcttc g 591

<210> 39

<211> 918
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 39
atctgggagc tcaaaaagga tgtttatgtg gtcgaacttg actggtaccc ggacgcacca 60

ggggagatgg tggtgttgac ctgcgacacc cccgaagagg acgggattac atggactttg 120

gaccagtcca gtgaagtcct gggctcggga aagaccctga ctatccaggt gaaggagttc 180

ggagatgctg gacaatatac atgccacaag ggcggggaag ttttgagcca ttccctcctg 240

ctgctgcata aaaaagagga tggtatttgg agcactgata ttctgaaaga ccagaaggaa 300

cccaagaaca aaacttttct gcggtgtgag gccaagaatt acagtggaag attcacctgt 360

tggtggttaa ccacaatctc taccgatctt acctttttccg tcaaatcaag tcgcggcagc 420

agcgatccac agggcgtgac gtgcggcgct gccacactaa gcgcggagag agtgcggggt 480

gacaacaagg aatacgagta ctccgttgag tgtcaagaag actctgcatg ccctgccgca 540

gaggaatcat taccgatcga agtaatggtg gatgctgttc acaaactgaa gtatgaaaac 600

tacacttctt catttttcat aagggacatt atcaagcctg atcctccaaa gaacctccaa 660

cttaaaccac tcaagaatag ccgtcaggta gaggtgtcct gggagtaccc cgatacctgg 720

tcaacgcccc actcatattt ctccctgacg ttctgtgtgc aggtgcaggg gaaatccaag 780

agggagaaga aagacagggt ctttacagat aagacatctg ccactgtcat ctgcagaaaa 840

aatgcctcta tatccgtgcg agcccaggac cgctactatt ctagtagctg gagcgagtgg 900

gctagtgtac cttgttcg 918

<210> 40
<211> 387
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 40
cacaagtgtg atattacact ccaagaaata atcaagaccc tgaacagcct aaccgagcag 60

aaaactctct gtacggaatt gaccgttacc gatatcttcg cagctagtaa gaatacaact 120

gaaaaagaga cgttttgtcg tgccgccaca gtcctgaggc agttttattc acatcacgag 180

aaagacaccc ggtgccttgg ggcaactgcc caacagtttc atcgccacaa acagctgatc 240

agattcttga agcggctgga caggaatctc tggggattag ctggcctgaa ttcttgcccc 300

gtgaaggagg cgaaccagag cactctggag aacttcctgg aacgacttaa gacaattatg 360

agagagaagt actccaaatg ctcctct 387

<210> 41
<211> 480
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 41
tcacccggac agggtactca atctgaaaat agttgcaccc attttccagg aaatctgcct 60

aacatgctga gggacttacg cgatgcattt tcgcgtgtaa aaacattctt tcagatgaaa 120

gatcaactgg ataacctgtt gctaaaagag agcctgcttg aggatttcaa gggctatctg 180

ggctgtcagg cgctctccga aatgattcaa ttctacctcg aagaggtgat gccccaggcc 240

gagaaccagg acccagacat caaggcccac gtgaattctc tgggggagaa tctgaaaacg 300

ctcagattgc gactcagacg gtgccacagg tttttacctt gtgaaaacaa gagcaaagcc 360

gttgagcagg tcaagaacgc ttttaataag cttcaggaaa aagggatcta taaggcaatg 420

tccgagttcg acatattcat taattacatt gaggcttaca tgaccatgaa gatccggaac 480

<210> 42
<211> 366
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 42
ttaacatgtc tgggcgggtt cgcctcacct ggaccagttc ccccttcaac cgctctcaga 60

gaactgattg aggagctcgt caatatcacc cagaaccaaa aagccccact ctgcaatgga 120

agtatggtgt ggtctattaa cttgactgcc ggcatgtact gtgccgcact ggagtctttg 180

atcaacgtgt ccgggtgcag tgcaatcgaa aagacgcagc ggatgctgag cggcttttgc 240

ccccacaagg tgagcgctgg tcagttttcc agccttcacg tgcgagatac aaagatagaa 300

gtagcgcagt tcgtcaagga cctgctgctg catcttaaaa aactatttcg cgagggtagg 360

ttcaat 366

<210> 43
<211> 471
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 43
tattttggca aactcgaaag taagctgagc gtgattcgga atcttaacga tcaggtgtta 60

ttcatcgatc aaggcaacag accactcttt gaagatatga cagattcaga ctgtagggat 120

aatgccccta ggaccatctt tattataagc atgtataagg actctcagcc ccgcggtatg 180

gcagtaacga ttagcgttaa gtgcgagaag atttctacac tttcatgcga aaacaaaatc 240

atctccttca aagagatgaa ccctcccgat aatatcaaag ataccaagtc ggacataatt 300

ttctttcaga gatccgtccc aggacacgac aataagatgc aattcgaatc cagcagttac 360

gagggatact ttctggcttg tgagaaggaa cgtgacttgt tcaaactgat cctgaagaaa 420

gaggacgagc taggggaccg atctatcatg ttcactgtgc agaacgagga c 471

<210> 44
<211> 1590
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 44
aagaacctga aatccccaca gaaagtcgag gtggacatca tcgatgacaa tttcatctta 60

agatggaacc gtagcgatga gtccgtcgga aatgtcacat tttcttttga ttatcagaag 120

accgggatgg acaactggat taagctgtcc ggttgccaga acataaccag taccaagtgt 180

aacttcagca gcctcaaact caatgtatat gaggaaatca agctgaggat ccgggccgag 240

aaggaaaaca caagctcctg gtatgaagtt gattcattta ctccatttcg aaaagcgcaa 300

ataggacccc cggaagttca cctcgaggct gaagataaag caattgtaat acacatatcg 360

cctggcacca aggactctgt gatgtgggct ttagatgggc tgtcattcac gtacagcctg 420

gtgatctgga agaacagttc tggggtggag gagagaatag aaaacattta tagtcgccac 480

aaaatctaca aattgtcacc cgaaacaacc tattgcctga aggtcaaggc ggcactattg 540

acgtcctgga agatcggcgt gtactcacca gtgcattgta taaagacaac agtggaaaac 600

gagcttcccc cgccggagaa tattgaggtt tccgtgcaga atcagaatta tgtgttgaag 660

tgggactaca catatgccaa tatgaccttc caggttcaat ggcttcatgc atttctgaaa 720

agaaaccctg gtaaccacct ttacaaatgg aagcagattc ctgactgcga gaatgtcaag 780

accacacagt gcgtgtttcc tcaaaacgtt ttccagaaag gcatctatct gctacgggtc 840

caggcttccg atggcaataa tacctcattt tggagcgagg aaattaaatt cgacactgaa 900

atccaagcct tcctactccc tcccgtattt aacatcagga gtctgtctga tagcttccat 960

atttacatcg gtgctcccaa gcagtctgga aacactcccg tgatccagga ttacccctc 1020

atctacgaga tcattttctg ggaaaacacc tctaacgccg aacggaagat tatagagaag 1080

aaaactgacg tcactgtgcc taacctgaaa ccattaactg tctattgcgt caaagctagg 1140

gcccacacca tggatgaaaa actgaacaag tctagcgtgt tcagcgacgc agtttgtgag 1200

aaaacgaagc caggaaatac ttctaagatt tggcttatcg tgggcatttg tatcgctctg 1260

ttcgcactgc cctttgtaat ctacgccgcc aaggtttttc tccgctgtat taattatgtg 1320

ttttcccat ccctgaagcc atcatcgtcg attgacgagt acttctctga gcaacctctt 1380

aaaaacctgt tgttgtccac cagtgaagag cagattgaga aatgcttcat tatcgaaaat 1440

atttcaacaa tcgccacagt ggaggagacg aatcagaccg acgaggacca taagaagtac 1500

agcagtcaga catctcagga ttccgggaat tacagcaatg aagatgaaag tgaatccaaa 1560

actagcgagg agctccaaca ggactttgtg 1590

<210> 45
<211> 1467
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 45
atcagctacg actcccccga ttacaccgac gagtcctgta cctttaaaat ctccctacgt 60

aacttcaggt ccattctctc ctgggaactg aaaaaccata gcattgtgcc gactcactat 120

acactgctgt ataccataat gtctaaaccc gaggatctga aggtggtgaa gaactgtgcg 180

aacaccacaa gatccttctg cgacctgaca gatgagtggc gatctaccca tgaagcctac 240

gtcacggtcc tcgagggctt cagcggtaat accacacttt tcagctgctc acataacttt 300

tggttggcca tcgatatgtc ctttgaacca cccgagttcg agattgtcgg tttcacaaac 360

cacatcaatg tcatggtgaa atttccttct attgtcgagg aagaactcca gtttgatttg 420

agcctcgtga ttgaggagca gtcagaggga atcgtgaaga agcataagcc cgaaataaag 480

ggaaatatga gtgggaactt cacttacata atcgacaagc tcatccccaa cacgaattat 540

tgtgtgtcag tgtatctcga gcactcggat gagcaagccg tgatcaagtc tccacttaag 600

tgcactctcc tgccgccagg ccaggagtca gagagcgctg aatcggctaa gataggcggg 660

atcattaccg tcttcctcat cgcactggtg ttgacttcta ctattgttac cctgaagtgg 720

atcggataca tctgcttgcg caactctctg ccaaaagttc taaactttca caattttctg 780

gcctggccct tccccaatct tcctcctctg gaggccatgg acatggttga ggttatctat 840

ataaatcgga aaaaaaaagt ctgggactac aattacgatg acgaaagtga ctcagacacg 900

gaggccgcac caaggacctc tggaggggc tatactatgc acggccttac cgtgagacct 960

ttaggacagg catctgctac aagcactgaa agccagctga ttgacccaga gagcgaggaa 1020

gagcctgatc taccagaagt ggatgtagag ctgccgacaa tgcctaagga ctccccccaa 1080

cagctcgaac tgttgagcgg cccttgtgaa aggcgcaaaa gtcccttgca agatccgttc 1140

cctgaagaag actatagcag taccgaagga tccggcggtc ggattacatt caacgtggat 1200

ttaaatagtg tatttttacg ggttctggac gatgaggaca gtgatgatct ggaggcgccc 1260

cttatgctgt cctcccatct ggaggagatg gtagaccccg aagatccaga taacgtgcag 1320

tctaatcacc ttctggcttc cggggaaggt actcagccaa cctttcctag tccttcttca 1380

gagggcttat ggtcagaaga cgcaccaagc gatcagtcag acacaagtga gagcgacgta 1440

gacctcgggg acgggtacat tatgaga 1467

<210> 46
<211> 1416
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 46
gaaatgggga ctgccgactt gggacctagc agtgtcccca ctcccaccaa cgtgaccatc 60

gagtcttata atatgaatcc tattgtttat tgggaatatc agatcatgcc tcaggttcca 120

gtgttcactg ttgaagtgaa aaattacgga gtgaagaact cagagtggat agacgcttgc 180

ataaacatat ctcaccatta ctgcaatatt tccgaccacg tgggcgaccc cagcaacagt 240

ttgtgggtca gagtgaaagc tcgcgtgggc cagaaggaga gtgcttatgc caaaagcgaa 300

gaattcgccg tttgtagaga tggcaagatc gggcccccca aattagacat tcgcaaagaa 360

gaaaaacaaa ttatgatcga tatcttccat ccctctgtct tcgtcaacgg cgacgaacag 420

gaggtagatt atgatccaga gacaacgtgt tacatcaggg tatacaacgt ttacgtgagg 480

atgaatgggt cagagatcca gtataagatc ctcactcaaa aggaggacga ctgtgacgaa 540

attcagtgtc aactcgccat cccagtgtct tcgctgaata gccagtactg cgtgtctgcc 600

gagggtgtgc ttcacgtttg gggagtcaca actgaaaagt ccaaagaagt ttgtattacc 660

atttttaaca gctctatcaa gggctccctg tggataccag tggtggcggc actgctgctg 720

ttccttgtac tcagcctggt cttcatctgc ttctatatta agaagatcaa ccctctgaag 780

gagaagagca tcatactacc caagtcgctt atctcagtcg tgcggtccgc caccctagaa 840

actaagcccg aatcaaaata tgtatccctg atcacaagct accagccatt ttcattagag 900

aaagaagtcg tgtgcgagga gcctctgtcc ccagcaactg tgccaggtat gcatacggag 960

gacaatccgg gtaaagtaga gcacaccgag gagctgtcca gcattacaga ggtcgtcacc 1020

acagaggaga acatacccga tgtggtgcct ggaagtcatc tcacacctat tgagcgtgaa 1080

tctagcagtc ccttgtcttc taatcagagt gaaccgggga gtattgcatt aaactcctac 1140

cactcccgga attgcagcga aagcgaccac tcgagaaatg ggtttgatac cgatagttct 1200

tgtctggaat cccactcatc actgagcgat tctgagtttc cgccaaacaa caagggcgaa 1260

attaaaacgg agggacaaga gctcatcacc gtcatcaagg ctccaaccag ttttggttac 1320

gacaagcctc atgttttggt ggatctgctt gtggatgact caggcaagga gtccctcatt 1380

ggataccgac ctacagagga ttccaaagag tttagc 1416

<210> 47
<211> 948
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 47
gccccccctg atcctctctc acagctaccc gccccacagc atcccaagat aagactgtac 60

aatgccgagc aggtgcttag ctgggagccc gtggcactat caaacagtac gagacccgtg 120

gtgtaccagg tacagttcaa gtacacagac agcaagtggt ttaccgctga cattatgagc 180

attggagtca attgcactca gatcaccgca accgagtgtg actttacagc agcttcaccc 240

tccgccggat tccctatgga cttcaacgtc actctgcggc ttcgtgcaga actgggcgct 300

cttcattccg cctgggtgac aatgccttgg ttccagcact atcggaacgt caccgtaggg 360

ccccctgaaa atatcgaagt aacccctgga gaaggttcgc tgataataag gttcagctct 420

ccgtttgaca ttgctgatac atccactgcg ttcttctgct actatgtgca ctactgggag 480

aagggcggga ttcaacaagt gaaagggcca ttcaggagca acagtatcag tctcgacaac 540

ctgaaacctt ctcgcgtcta ttgcctccaa gtgcaggctc aactgctgtg gaacaaaagt 600

aatattttcc gagttggcca cctgtctaat atctcctgtt atgagaccat ggccgacgca 660

tctacggagt tgcagcaggt catcctcatt tctgtgggca cattttccct gctgtcggtt 720

ctggccggtg cctgtttttt tctcgttttg aaataccgcg gcttgatcaa atactggttt 780

catacccccac catcaatacc attacagatc gaagagtatc ttaaagatcc aactcagcca 840

attttagagg cgctcgataa ggactctagc ccgaaggacg atgtgtggga ttccgtgtcc 900

atcatcagct ttcccgaaaa ggagcaggaa gatgttctgc aaactttg 948

<210> 48
<211> 1278
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 48
ttggtacccc atcttggcga ccgagagaaa cgggatagtg tctgtcccca agggaaatat 60

atacacccac agaataactc tatctgctgc actaagtgcc ataaaggaac gtacctttat 120

aacgactgcc caggccccgg ccaagatact gactgcagag agtgcgagtc tgggagcttc 180

accgcctccg agaatcactt gagacattgc ctgagttgta gcaagtgcag gaaggagatg 240

gggcaggttg agatctcatc atgtaccgtt gatcgggaca ccgtctgtgg atgccgcaaa 300

aatcagtatc ggcattattg gtccgaaaac ctatttcagt gttttaactg ttctttgtgc 360

ctgaacggaa cagtccacct gagttgccag gaaaaacaga atacagtttg cacttgccac 420

gctggctttt ttctccgcga gaacgaatgt gtgtcctgtt ccaattgtaa gaagtctcta 480

gaatgtacaa agctgtgtct gccccaaatc gagaacgtga aaggaactga ggacagtggt 540

acaaccgtgt tgctgcctct ggtgatcttc ttcgggctct gcctcctcag tctgcttttc 600

attgggctaa tgtaccggta ccagcgttgg aaatctaagt tatactcaat tgtctgtggg 660

aagtccaccc ctgagaagga aggagaactg gaaggtacta ccaccaaacc actggctcca 720

aacccctcct tctctcctac acccggcttt actcctaccc tgggcttctc accggtgccc 780

agctcaacgt tcaccagctc gagcacatac acccctggcg attgtcccaa cttcgcagca 840

ccaaggcgtg aagtggcccc accctaccag ggtgctgatc caatacttgc caccgcatta 900

gccagcgatc cgattcctaa tcctttacag aagtgggagg attcggccca caaaccccag 960

agcctggaca ctgacgaccc cgccacgctg tatgctgtgg tcgagaatgt accgcctctc 1020

agatggaagg aatttgtgag gcgactgggc ctgtccgatc acgagatcga cagactggag 1080

ttgcaaaatg gtcgatgcct ccgggaggcc cagtacagca tgctggctac atggaggagg 1140

cgcacacctc gcagggaggc gactcttgaa ttgctgggac gcgtgctcag agatatggac 1200

ttactcggat gtcttgaaga cattgaagag gcgctctgcg gcccagcagc cctgcctccg 1260

gcaccatccc tgctcaga 1278

<210> 49
<211> 1317
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 49
ctgcctgccc aggtcgcttt tacaccatat gcacctgagc ctggttccac gtgtaggctt 60

agggagtact acgatcaaac cgctcagatg tgttgctcca agtgtagtcc aggccagcac 120

gcaaaagtct tttgtacaaa gacgtcagat accgtgtgcg acagctgcga agatagcacc 180

tatacccagc tgtggaattg ggttcccgaa tgtttgtctt gtggctcccg ctgctctagt 240

gaccaggtgg aaacacaggc ctgcactcgg gaacagaacc gtatttgtac ctgcaggccc 300

ggttggtact gcgcactgtc caaacaagag gggtgtagac tgtgtgcccc tttgcgcaag 360

tgtcgtccag gcttcggtgt ggcaagacct ggaacagaga cttcagacgt cgtttgtaag 420

ccctgcgccc ctggcacatt ctccaatacc acctcatcta ccgacatatg cagaccccac 480

caaatatgca acgtggtggc tatccctggg aacgcctcca tggacgctgt ttgcacttcc 540

acttctccca ctcggtctat ggctcccggt gccgtgcatt taccccaacc cgtgagcact 600

cggagccaac acacacagcc aacacccgag ccaagtaccg ccccgagtac cagcttccta 660

ctccccatgg gcccatctcc accggctgag ggatctaccg gggattttgc tctgcctgtc 720

gggctaatcg tcggggtgac ggcgctcgga ttgctcatta tcggagtggt aaactgcgtg 780

attatgactc aggtgaaaaa gaagccttta tgcctccaga gagaagcgaa agttccccac 840

ctgcctgcag acaaggccag gggtacacag ggcccggaac agcaacatct gctgatcacc 900

gccccctctt caagctccag cagcctggaa tccagtgcca gtgcacttga tcggcgcgca 960

ccaacgcgaa accagcccca ggcccctggg gtagaggcat caggcgctgg agaagcgcgc 1020

gctagcacag gcagttccga ttccagccct ggagggcatg gaacacaggt aaatgtcacc 1080

tgcatcgtta atgtgtgctc gtcctcggac cacagctctc aatgttcaag ccaggcctca 1140

agcactatgg gcgacactga tagctctccc tccgagtcac cgaaggacga gcaggtccca 1200

tttagtaaag aggagtgtgc cttccgaagt cagctggaga caccagaaac cctgcttggg 1260

tctactgaag agaaaccact ccctcttggc gtgccagatg cgggaatgaa gccgtcg 1317

<210> 50
<211> 1656
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 50
ctcgaggccg ataagtgcaa agaaagagag gaaaaaatca ttctggtttc tagcgccaac 60

gaaatcgatg tccgcccctg tccactgaat cctaacgagc ataaggggac tataacatgg 120

tataaggacg acagcaagac ccctgtgtct acagaacaag caagcaggat acaccagcac 180

aaagaaaagc tttggtttgt accagcaaag gtcgaggaca gcgggcatta ttattgcgtg 240

gtacgaaaca gttcttactg cctcagaatc aagatttccg ctaagtttgt cgagaacgaa 300

cctaacttat gttacaacgc acaggctatt tttaaacaga agctcccagt tgctggggat 360

ggcggcctgg tgtgtcccta catggagttt tttaaaaatg agaataatga gctacctaaa 420

ctgcaatggt acaaggactg caaacccctt ttgctcgaca atattcactt cagcggagtg 480

aaagatcggc tgattgtgat gaacgtggct gagaaacacc gcgggaacta tacatgccac 540

gcctcttata cgtacctggg caagcagtac ccgatcacta gagtgattga atttataaca 600

ctggaagaga acaagccaac tcgtcctgtc atagtatccc ccgcaaacga aaccatggag 660

gtggacttgg gttctcagat ccagctgatt tgcaatgtta ccgggcaatt gagtgatatc 720

gcctattgga agtggaatgg ttctgtcatt gacgaagacg atccagtgtt aggagaggac 780

tattatagcg tagaaaatcc tgcgaacaag aggcggtcga ctctgataac tgtcctgaac 840

atcagtgaga tcgagagccg attttataaa catccattca catgtttcgc caaaaataca 900

cacgggatcg acgccgccta cattcagctg atctaccccg taaccaattt ccagaagcac 960

atgatcggga tatgcgtgac gctaaccgtg atcattgttt gctcagtgtt catttacaag 1020

atcttcaaga tcgacatcgt cctttggtat agggatagct gttacgactt tctgcccatt 1080

aaggcatcgg atggcaaaac ctacgacgct tacatcttgt acccaaagac cgtgggagaa 1140

ggctcaacct ccgactgtga cattttcgtc tttaaggtgc tccctgaggt cctcgagaaa 1200

cagtgtggct ataaactgtt catctatggc cgggatgact acgtgggcga ggatatagtt 1260

gaagtcataa atgaaaatgt taagaaatca cggaggctga tcatcattct agtgcgggag 1320

acctcaggtt tttcctggct cggcggctcc tcagaggagc agattgcgat gtacaacgct 1380

ctggtgcaag atggaatcaa ggtggttctg ttggagctcg aaaagatcca ggattacgag 1440

aaaatgcccg agagcattaa gttcatcaaa caaaaacacg gagccattag atggagtggt 1500

gatttcacgc aaggaccgca gtccgccaag acacgtttct ggaaaaacgt gcgctatcat 1560

atgcccgtgc agaggagatc cccctccagt aaacatcagc tgttatctcc ggcgactaag 1620

gaaaagcttc agcgcgaagc ccatgttcct cttgga 1656

<210> 51
<211> 1650
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 51
tccgagcggt gcgatgattg gggcttagat accatgcggc agattcaggt gttcgaagac 60

gagcctgctc gcattaaatg cccgctcttt gagcacttcc tgaagtttaa ttacagcact 120

gctcactccg caggactcac actgatctgg tattggacac gccaagacag agatctggag 180

gagcccatta attttaggct ccccgagaac aggatctcta aggagaagga cgtgctgtgg 240

tttcggccga cactactgaa cgatactggg aattacacat gtatgcttcg aaatactacc 300

tattgctcca aggtggcttt tccacttgag gtggtgcaga aagacagctg ttttaatagc 360

ccaatgaaac tgcccgtgca caagctgtac atcgaatatg gcatacagag aatcacatgc 420

cctaacgtcg acggctactt ccctagctca gttaagccga ccataacttg gtatatgggc 480

tgctataaaa tacagaactt caataatgta atccccgagg gtatgaactt gagtttcctg 540

atcgcactga tatctaacaa cgggaactac acctgtgtgg tgacttatcc cgagaacgga 600

cgcacattcc atttgacaag gacgttaact gtcaaggtag tgggtagtcc taagaatgca 660

gttcctcccg tgattcacag ccctaatgat cacgtggtgt atgaaaaaga accaggtgaa 720

gaactcctga tcccctgcac ggtgtacttc tctttttttaa tggactcccg taatgaagtt 780

tggtggacca tcgacggcaa aaaacctgat gatattacca tcgacgtgac aatcaacgag 840

agcatttcac atagtcggac cgaagatgag acaagaaccc agattcttag cataaaaaaa 900

gtgacttctg aagacctgaa gcgcagttac gtatgtcacg cgcgatccgc aaaaggggaa 960

gttgccaagg ctgccaaggt gaagcagaaa gtccctgccc cacggtacac cgtagagctg 1020

gcctgtggct tcggagctac ggttttgctg gttgttatcc ttatcgtcgt ctatcatgtg 1080

tactggttgg agatggtgct tttttatcgg gcccatttcg ggaccgatga gacgattcta 1140

gacggaaagg agtacgatat ttacgtctcg tacgccagaa atgcggagga agaggaattc 1200

gtgctcttaa ccctgagggg agtactggaa aacgagtttg gctacaagtt gtgtattttt 1260

gacagagatt cactgccagg aggaattgtc actgacgaga cactctcatt catccagaaa 1320

tctaggaggt tgctcgttgt cctgagtcca aattatgtgc tccaaggcac ccaggccttg 1380

ctagaactga aggcggggct tgaaaacatg gcctctcgcg ggaacatcaa cgtaattctg 1440

gtgcagtaca aagcagtgaa ggagaccaaa gttaaagagc tgaaacgagc caagacagtc 1500

ctcactgtca tcaagtggaa aggtgaaaaa tcaaagtatc cacaagggag attctggaag 1560

cagcttcaag tcgctatgcc cgtgaagaag tccccccgtc gttcctcctc ggacgagcag 1620

ggcctgagct acagctctct caagaatgtc 1650

<210> 52
<211> 1347
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 52
cttgcaccaa gacgctgtcc ggctcaggag gtcgctaggg gagtgctgac ctcgctgccg 60

ggcgactccg tgaccctgac atgtcctgga gtggagcctg aggacaacgc aacagttcac 120

tgggtgctac ggaagcccgc cgctggctcc catccttcca ggtgggccgg gatggggcgc 180

agactgcttc tcagatcagt gcagttacat gatagcggta attacagctg ctaccgcgct 240

ggaaggccgg caggcactgt gcacctccta gtggatgttc cacctgagga gccacagttg 300

agctgctttc gaaaaagtcc cttgtctaac gtcgtatgcg agtggggccc tagatcaact 360

ccctccctca ccaccaaagc ggttctcctc gtacgtaagt tccaaaactc tcctgccgaa 420

gattttcaag agccatgtca gtatagccag gagagtcaga agttctcatg ccagcttgca 480

gtcccggagg gtgactcatc cttctatatt gttagtatgt gcgtcgcctc gtctgtgggg 540

tctaagttta gcaagactca aacttttcag ggctgcggca tcctccaacc agacccccct 600

gccaacatta cagtgaccgc agttgccaga aaccctaggt ggttgagcgt gacgtggcag 660

gatccccatt cctggaattc atcattctac agactgcggt tcgagctccg atacagggcg 720

gaacgtagca agacattcac cacgtggatg gtcaaagacc tgcagcacca ctgtgtaatc 780

catgacgctt ggagcggtct gcgccacgtg gtccagctgc gggcacaaga ggaattcgga 840

cagggtgaat ggagtgaatg gtctcctgag gctatgggca ctccgtggac cgaatctcgg 900

tctccaccag ccgaaaacga agtgtccacc cctatgcagg ctctgactac taataaggat 960

gacgataata tcttgtttag ggactccgca aatgctacat cactgcctgt acaggattcc 1020

agtagtgttc ccctaccaac ctttttagtc gccggagggt ctctggcgtt cgggacgttg 1080

ctctgtatag ccattgtgct gcgtttcaaa aagacctgga aactgcgcgc cttaaaggag 1140

ggaaaaacaa gcatgcaccc cccatattct cttgggcagc tggtgcccga acggcccaga 1200

ccaacaccag tcctggtgcc tcttatatcc ccccccgtga gcccctctag cctgggcagt 1260

gacaatacca gtagccataa taggcccgac gcccgagacc ctcgctcccc atacgatatc 1320

tcaaacacag attatttttt tccccgg 1347

<210> 53
<211> 2688
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 53
gaactcctgg acccctgcgg gtatattagc cccgagtctc ccgtggtgca actgcattct 60

aacttcaccg cagtttgtgt gctcaaagaa aagtgtatgg attacttcca tgttaacgcc 120

aactacattg tgtggaaaac taatcatttt acgataccaa aggagcagta cacaattatc 180

aacagaaccg catcatccgt cacatttacc gatatcgcct ccttgaacat tcagctgaca 240

tgtaatatct taacattcgg tcaactggaa caaaacgtgt atggcatcac catcatctct 300

ggacttcctc cagaaaaacc caaaaatttg tcgtgtatcg tgaatgaggg aaaaaaaatg 360

cgctgtgaat gggacggggg ccgggagact cacctcgaga cgaacttcac ccttaagtca 420

gagtgggcga cacataaatt tgccgactgc aaagcaaaga gagatacccc cacttcctgc 480

accgtcgact attcaactgt gtacttcgtc aacattgagg tgtgggtgga ggcggagaat 540

gcccttggca aggttacttc cgaccacatc aactttgatc ccgtctacaa ggtgaaaccg 600

aacccacccc acaacctgtc cgtcattaat tcagaggagc taagttctat actcaagtta 660

acttggacga atccctccat aaagagtgta attattctca agtataacat ccaatatagg 720

actaaagatg cttcaacctg gtcacagatc ccaccggagg acaccgcctc tacaaggtca 780

tcgttcaccg tgcaggatct taagcctttc accgagtatg tgttcagaat ccgatgcatg 840

aaagaggacg gcaaggggta ttggagcgat tggagcgaag aagcttccgg cattacctac 900

gaggacaggc cttcgaaagc accttctttc tggtacaaaa tcgatccttc tcacactcag 960

ggctaccgga ccgtgcagct tgtgtggaag actttgccac cattcgaggc aaatggaaag 1020

atactggatt atgaggtcac actgacccgc tggaaaagtc acttgcagaa ctatacagta 1080

aacgccacca aactgacagt caatctcact aacgatagat atttagcaac cctgactgta 1140

cgaaacctgg tgggaaaatc tgacgccgcg gtactgacta tccctgcttg tgactttcag 1200

gctacccacc ctgttatgga tctgaaggcc ttccctaagg ataacatgct atgggtcgag 1260

tggaccacac caagggaaag cgtcaaaaag tatattctcg agtggtgcgt tctgagcgac 1320

aaggccccat gtattacaga ctggcaacag gaggacggga cagttcatcg gacatatctg 1380

cgcggcaatc tagctgaaag taaatgctac cttatcaccg tcacgccagt ctacgccgac 1440

ggcccgggct ctccagagtc aatcaaggct tacctaaagc aggcccctcc ctctaagggg 1500

ccaactgtga gaacaaaaaa ggtaggtaag aatgaagccg tcctggagtg ggatcaactg 1560

ccagtggacg tacagaacgg tttcattcgc aactacacca tcttttacag gacgatcatt 1620

gggaatgaga cagcagtgaa cgtggattct tcccataccg aatacacgct cagcagtctg 1680

acgtcggaca cattgtacat ggtcaggatg gctgcatata cagacgaagg agggaaggat 1740

gggcctgagt tcacctttac cacccctaag ttcgctcagg gcgagattga agcaattgtg 1800

gtgcccgtat gcctggcctt tctccttacg acactgctgg gtgttctctt ttgctttaat 1860

aagcgggacc tcatcaagaa acacatttgg cctaatgtgc ccgaccccag caaaagtcac 1920

atagcccagt ggagccctca tactcccccc cgtcataatt ttaatagcaa ggatcagatg 1980

tacagcgacg gcaattttac agacgtgtcc gtcgtcgaaa tagaagctaa tgataagaag 2040

ccctttcctg aagacctgaa atccttggac ttattcaaaa aggagaagat caataccgaa 2100

gggcactcct cagggatagg gggcagcagt tgcatgtcct catcccgtcc ctctatcagc 2160

tccagcgatg agaacgagag cagccagaat actagttcca ctgttcagta cagcactgta 2220

gttcacagtg gctatagaca tcaggtcccg agtgttcagg tgttctccag gagtgaatct 2280

acccagccgt tgttagactc agaagaacgc ccagaagacc tgcagctggt ggaccacgtg 2340

gatggaggtg atggcattct gccgcgccag caatacttta agcagaactg ttctcagcat 2400

gaatccagcc ctgacatctc tcactttgag cgaagcaaac aggtgtcaag cgtgaacgaa 2460

gaggatttcg ttcggcttaa gcaacagata tctgaccaca tctcacaatc ctgcggaagt 2520

ggacaaatga agatgtttca ggaggttagt gcggccgatg ctttcggccc tggcactgag 2580

ggtcaggtgg aaagattcga gacagtgggt atggaagccg ctacagatga gggaatgccc 2640

aaaagctacc tcccacaaac cgtgcggcag ggaggatata tgccacag 2688

<210> 54
<211> 1917
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 54
tgcagaacta gcgaatgttg tttccaggac cccccgtatc ccgacgccga ttccggaagc 60

gcatccggac cacgtgacct gcggtgctat cggatttcta gcgataggta cgaatgctca 120

tggcagtacg aggggcccac tgctggggtg agtcacttct taagatgctg tttaagttcc 180

gggaggtgct gctatttcgc cgcagggtca gctactcgac tacagttttc tgaccaggct 240

ggagtaagcg tgctttatac agtgacactg tgggtcgaat cctgggccag gaaccaaacg 300

gagaagtcac ccgaggtgac cctgcaactg tataactcag tcaaatacga gcctcctctg 360

ggtgacatta aagtgtcgaa actcgccgga cagcttagaa tggagtggga gacccccgat 420

aaccaggttg gcgcagaggt gcagttccgg caccgaacac cctcatctcc ttggaaactg 480

ggcgattgtg gtccgcagga cgacgatacc gagagttgct tgtgtcccct agagatgaat 540

gtcgcacagg agtttcagct gaggaggcgt cagctcggca gccaaggcag ttcttggtca 600

aaatggtcct cccccgtctg cgttcccccc gaaaatcctc cacagccgca ggttcgattc 660

agcgtggaac aactcgggca ggacgggaga cgccgcttga ctcttaagga gcaaccaacg 720

cagctcgaac tcccagaagg ttgccagggc ctggcacctg gcaccgaggt gacctaccgt 780

ttgcagttac atatgcttag ttgcccttgt aaggccaagg ctacacggac ccttcaccta 840

ggcaaaatgc catacctaag cggtgctgca tacaacgtgg cggtcatttc ttccaaccag 900

ttcggacccg gtctgaatca gacctggcac atccccgcag atacccatac cgaacctgtg 960

gcgctgaata tcagcgtggg cacaaatggc actacgatgt attggccggc ccgcgctcaa 1020

tctatgactt actgcatcga atggcagcct gttgggcaag atggaggact cgcgacatgc 1080

agccttactg ccccgcagga ccctgatcca gcaggtatgg ccacttattc ttggagccgc 1140

gagtccgggg ccatgggaca ggagaagtgt tactacatca ccatatttgc gtcagctcat 1200

ccagaaaagc tgaccctgtg gtcaaccgtt ctgagcacat accacttcgg gggcaatgcg 1260

tccgctgcag gcaccccaca ccacgtgtcg gtgaaaaacc actctctgga cagtgtgagt 1320

gttgactggg ccccaagcct gttgtccaca tgtcccgggg tgctcaagga atatgttgtc 1380

cgctgtcgag acgaggactc caaacaagtg tcggaacatc ccgtacagcc aacggagacc 1440

caagtcactc tgtctggact gagagccggc gtggcctaca cagtccaagt gcgggcagat 1500

acagcttggt tacggggcgt atggagccag ccacaaaggt tcagcattga ggtacaggtc 1560

tctgattggt tgatttttt tgccagtctg ggcagttttc tctctatcct gttggtcgga 1620

gtgttgggct atctgggact gaatcgcgcc gccagacatc tgtgcccccc actcccaacc 1680

ccatgtgcct cctccgccat agaatttcct gggggtaaag agacatggca gtggatcaac 1740

cctgtagact tccaggagga ggctagcctc caggaagccc tggttgtgga aatgtcatgg 1800

gataagggcg agagaacgga acctctcgag aagactgaac ttcccgaggg agctcctgag 1860

ctcgcacttg acacagaact gtctttagag gatggggata ggtgtaaggc taagatg 1917

<210> 55
<211> 2517
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 55
aaaattgatg cgtgcaaacg cggcgatgtg accgtgaaac cgagccatgt gattctgctg 60

ggcagcaccg tgaacattac ctgcagcctg aaaccgcgcc agggctgctt tcattatagc 120

cgccgcaaca aactgattct gtataaattt gatcgccgca ttaactttca tcatggccat 180

agcctgaaca gccaggtgac cggcctgccg ctgggcacca ccctgtttgt gtgcaaactg 240

gcgtgcatta acagcgatga attcagatt tgcggcgcgg aaatttttgt gggcgtggcg 300

ccggaacagc cgcagaacct gagctgcatt cagaaaggcg aacagggcac cgtggcgtgc 360

acctgggaac gcggccgcga tacccatctg tataccgaat ataccctgca gctgagcggc 420

ccgaaaaacc tgacctggca gaaacagtgc aaagatattt attgcgatta tctggatttt 480

ggcattaacc tgaccccgga aagcccggaa agcaacttta ccgcgaaagt gaccgcggtg 540

aacagcctgg gcagcagcag cagcctgccg agcaccttta cctttctgga tattgtgcgc 600

ccgctgccgc cgtgggatat tcgcattaaa tttcagaaag cgagcgtgag ccgctgcacc 660

ctgtattggc gcgatgaagg cctggtgctg ctgaaccgcc tgcgctatcg cccgagcaac 720

agccgcctgt ggaacatggt gaacgtgacc aaagcgaaag gccgccatga tctgctggat 780

ctgaaaccgt ttaccgaata tgaatttcag attagcagca aactgcatct gtataaaggc 840

agctggagcg attggagcga aagcctgcgc gcgcagaccc cggaagaaga accgaccggc 900

atgctggatg tgtggtatat gaaacgccat attgattata gccgccagca gattagcctg 960

ttttggaaaa acctgagcgt gagcgaagcg cgcggcaaaa ttctgcatta tcaggtgacc 1020

ctgcaggaac tgaccggcgg caaagcgatg acccagaaca ttaccggcca taccagctgg 1080

accaccgtga ttccgcgcac cggcaactgg gcggtggcgg tgagcgcggc gaacagcaaa 1140

ggcagcagcc tgccgacccg cattaacatt atgaacctgt gcgaagcggg cctgctggcg 1200

ccgcgccagg tgagcgcgaa cagcgaaggc atggataaca ttctggtgac ctggcagccg 1260

ccgcgcaaag atccgagcgc ggtgcaggaa tatgtggtgg aatggcgcga actgcatccg 1320

ggcggcgata cccaggtgcc gctgaactgg ctgcgcagcc gcccgtataa cgtgagcgcg 1380

ctgattagcg aaaacattaa aagctatatt tgctatgaaa ttcgcgtgta tgcgctgagc 1440

ggcgatcagg gcggctgcag cagcattctg ggcaacagca aacataaagc gccgctgagc 1500

ggcccgcata ttaacgcgat taccgaagaa aaaggcagca ttctgattag ctggaacagc 1560

attccggtgc aggaacagat gggctgcctg ctgcattatc gcatttattg gaaagaacgc 1620

gatagcaaca gccagccgca gctgtgcgaa attccgtatc gcgtgagcca gaacagccat 1680

ccgattaaca gcctgcagcc gcgcgtgacc tatgtgctgt ggatgaccgc gctgaccgcg 1740

gcgggcgaaa gcagccatgg caacgaacgc gaattttgcc tgcagggcaa agcgaactgg 1800

atggcgtttg tggcgccgag catttgcatt gcgattatta tggtgggcat ttttagcacc 1860

cattattttc agcagaaagt gtttgtgctg ctggcggcgc tgcgcccgca gtggtgcagc 1920

cgcgaaattc cggatccggc gaacagcacc tgcgcgaaaa aatatccgat tgcggaagaa 1980

aaaacccagc tgccgctgga tcgcctgctg attgattggc cgaccccgga agatccggaa 2040

ccgctggtga ttagcgaagt gctgcatcag gtgaccccgg tgtttcgcca tccgccgtgc 2100

agcaactggc cgcagcgcga aaaaggcatt cagggccatc aggcgagcga aaaagatatg 2160

atgcatagcg cgagcagccc gccgccgccg cgcgcgctgc aggcggaaag ccgccagctg 2220

gtggatctgt ataaagtgct ggaaagccgc ggcagcgatc cgaaaccgga aaacccggcg 2280

tgcccgtgga ccgtgctgcc ggcgggcgat ctgccgaccc atgatggcta tctgccgagc 2340

aacattgatg atctgccgag ccatgaagcg ccgctggcgg atagcctgga agaactggaa 2400

ccgcagcata ttagcctgag cgtgtttccg agcagcagcc tgcatccgct gacctttagc 2460

tgcggcgata aactgaccct ggatcagctg aaaatgcgct gcgatagcct gatgctg 2517

<210> 56
<211> 2400
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 56
atgaaagtgc tgcaggaacc gacctgcgtg agcgattata tgagcattag cacctgcgaa 60

tggaaaatga acggcccgac caactgcagc accgaactgc gcctgctgta tcagctggtg 120

tttctgctga gcgaagcgca tacctgcatt ccggaaaaca acggcggcgc gggctgcgtg 180

tgccatctgc tgatggatga tgtggtgagc gcggataact ataccctgga tctgtgggcg 240

ggccagcagc tgctgtggaa aggcagcttt aaaccgagcg aacatgtgaa accgcgcgcg 300

ccgggcaacc tgaccgtgca taccaacgtg agcgataccc tgctgctgac ctggagcaac 360

ccgtatccgc cggataacta tctgtataac catctgacct atgcggtgaa catttggagc 420

gaaaacgatc cggcggattt tcgcatttat aacgtgacct atctggaacc gagcctgcgc 480

attgcggcga gcaccctgaa aagcggcatt agctatcgcg cgcgcgtgcg cgcgtgggcg 540

cagtgctata acaccacctg gagcgaatgg agcccgagca ccaaatggca taacagctat 600

cgcgaaccgt ttgaacagca tctgctgctg ggcgtgagcg tgagctgcat tgtgattctg 660

gcggtgtgcc tgctgtgcta tgtgagcatt accaaaatta aaaaagaatg gtgggatcag 720

attccgaacc cggcgcgcag ccgcctggtg gcgattatta ttcaggatgc gcagggcagc 780

cagtgggaaa aacgcagccg cggccaggaa ccggcgaaat gcccgcattg gaaaaactgc 840

ctgaccaaac tgctgccgtg ctttctggaa cataacatga aacgcgatga agatccgcat 900

aaagcggcga aagaaatgcc gtttcagggc agcggcaaaa gcgcgtggtg cccggtggaa 960

attagcaaaa ccgtgctgtg gccggaaagc attagcgtgg tgcgctgcgt ggaactgttt 1020

gaagcgccgg tggaatgcga agaagaagaa gaagtggaag aagaaaaagg cagcttttgc 1080

gcgagcccgg aaagcagccg cgatgatttt caggaaggcc gcgaaggcat tgtggcgcgc 1140

ctgaccgaaa gcctgtttct ggatctgctg ggcgaagaaa acggcggctt ttgccagcag 1200

gatatgggcg aaagctgcct gctgccgccg agcggcagca ccagcgcgca tatgccgtgg 1260

gatgaatttc cgagcgcggg cccgaaagaa gcgccgccgt ggggcaaaga acagccgctg 1320

catctggaac cgagcccgcc ggcgagcccg acccagagcc cggataacct gacctgcacc 1380

gaaaccccgc tggtgattgc gggcaacccg gcgtatcgca gctttagcaa cagcctgagc 1440

cagagcccgt gcccgcgcga actgggcccg gatccgctgc tggcgcgcca tctggaagaa 1500

gtggaaccgg aaatgccgtg cgtgccgcag ctgagcgaac cgaccaccgt gccgcagccg 1560

gaaccggaaa cctgggaaca gattctgcgc cgcaacgtgc tgcagcatgg cgcggcggcg 1620

gcgccggtga gcgcgccgac cagcggctat caggaatttg tgcatgcggt ggaacagggc 1680

ggcacccagg cgagcgcggt ggtgggcctg ggcccgccgg gcgaagcggg ctataaagcg 1740

tttagcagcc tgctggcgag cagcgcggtg agcccggaaa aatgcggctt tggcgcgagc 1800

agcggcgaag aaggctataa accgtttcag gatctgattc cgggctgccc gggcgatccg 1860

gcgccggtgc cggtgccgct gtttaccttt ggcctggatc gcgaaccgcc gcgcagcccg 1920

cagagcagcc atctgccgag cagcagcccg gaacatctgg gcctggaacc gggcgaaaaa 1980

gtggaagata tgccgaaacc gccgctgccg caggaacagg cgaccgatcc gctggtggat 2040

agcctgggca gcggcattgt gtatagcgcg ctgacctgcc atctgtgcgg ccatctgaaa 2100

cagtgccatg gccaggaaga tggcggccag accccggtga tggcgagccc gtgctgcggc 2160

tgctgctgcg gcgatcgcag cagcccgccg accaccccgc tgcgcgcgcc ggatccgagc 2220

ccgggcggcg tgccgctgga agcgagcctg tgcccggcga gcctggcgcc gagcggcatt 2280

agcgaaaaaa gcaaaagcag cagcagcttt catccggcgc cgggcaacgc gcagagcagc 2340

agccagaccc cgaaaattgt gaactttgtg agcgtgggcc cgacctatat gcgcgtgagc 2400

<210> 57
<211> 1041
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 57
ctgaacacaa caattctcac ccctaacggc aacgaagaca ctaccgcaga ttttttcctc 60

actactatgc ccactgattc cctttccgtg tcgaccttgc cgctgccaga agtgcagtgc 120

ttcgtcttta atgttgagta tatgaattgt acatggaatt ctagcagcga accgcagcca 180

accaatttga cattgcacta ctggtataaa aactcagata acgacaaagt gcagaagtgt 240

tcccactact tatttagcga ggaaataacc tctgggtgcc agctgcagaa gaaggagatc 300

catctgtacc agaccttcgt cgtgcagctc caggatccac gggaaccacg ccggcaagct 360

acccaaatgc taaagctgca aaatctcgtt atcccatggg cacctgagaa tttgacactt 420

cataagctgt cggaatccca gctggagctc aattggaaca accgtttcct caaccattgt 480

ctggagcacc tggtgcagta cagaaccgac tgggaccata gttggacgga gcagagtgtc 540

gattatagac acaaattctc actaccctca gtggacgggc agaagaggta cacatttaga 600

gtaaggagtc ggttcaatcc cctgtgcggg tccgcccaac actggagtga gtggtctcat 660

cctattcact ggggcagcaa cacgtccaag gagaaccctt tcttgtttgc tctggaagct 720

gttgtgattt cagtaggctc tatgggatta atcatcagcc tcctgtgtgt ctatttttgg 780

ctggagcgaa caatgcccag gatccccact ctcaaaaatc tggaagacct tgtgacggag 840

tatcacggca acttcagcgc gtggtctggc gtctctaaag gtcttgccga gagcctgcag 900

cctgattaca gtgagcgctt atgcctggtg agcgagatac cacctaaagg aggagccctt 960

ggtgaaggac cgggggcatc cccctgtaat caacactcac catactgggc ccccccctgc 1020

tataccctaa agcctgaaac t 1041

<210> 58
<211> 1218
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 58
ggcggcggcg gcgcggcgcc gaccgaaacc cagccgccgg tgaccaacct gagcgtgagc 60

gtggaaaacc tgtgcaccgt gatttggacc tggaacccgc cggaaggcgc gagcagcaac 120

tgcagcctgt ggtattttag ccattttggc gataaacagg ataaaaaaat tgcgccggaa 180

acccgccgca gcattgaagt gccgctgaac gaacgcattt gcctgcaggt gggcagccag 240

tgcagcacca acgaaagcga aaaaccgagc attctggtgg aaaaatgcat tagcccgccg 300

gaaggcgatc cggaaagcgc ggtgaccgaa ctgcagtgca tttggcataa cctgagctat 360

atgaaatgca gctggctgcc gggccgcaac accagcccgg ataccaacta taccctgtat 420

tattggcatc gcagcctgga aaaaattcat cagtgcgaaa acatttttcg cgaaggccag 480

tattttggct gcagctttga tctgaccaaa gtgaaagata gcagctttga acagcatagc 540

gtgcagatta tggtgaaaga taacgcgggc aaaattaaac cgagctttaa cattgtgccg 600

ctgaccagcc gcgtgaaacc ggatccgccg catattaaaa acctgagctt tcataacgat 660

gatctgtatg tgcagtggga aaacccgcag aactttatta gccgctgcct gttttatgaa 720

gtggaagtga acaacagcca gaccgaaacc cataacgtgt tttatgtgca ggaagcgaaa 780

tgcgaaaacc cggaatttga acgcaacgtg gaaaacacca gctgctttat ggtgccgggc 840

gtgctgccgg ataccctgaa caccgtgcgc attcgcgtga aaaccaacaa actgtgctat 900

gaagatgata aactgtggag caactggagc caggaaatga gcattggcaa aaaacgcaac 960

agcaccctgt atattaccat gctgctgatt gtgccggtga ttgtggcggg cgcgattatt 1020

gtgctgctgc tgtatctgaa acgcctgaaa attattattt ttccgccgat tccggatccg 1080

ggcaaaattt ttaaagaaat gtttggcgat cagaacgatg ataccctgca ttggaaaaaa 1140

tatgatattt atgaaaaaca gaccaaagaa gaaaccgata gcgtggtgct gattgaaaac 1200

ctgaaaaaag cgagccag 1218

<210> 59
<211> 1671
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 59
catgggaccg agctccccag tcctccttct gtttggttcg aagccgaatt ctttcaccat 60

attctgcact ggactcctat cccaaatcaa tcagaatcaa catgttacga ggtggcactg 120

ctgaggtacg gaatcgagtc ttggaatagc atttcaaact gtagccaaac cctgtcttac 180

gatcttaccg ctgtgacgct ggacctgtat catagcaacg gctaccgtgc cagggttagg 240

gcagttgatg gcagcagaca ctccaattgg acagttacga atacccgatt cagtgtcgac 300

gaggtgactt taactgtcgg gagtgttaac cttgaaattc acaacgggtt catattggga 360

aagatccagc tccccggcc aaaaatggcc ccagccaacg acacatacga gagtatattt 420

tctcatttta gagagtatga gatcgcaatc cgcaaggtgc ctgggaattt cacatttact 480

cataagaagg taaaacacga gaacttctcc ttgctcacct ccggcgaagt gggggagttc 540

tgcgtgcagg tgaagccctc ggtggcttca cgctccaata aaggcatgtg gagcaaagaa 600

gaatgtattt ctctgactcg gcagtacttt accgtgacta acgtaatcat atttttgcc 660

ttcgtgctcc tgctgtctgg tgccctggcc tattgcctgg cgcttcaact ttatgtgcgg 720

aggaggaaga agctgccgtc cgtgctgttg tttaagaaac cgtctccctt catttttatc 780

agccagcgcc cctcacccga aacacaggat actattcacc cccttgacga agaagccttc 840

cttaaagtgt cccccgagct aaaaaacctc gacctgcacg ggtccaccga tagcgggttt 900

ggtagcacca aaccatcctt gcaaaccgag gagccccagt tcttgctccc tgatccacac 960

ccacaggctg acagaacgtt gggaaacaga gagcccccag tcctgggggа ttcctgttcg 1020

tcagggtcta gtaatagtac cgatagcggg atttgcctgc aggagccgag cctgtcaccc 1080

tcaaccggtc cgacctggga gcagcaagta ggatctaact cccgcgggca ggatgactcc 1140

ggcatagacc tcgtacagaa ttcggaaggc cgggcgggtg acacacaggg cggctccgct 1200

ctgggccacc attccccacc agagcccgag gtccctggcg aggaggaccc tgcagccgtc 1260

gcttttcaag gctatctgcg tcagacacga tgtgctgaag agaaagctac taagacggga 1320

tgtcttgaag aggaatctcc gcttacagac ggattgggac caaagttcgg cagatgccta 1380

gtggatgagg cgggactaca tcctcccgca ttagcaaagg gctacctgaa gcaggatcca 1440

ctagaaatga cactggcctc atctggcgcc cctacaggac agtggaacca gccaaccgaa 1500

gagtggtcct tgctcgcttt aagctcttgc agtgacctgg gtatctcaga ttggagtttt 1560

gcacacgacc tcgcccctct gggttgcgtc gccgctcctg gtggactctt aggaagtttc 1620

aatagcgatc tcgtcactct gcctctcatc agtagcttac agagcagcga a 1671

<210> 60
<211> 918
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 60
atggtaccac cacctgaaaa tgtgaggatg aactctgtga attttaagaa cattctccag 60

tgggaaagtc ccgcttttgc taaggggaac ctgaccttca cagcccaata cttatcctac 120

cgaatcttcc aagacaagtg catgaatacc actttaactg aatgcgactt ctcaagcctg 180

tctaagtatg gcgatcatac actgcgggtt cgtgccgagt ttgccgacga gcactctgac 240

tgggtgaata taaccttctg ccccgtcgat gatactataa ttgggccacc aggtatgcaa 300

gttgaagtgt tggcagattc gctgcacatg aggtttctcg cccccaaaat cgagaacgag 360

tacgagacct ggacgatgaa gaatgtctac aactcttgga catataatgt tcagtattgg 420

aaaaacggaa ccgacgagaa gtttcagatc actccgcagt atgatttcga agtcctgaga 480

aacctcgagc cttggacaac ttactgtgtc caagtgcgcg gctttctccc tgaccggaac 540

aaggcaggag agtggtcaga accggtgtgt gagcagacca cccacgacga gacagtaccc 600

agctggatgg tagctgtgat ccttatggcc tccgtgttca tggtttgtct agctttgttg 660

ggctgttttg cccttctatg gtgcgtctat aaaaagacca aatacgcgtt ttcacctaga 720

aacagccttc cacagcacct caaggagttc ctggggcatc ctcatcacaa tacactgctg 780

ttcttctcct tccccctgag tgacgaaaac gatgtgtttg ataaactgtc cgtgattgca 840

gaagacagtg agtccggcaa acagaatcca ggagatagtt gcagcctggg tacgcctccc 900

ggacagggcc cccagagc 918

<210> 61
<211> 1569
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 61
gccgagagct gcactagccg gccccatata actgtggtcg aaggggagcc attctatctg 60

aaacattgtt cctgctccct tgcccatgaa attgaaacca caaccaagag ctggtacaaa 120

tctagtgggt ctcaagagca cgtcgagttg aacccaagat catctagtag gatcgccctg 180

catgactgcg ttctagagtt ttggccggtg gaattaaatg acaccggatc ttacttcttc 240

cagatgaaga attacaccca gaaatggaag ctgaacgtga tacgacgcaa caagcactca 300

tgcttcacag aacgtcaggt gacctcgaaa atcgtggaag tgaaaaagtt ctttcagatt 360

acatgcgaga acagttacta tcaaacgcta gtgaatagca cgagcctgta caaaaactgt 420

aagaaacttc tgctggagaa caataaaaac cctactatca aaaaaaatgc agaattcgag 480

gatcagggct attacagttg tgtgcatttt ctccaccaca atggtaagct attcaatatc 540

accaagacgt tcaacatcac cattgtggag gatcgctcca acatagtacc tgtgttattg 600

ggtcctaaac ttaaccacgt ggcagtggag ctggggaaaa acgtgagact caattgctca 660

gccttgctga acgaagagga tgttatttat tggatgtttg gggaagaaaa tggaagtgac 720

ccgaacattc acgaagagaa ggagatgcga atcatgacac cagaggggaa atggcacgcg 780

agtaaggtcc tcagaattga aaatattggc gaatcaaatc tcaacgtcct ctataactgt 840

accgtagcat ccacaggcgg cactgatact aagtccttta tccttgtgcg taaggccgat 900

atggctgaca tccccggcca cgtattcaca cggggaatga tcattgctgt tctgatcctg 960

gtggcagtag tgtgtttggt tactgtatgt gttatctacc gcgtggactt agttctgttt 1020

tataggcacc tgacccgaag agacgaaacc cttacagatg gcaagactta tgacgcgttc 1080

gtgtcgtatc ttaaagaatg ccggcccgag aatggagagg agcacacgtt tgctgtcgaa 1140

attctcccca gagtcctgga gaagcatttt ggttacaagc tgtgcatctt cgaaagagac 1200

gtcgtgcccg gtggcgccgt ggtcgacgag atacattccc tgatcgagaa gtcccgcagg 1260

ttgatcatag tcctctcaaa gtcttacatg agcaatgagg tgcggtacga actcgagagc 1320

ggactgcatg aggctttagt cgagaggaag attaagatta ttttgatcga gtttacacct 1380

gtgactgact ttaccttcct ccctcagtca ctgaaactcc ttaagtctca cagggtactg 1440

aagtggaaag ctgataaatc cctctcttat aatagccggt tttggaagaa cctattgtac 1500

ctgatgccag ccaaaacagt caagcctgga cgcgatgagc ccgaagttct gccagttctg 1560

agcgagtcc 1569

<210> 62
<211> 1740
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 62
tttaatatct ctggatgcag tacgaagaaa ttgctctgga catactctac taggagcgag 60

gaagagttcg tgcttttctg cgatttacca gaaccacaga aatcccattt ttgtcacaga 120

aatcgtcttt ctcctaagca ggttcccgaa cacctgccct tcatgggctc caacgacctt 180

agtgacgttc aatggtacca gcaaccaagc aatggcgacc ctctggaaga catacgcaag 240

agttaccccc atattatcca ggataaatgc acgctacatt tcctgacccc aggcgtcaac 300

aacagtggat cttatatatg taggcctaag atgatcaaat ccccctacga cgtggcttgt 360

tgcgtcaaga tgattctcga ggtgaagccc cagaccaatg cctcatgtga gtactccgcc 420

tctcacaaac aggaccttct gctggggtcg accggcagta taagctgccc atcgctctct 480

tgtcagagtg atgcgcagag ccctgctgtg acatggtaca aaaacggaaa gctactgtca 540

gtggagcgct caaaccgtat tgtagtagac gaagtctacg actatcacca aggcacctac 600

gtgtgcgatt atacacagtc tgatacggtc tccagttgga ctgtgcgggc cgtggtgcag 660

gtacggacca tcgtggggga cacaaaactg aagcccgaca tccttgatcc agttgaggac 720

accctggagg tggagctcgg gaagcccctg actatctcct gtaaagcaag atttggcttc 780

gagcgagtat ttaaccctgt tatcaagtgg tatattaaag atagcgatct cgagtgggag 840

gtatcagtgc ctgaagccaa atccatcaaa tcaactctga aggatgaaat cattgagcga 900

aatattattc ttgagaaggt tacccagcgc gatctccgcc gcaaatttgt ctgcttcgtg 960

caaaacagca taggcaatac tactcagagc gtgcagctga aagagaagcg tggtgtcgtc 1020

ttgttgtaca tcctgctcgg aacaattggt acactcgtag ccgtgttggc cgcctcagcc 1080

ctgctctaca ggcattggat tgaaatcgtg ttgctttaca ggacatatca gagcaaggac 1140

cagactctgg gcgacaaaaa ggatttcgat gcattcgtta gctatgctaa atggtcttca 1200

tttcctagcg aagctacatc ctccctgagc gaggaacact tagccttatc actgtttcca 1260

gatgtgttag aaaataaata tggctatagc ctgtgtttgc tggagcgcga cgttgcacca 1320

ggggggggtgt atgctgaaga catcgtcagc atcatcaagc ggtccaggag gggaatattt 1380

atattaagcc ctaactacgt caacggtcca tcgattttcg aactgcaggc tgcagtgaac 1440

ttggcgctcg atgaccagac gctcaagctg attctcatca agttctgcta ctttcaagag 1500

cccgagtctc ttcctcacct agtcaagaag gcgctgagag tcctgccgac cgtgacatgg 1560

cgaggactaa agtctgtgcc gccgaattcc agattctggg caaagatgcg gtatcatatg 1620

cccgttaaaa attcccaagg ttttacttgg aaccagctgc ggattaccag tcggatcttc 1680

cagtggaagg ggctgtctag aaccgagacc accggaagat ccagtcaacc caaagaatgg 1740

<210> 63
<211> 262
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 63
Gln Asp Pro Tyr Val Lys Glu Ala Glu Asn Leu Lys Lys Tyr Phe Asn
1 5 10 15

Ala Gly His Ser Asp Val Ala Asp Asn Gly Thr Leu Phe Leu Gly Ile
20 25 30

Leu Lys Asn Trp Lys Glu Glu Ser Asp Arg Lys Ile Met Gln Ser Gln

```
        35                  40                  45

Ile Val Ser Phe Tyr Phe Lys Leu Phe Lys Asn Phe Lys Asp Asp Gln
    50                  55                  60

Ser Ile Gln Lys Ser Val Glu Thr Ile Lys Glu Asp Met Asn Val Lys
65                  70                  75                  80

Phe Phe Asn Ser Asn Lys Lys Lys Arg Asp Asp Phe Glu Lys Leu Thr
                85                  90                  95

Asn Tyr Ser Val Thr Asp Leu Asn Val Gln Arg Lys Ala Ile His Glu
            100                 105                 110

Leu Ile Gln Val Met Ala Glu Leu Gly Ala Asn Val Ser Gly Glu Phe
        115                 120                 125

Val Lys Glu Ala Glu Asn Leu Lys Lys Tyr Phe Asn Ala Gly His Ser
    130                 135                 140

Asp Val Ala Asp Asn Gly Thr Leu Phe Leu Gly Ile Leu Lys Asn Trp
145                 150                 155                 160

Lys Glu Glu Ser Asp Arg Lys Ile Met Gln Ser Gln Ile Val Ser Phe
                165                 170                 175

Tyr Phe Lys Leu Phe Lys Asn Phe Lys Asp Asp Gln Ser Ile Gln Lys
            180                 185                 190

Ser Val Glu Thr Ile Lys Glu Asp Met Asn Val Lys Phe Phe Asn Ser
        195                 200                 205

Asn Lys Lys Lys Arg Asp Asp Phe Glu Lys Leu Thr Asn Tyr Ser Val
    210                 215                 220

Thr Asp Leu Asn Val Gln Arg Lys Ala Ile His Glu Leu Ile Gln Val
225                 230                 235                 240
```

Met Ala Glu Leu Ser Pro Ala Ala Lys Thr Gly Lys Arg Lys Arg Ser
245 250 255

Gln Met Leu Phe Arg Gly
260

<210> 64
<211> 168
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 64
Asn Tyr Pro Lys Lys Lys Met Glu Lys Arg Phe Val Phe Asn Lys Ile
1 5 10 15

Glu Ile Asn Asn Lys Leu Glu Phe Glu Ser Ala Gln Phe Pro Asn Trp
20 25 30

Tyr Ile Ser Thr Ser Gln Ala Glu Asn Met Pro Val Phe Leu Gly Gly
35 40 45

Thr Lys Gly Gly Gln Asp Ile Thr Asp Phe Thr Met Gln Phe Val Ser
50 55 60

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
65 70 75 80

Ala Pro Val Arg Ser Leu Asn Cys Thr Leu Arg Asp Ser Gln Gln Lys
85 90 95

Ser Leu Val Met Ser Gly Pro Tyr Glu Leu Lys Ala Leu His Leu Gln
100 105 110

Gly Gln Asp Met Glu Gln Gln Val Val Phe Ser Met Ser Phe Val Gln
115 120 125

Gly Glu Glu Ser Asn Asp Lys Ile Pro Val Ala Leu Gly Leu Lys Glu
130 135 140

Lys Asn Leu Tyr Leu Ser Cys Val Leu Lys Asp Asp Lys Pro Thr Leu
145 150 155 160

Gln Leu Glu Ser Val Asp Pro Lys
165

<210> 65
<211> 521
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 65
Ile Trp Glu Leu Lys Lys Asp Val Tyr Val Val Glu Leu Asp Trp Tyr
1 5 10 15

Pro Asp Ala Pro Gly Glu Met Val Val Leu Thr Cys Asp Thr Pro Glu
20 25 30

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

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

Gln Tyr Thr Cys His Lys Gly Gly Glu Val Leu Ser His Ser Leu Leu
65 70 75 80

Leu Leu His Lys Lys Glu Asp Gly Ile Trp Ser Thr Asp Ile Leu Lys
85 90 95

Asp Gln Lys Glu Pro Lys Asn Lys Thr Phe Leu Arg Cys Glu Ala Lys
100 105 110

```
Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp Leu Thr Thr Ile Ser Thr
        115                 120                 125

Asp Leu Thr Phe Ser Val Lys Ser Ser Arg Gly Ser Ser Asp Pro Gln
    130                 135                 140

Gly Val Thr Cys Gly Ala Ala Thr Leu Ser Ala Glu Arg Val Arg Gly
145                 150                 155                 160

Asp Asn Lys Glu Tyr Glu Tyr Ser Val Glu Cys Gln Glu Asp Ser Ala
                165                 170                 175

Cys Pro Ala Ala Glu Glu Ser Leu Pro Ile Glu Val Met Val Asp Ala
            180                 185                 190

Val His Lys Leu Lys Tyr Glu Asn Tyr Thr Ser Ser Phe Phe Ile Arg
        195                 200                 205

Asp Ile Ile Lys Pro Asp Pro Pro Lys Asn Leu Gln Leu Lys Pro Leu
    210                 215                 220

Lys Asn Ser Arg Gln Val Glu Val Ser Trp Glu Tyr Pro Asp Thr Trp
225                 230                 235                 240

Ser Thr Pro His Ser Tyr Phe Ser Leu Thr Phe Cys Val Gln Val Gln
                245                 250                 255

Gly Lys Ser Lys Arg Glu Lys Lys Asp Arg Val Phe Thr Asp Lys Thr
            260                 265                 270

Ser Ala Thr Val Ile Cys Arg Lys Asn Ala Ser Ile Ser Val Arg Ala
        275                 280                 285

Gln Asp Arg Tyr Tyr Ser Ser Ser Trp Ser Glu Trp Ala Ser Val Pro
    290                 295                 300

Cys Ser Gly Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly
```

```
305                 310                 315                 320

Ser Thr Lys Gly Arg Asn Leu Pro Val Ala Thr Pro Asp Pro Gly Met
                325                 330                 335

Phe Pro Cys Leu His His Ser Gln Asn Leu Leu Arg Ala Val Ser Asn
            340                 345                 350

Met Leu Gln Lys Ala Arg Gln Thr Leu Glu Phe Tyr Pro Cys Thr Ser
        355                 360                 365

Glu Glu Ile Asp His Glu Asp Ile Thr Lys Asp Lys Thr Ser Thr Val
    370                 375                 380

Glu Ala Cys Leu Pro Leu Glu Leu Thr Lys Asn Glu Ser Cys Leu Asn
385                 390                 395                 400

Ser Arg Glu Thr Ser Phe Ile Thr Asn Gly Ser Cys Leu Ala Ser Arg
                405                 410                 415

Lys Thr Ser Phe Met Met Ala Leu Cys Leu Ser Ser Ile Tyr Glu Asp
            420                 425                 430

Leu Lys Met Tyr Gln Val Glu Phe Lys Thr Met Asn Ala Lys Leu Leu
        435                 440                 445

Met Asp Pro Lys Arg Gln Ile Phe Leu Asp Gln Asn Met Leu Ala Val
    450                 455                 460

Ile Asp Glu Leu Met Gln Ala Leu Asn Phe Asn Ser Glu Thr Val Pro
465                 470                 475                 480

Gln Lys Ser Ser Leu Glu Glu Pro Asp Phe Tyr Lys Thr Lys Ile Lys
                485                 490                 495

Leu Cys Ile Leu Leu His Ala Phe Arg Ile Arg Ala Val Thr Ile Asp
            500                 505                 510
```

Arg Val Met Ser Tyr Leu Asn Ala Ser
515 520

<210> 66
<211> 134
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 66
Asn Thr Thr Glu Lys Glu Thr Phe Cys Arg Ala Ala Thr Val Leu Arg
1 5 10 15

Gln Phe Tyr Ser His His Glu Lys Asp Thr Arg Cys Leu Gly Ala Thr
20 25 30

Ala Gln Gln Phe His Arg His Lys Gln Leu Ile Arg Phe Leu Lys Arg
35 40 45

Leu Asp Arg Asn Leu Trp Gly Leu Ala Gly Leu Asn Ser Cys Pro Val
50 55 60

Lys Glu Ala Asn Gln Ser Thr Leu Glu Asn Phe Leu Glu Arg Leu Lys
65 70 75 80

Thr Ile Met Arg Glu Lys Tyr Ser Lys Cys Ser Ser Gly Gly Asn Gly
85 90 95

Gly His Lys Cys Asp Ile Thr Leu Gln Glu Ile Ile Lys Thr Leu Asn
100 105 110

Ser Leu Thr Glu Gln Lys Thr Leu Cys Thr Glu Leu Thr Val Thr Asp
115 120 125

Ile Phe Ala Ala Ser Lys
130

<210> 67
<211> 166
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 67
Ser Pro Gly Gln Gly Thr Gln Ser Glu Asn Ser Cys Thr His Phe Pro
1 5 10 15

Gly Asn Leu Pro Asn Met Leu Arg Asp Leu Arg Asp Ala Phe Ser Arg
20 25 30

Val Lys Thr Phe Phe Gln Met Lys Asp Gln Leu Asp Asn Leu Leu Leu
35 40 45

Lys Glu Ser Leu Leu Glu Asp Phe Lys Gly Tyr Leu Gly Cys Gln Ala
50 55 60

Leu Ser Glu Met Ile Gln Phe Tyr Leu Glu Glu Val Met Pro Gln Ala
65 70 75 80

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

Asn Leu Lys Thr Leu Arg Leu Arg Leu Arg Arg Cys His Arg Phe Leu
100 105 110

Pro Cys Glu Asn Gly Gly Gly Ser Gly Gly Lys Ser Lys Ala Val Glu
115 120 125

Gln Val Lys Asn Ala Phe Asn Lys Leu Gln Glu Lys Gly Ile Tyr Lys
130 135 140

Ala Met Ser Glu Phe Asp Ile Phe Ile Asn Tyr Ile Glu Ala Tyr Met
145 150 155 160

Thr Met Lys Ile Arg Asn
165

<210> 68
<211> 175
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 68
Gly Tyr Leu Gly Cys Gln Ala Leu Ser Glu Met Ile Gln Phe Tyr Leu
1 5 10 15

Glu Glu Val Met Pro Gln Ala Glu Asn Gln Asp Pro Asp Ile Lys Ala
20 25 30

His Val Asn Ser Leu Gly Glu Asn Leu Lys Thr Leu Arg Leu Arg Leu
35 40 45

Arg Arg Cys His Arg Phe Leu Pro Cys Glu Asn Lys Ser Lys Ala Val
50 55 60

Glu Gln Val Lys Asn Ala Phe Asn Lys Leu Gln Glu Lys Gly Ile Tyr
65 70 75 80

Lys Ala Met Ser Glu Phe Asp Ile Phe Ile Asn Tyr Ile Glu Ala Tyr
85 90 95

Met Thr Met Lys Ile Arg Asn Gly Gly Gly Gly Ser Gly Gly Gly Gly
100 105 110

Ser Gly Gly Gly Gly Ser Ser Pro Gly Gln Gly Thr Gln Ser Glu Asn
115 120 125

Ser Cys Thr His Phe Pro Gly Asn Leu Pro Asn Met Leu Arg Asp Leu
130 135 140

Arg Asp Ala Phe Ser Arg Val Lys Thr Phe Phe Gln Met Lys Asp Gln
145 150 155 160

Leu Asp Asn Leu Leu Leu Lys Glu Ser Leu Leu Glu Asp Phe Lys
165 170 175

<210> 69
<211> 335
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 69
Ser Pro Gly Gln Gly Thr Gln Ser Glu Asn Ser Cys Thr His Phe Pro
1 5 10 15

Gly Asn Leu Pro Asn Met Leu Arg Asp Leu Arg Asp Ala Phe Ser Arg
20 25 30

Val Lys Thr Phe Phe Gln Met Lys Asp Gln Leu Asp Asn Leu Leu Leu
35 40 45

Lys Glu Ser Leu Leu Glu Asp Phe Lys Gly Tyr Leu Gly Cys Gln Ala
50 55 60

Leu Ser Glu Met Ile Gln Phe Tyr Leu Glu Glu Val Met Pro Gln Ala
65 70 75 80

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

Asn Leu Lys Thr Leu Arg Leu Arg Leu Arg Arg Cys His Arg Phe Leu
100 105 110

Pro Cys Glu Asn Lys Ser Lys Ala Val Glu Gln Val Lys Asn Ala Phe
115 120 125

```
Asn Lys Leu Gln Glu Lys Gly Ile Tyr Lys Ala Met Ser Glu Phe Asp
    130                 135                 140

Ile Phe Ile Asn Tyr Ile Glu Ala Tyr Met Thr Met Lys Ile Arg Asn
145                 150                 155                 160

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser
                165                 170                 175

Pro Gly Gln Gly Thr Gln Ser Glu Asn Ser Cys Thr His Phe Pro Gly
            180                 185                 190

Asn Leu Pro Asn Met Leu Arg Asp Leu Arg Asp Ala Phe Ser Arg Val
        195                 200                 205

Lys Thr Phe Phe Gln Met Lys Asp Gln Leu Asp Asn Leu Leu Leu Lys
    210                 215                 220

Glu Ser Leu Leu Glu Asp Phe Lys Gly Tyr Leu Gly Cys Gln Ala Leu
225                 230                 235                 240

Ser Glu Met Ile Gln Phe Tyr Leu Glu Glu Val Met Pro Gln Ala Glu
                245                 250                 255

Asn Gln Asp Pro Asp Ile Lys Ala His Val Asn Ser Leu Gly Glu Asn
            260                 265                 270

Leu Lys Thr Leu Arg Leu Arg Leu Arg Arg Cys His Arg Phe Leu Pro
        275                 280                 285

Cys Glu Asn Lys Ser Lys Ala Val Glu Gln Val Lys Asn Ala Phe Asn
    290                 295                 300

Lys Leu Gln Glu Lys Gly Ile Tyr Lys Ala Met Ser Glu Phe Asp Ile
305                 310                 315                 320

Phe Ile Asn Tyr Ile Glu Ala Tyr Met Thr Met Lys Ile Arg Asn
```

325 330 335

<210> 70
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 70
Val Ser Ala Gly Gln Phe Ser Ser Leu His Val Arg Asp Thr Lys Ile
1 5 10 15

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

Phe Arg Glu Gly Arg Phe Asn Gly Gly Gly Gly Ser Leu Thr Cys Leu
35 40 45

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

Glu Leu Ile Glu Glu Leu Val Asn Ile Thr Gln Asn Gln Lys Ala Pro
65 70 75 80

Leu Cys Asn Gly Ser Met Val Trp Ser Ile Asn Leu Thr Ala Gly Met
85 90 95

Tyr Cys Ala Ala Leu Glu Ser Leu Ile Asn Val Ser Gly Cys Ser Ala
100 105 110

Ile Glu Lys Thr Gln Arg Met Leu Ser Gly Phe Cys Pro His Lys
115 120 125

<210> 71
<211> 786
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 71
caggatccct acgtgaaaga agccgagaac ttaaagaaat atttcaacgc aggccattca 60

gacgtcgctg ataatggaac actttttttg ggcattctga aaaattggaa ggaagaatcg 120

gaccgaaaaa ttatgcagag ccagatagta tccttttatt tcaagttatt taaaaacttc 180

aaagacgatc agtctatcca aaaaagtgtg gagactatca aggaggacat gaatgtgaag 240

ttcttcaaca gcaataaaaa gaaacgggat gactttgaaa agctcaccaa ttactcagtc 300

actgatctga acgtgcagag aaaggcgatt catgagctaa tccaagtgat ggctgagctc 360

ggagccaacg tgagcggaga gtttgtgaag gaagccgaga atctgaagaa gtatttcaac 420

gctggtcact ctgacgtggc agataacggc acgctgttcc tggggatcct gaagaattgg 480

aaagaagagt ccgacaggaa gattatgcaa tcccagatcg tcagtttcta ctttaagctt 540

ttcaagaatt tcaaagacga tcagagtatc cagaagtctg tcgagaccat aaaagaagac 600

atgaatgtaa agtttttaa ttcaaacaaa aagaagcgtg acgatttcga aaaactcacc 660

aactactccg ttacagatct gaacgttcag agaaaagcca ttcacgagtt gatccaagtt 720

atggccgagc tctctcctgc agctaagaca ggtaagagga aacggagcca gatgctgttt 780

cgcggg 786

<210> 72
<211> 504
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 72
aactacccca aaaaaaagat ggagaagcgg tttgttttta acaagattga gatcaacaat 60

aagctggaat tcgagtctgc gcagttccca aactggtata ttagcacatc gcaagcagaa 120

aatatgcccg tgttcctcgg cggaaccaaa ggcgggcagg atatcacaga ctttacgatg 180

cagttcgtgt catctggtgg tggtggaagc ggcgggggag gcagtggggg aggcgggtcc 240

gccccagtga ggtccctgaa ctgtacctta agagactcac agcaaaagtc cctggtcatg 300

tctggcccct acgaactgaa agcccttcac ctgcaggggc aagatatgga gcagcaggtg 360

gttttcagca tgagttttgt acagggcgaa gagagtaatg acaagatacc tgtggctcta 420

ggactcaagg aaaagaattt gtatctcagc tgcgtcctga aggacgataa acctactctt 480

cagttggagt ccgtcgatcc gaaa 504

<210> 73
<211> 1563
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 73
atctgggagc tcaaaaagga tgtttatgtg gtcgaacttg actggtaccc ggacgcacca 60

ggggagatgg tggtgttgac ctgcgacacc cccgaagagg acgggattac atggactttg 120

gaccagtcca gtgaagtcct gggctcggga aagaccctga ctatccaggt gaaggagttc 180

ggagatgctg gacaatatac atgccacaag ggcggggaag ttttgagcca ttccctcctg 240

ctgctgcata aaaaagagga tggtatttgg agcactgata ttctgaaaga ccagaaggaa 300

cccaagaaca aaacttttct gcggtgtgag gccaagaatt acagtggaag attcacctgt 360

tggtggttaa ccacaatctc taccgatctt acctttttccg tcaaatcaag tcgcggcagc 420

agcgatccac agggcgtgac gtgcggcgct gccacactaa gcgcggagag agtgcggggt 480

gacaacaagg aatacgagta ctccgttgag tgtcaagaag actctgcatg ccctgccgca 540

gaggaatcat taccgatcga agtaatggtg gatgctgttc acaaactgaa gtatgaaaac 600

tacacttctt catttttcat aagggacatt atcaagcctg atcctccaaa gaacctccaa 660

cttaaaccac tcaagaatag ccgtcaggta gaggtgtcct gggagtaccc cgatacctgg 720

tcaacgcccc actcatattt ctccctgacg ttctgtgtgc aggtgcaggg gaaatccaag 780

agggagaaga aagacagggt ctttacagat aagacatctg ccactgtcat ctgcagaaaa 840

aatgcctcta tatccgtgcg agcccaggac cgctactatt ctagtagctg gagcgagtgg 900

gctagtgtac cttgttcggg ctcaaccagc ggatccggga aacccggttc tggcgagggg 960

agtacaaagg gacgaaatct gccagtggct acccccgacc cgggcatgtt tccctgcctc 1020

catcatagcc agaatctgct cagagcggtc agcaacatgc tacagaaggc ccgccagacc 1080

ttagagtttt acccttgcac ctctgaggaa atcgatcacg aagacatcac caaagataag 1140

actagcaccg ttgaagcctg tctcccattg gaacttacaa aaaatgaatc ttgtctgaat 1200

tccagagaga catcttttat cactaatgga agttgcctcg ccagtcggaa aacttccttc 1260

atgatggccc tgtgtctgag ttcaatctac gaggatctta agatgtatca agtggaattc 1320

aaaacgatga acgcaaaact gttgatggat cctaagaggc agatattttt ggatcagaac 1380

atgttagctg tgatcgacga gctgatgcaa gcactcaact tcaactcaga gacagtcccc 1440

cagaagtcct ccctggagga gcctgacttc tacaagacga aaattaagct atgcattctg 1500

cttcacgcat tcaggatacg ggccgtaaca attgaccgtg tgatgagcta tctgaacgct 1560

tcg 1563

<210> 74
<211> 402
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 74
aatacgactg agaaagagac cttttgtagg gctgccacag tcctgcggca gttctatagt 60

caccatgaga aagacaccag atgtctgggg gcaaccgctc agcaattcca tagacacaag 120

cagttaatcc gatttctgaa gcggcttgat cgtaacttgt ggggactagc cggcctgaac 180

tcatgccccg tgaaagaagc gaatcagtcc actcttgaga acttcctcga aaggctcaag 240

acaattatgc gcgaaaagta cagcaagtgc agctctggcg gaaacggtgg gcacaagtgt 300

gatattacgc tccaagaaat catcaagact ctgaactccc tgaccgagca gaaaacactt 360

tgcactgagt tgacagtgac cgacatattc gccgctagca aa 402

<210> 75
<211> 498
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 75
tcgcctggcc agggaacgca gagtgaaaat agctgtaccc actttcccgg caacctacca 60

aatatgctca gagatctgcg ggatgcattc tcccgggtga agacattttt ccaaatgaag 120

gatcagttgg acaaccttct gttgaaggag tcactcttag aggacttcaa gggatacctg 180

gggtgccaag ccctgtctga gatgattcag ttctacctcg aagaggtaat gccacaggcc 240

gaaaaccagg accctgatat aaaagctcat gtcaatagtt taggcgagaa tctgaaaact 300

ctcaggctgc gtctgcgaag atgccaccgc tttctgccct gtgagaacgg gggagggtct 360

ggtggcaaaa gcaaagctgt ggagcaagtt aaaaatgcat tcaacaaact tcaggagaag 420

ggtatttata aggcgatgtc cgaatttgac atctttatta attacatcga agcctatatg 480

accatgaaga tcaggaac 498

<210> 76
<211> 525
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 76
ggttacttgg gctgtcaggc tctgagtgaa atgattcagt tctatcttga agaggttatg 60

cctcaggcgg agaaccaaga cccagacatc aaggcccatg tgaactctct cggggagaat 120

ctgaaaacac tgcgactgcg gttaagacgt tgccacaggt tcctaccctg cgaaaataaa 180

agcaaggccg tcgagcaagt gaaaaacgca ttcaataaac tccaggaaaa gggaatttac 240

aaggccatgt ccgagtttga tatctttata aactatattg aggcttacat gaccatgaag 300

atccgcaatg gtggtggtgg aagcggcggg ggaggcagtg ggggaggcgg gtcctcccct 360

ggccagggaa ctcagtcaga aaatagctgc acacactttc cagggaatct ccccaacatg 420

ttgagagatc tgagggacgc cttctctcgg gtgaaaacct ttttccaaat gaaagaccag 480

ctggacaacc tccttctgaa ggagagttta ctagaggatt tcaag 525

<210> 77
<211> 1005
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 77
tctccgggac agggaaccca gagcgaaaac tcctgcactc attttcctgg caacctcccc 60

aatatgctgc gagacttgcg cgacgcattc tcaagggtga agacgttctt ccagatgaag 120

gatcaactgg acaacttatt gctgaaagaa tctctgctcg aggatttcaa aggatacctg 180

ggatgtcagg cactgagcga gatgatccaa ttttacctgg aggaggtcat gcctcaggct 240

gagaatcagg atcctgacat caaggcccac gtgaacagtc ttggagagaa tcttaagacc 300

cttaggctga gacttagacg gtgtcaccgc tttctgccct gcgaaaataa atcaaaagcg 360

gtggaacagg ttaagaacgc ttttaataag ctgcaggaaa agggcattta taaagctatg 420

agtgaatttg acattttcat taactatatc gaggcctata tgacaatgaa aattaggaac 480

gggggaggcg ggagcggggg cggcggctca ggcggtgggg ggtcctctcc aggtcaagga 540

acacaatctg agaactcctg cacacacttc cccggcaatc taccaaacat gctcagagat 600

ctcagggacg cgttcagtcg agtgaaaact ttcttccaga tgaaggatca gctggacaat 660

ctactgctga aagaaagctt gcttgaggat tttaaaggct atctgggttg tcaggcctta 720

tcggagatga tccagtttta cttggaggaa gttatgcctc aggcagaaaa ccaagacccc 780

gatatcaagg ctcatgtgaa ttccctcggt gaaaacctaa agaccttacg cctgcgtctc 840

agacggtgtc atcggttttt gccatgcgag aataagtcca aagccgtaga gcaggtcaag 900

aatgccttca ataagctcca ggagaagggg atatacaaag caatgagcga atttgacatt 960

ttcatcaact acatagaggc ctacatgacc atgaagatcc ggaac 1005

<210> 78
<211> 381
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 78
gtgagcgcgg gccagtttag cagcctgcat gtgcgcgata ccaaaattga agtggcgcag 60

tttgtgaaag atctgctgct gcatctgaaa aaactgtttc gcgaaggccg ctttaacgga 120

ggaggtggat ctctgacctg cctgggcggc tttgcgagcc cgggcccggt gccgccgagc 180

accgcgctgc gcgaactgat tgaagaactg gtgaacatta cccagaacca gaaagcgccg 240

ctgtgcaacg gcagcatggt gtggagcatt aacctgaccg cgggcatgta ttgcgcggcg 300

ctggaaagcc tgattaacgt gagcggctgc agcgcgattg aaaaaaccca gcgcatgctg 360

agcggctttt gcccgcataa a 381

<210> 79
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 79
ggtggtggtg gaagcggcgg gggaggcagt gggggaggcg ggtcc 45

<210> 80
<211> 54
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 80
ggctcaacca gcggatccgg gaaacccggt tctggcgagg ggagtacaaa ggga 54

<210> 81
<211> 78
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 81
tctggaggcg gaagcggggg tggcggcagc ggcggtggag gatcaggtgg cgggggggtcc 60

gggggcggaa gtctgcag 78

<210> 82
<211> 63
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 82
atggccttgc ctgtgaccgc attactgctt ccactcgccc tgctcctgca cgctgcgaga 60

ccc 63

<210> 83
<211> 742
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 83
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

```
His Ala Ala Arg Pro Cys Asp Leu Pro Gln Thr His Ser Leu Gly Ser
            20                  25                  30

Arg Arg Thr Leu Met Leu Leu Ala Gln Met Arg Lys Ile Ser Leu Phe
        35                  40                  45

Ser Cys Leu Lys Asp Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe
    50                  55                  60

Gly Asn Gln Phe Gln Lys Ala Glu Thr Ile Pro Val Leu His Glu Met
65                  70                  75                  80

Ile Gln Gln Ile Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala
                85                  90                  95

Trp Asp Glu Thr Leu Leu Asp Lys Phe Tyr Thr Glu Leu Tyr Gln Gln
            100                 105                 110

Leu Asn Asp Leu Glu Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu
        115                 120                 125

Thr Pro Leu Met Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe
    130                 135                 140

Gln Arg Ile Thr Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala
145                 150                 155                 160

Trp Glu Val Val Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr
                165                 170                 175

Asn Leu Gln Glu Ser Leu Arg Ser Lys Glu Ser Gly Gly Gly Ser Gly
            180                 185                 190

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
        195                 200                 205

Gly Ser Leu Gln Lys Asn Leu Lys Ser Pro Gln Lys Val Glu Val Asp
```

```
    210                 215                 220

Ile Ile Asp Asp Asn Phe Ile Leu Arg Trp Asn Arg Ser Asp Glu Ser
225                 230                 235                 240

Val Gly Asn Val Thr Phe Ser Phe Asp Tyr Gln Lys Thr Gly Met Asp
                245                 250                 255

Asn Trp Ile Lys Leu Ser Gly Cys Gln Asn Ile Thr Ser Thr Lys Cys
            260                 265                 270

Asn Phe Ser Ser Leu Lys Leu Asn Val Tyr Glu Glu Ile Lys Leu Arg
        275                 280                 285

Ile Arg Ala Glu Lys Glu Asn Thr Ser Ser Trp Tyr Glu Val Asp Ser
    290                 295                 300

Phe Thr Pro Phe Arg Lys Ala Gln Ile Gly Pro Pro Glu Val His Leu
305                 310                 315                 320

Glu Ala Glu Asp Lys Ala Ile Val Ile His Ile Ser Pro Gly Thr Lys
                325                 330                 335

Asp Ser Val Met Trp Ala Leu Asp Gly Leu Ser Phe Thr Tyr Ser Leu
            340                 345                 350

Val Ile Trp Lys Asn Ser Ser Gly Val Glu Glu Arg Ile Glu Asn Ile
        355                 360                 365

Tyr Ser Arg His Lys Ile Tyr Lys Leu Ser Pro Glu Thr Thr Tyr Cys
    370                 375                 380

Leu Lys Val Lys Ala Ala Leu Leu Thr Ser Trp Lys Ile Gly Val Tyr
385                 390                 395                 400

Ser Pro Val His Cys Ile Lys Thr Thr Val Glu Asn Glu Leu Pro Pro
                405                 410                 415
```

```
Pro Glu Asn Ile Glu Val Ser Val Gln Asn Gln Asn Tyr Val Leu Lys
            420                 425                 430

Trp Asp Tyr Thr Tyr Ala Asn Met Thr Phe Gln Val Gln Trp Leu His
        435                 440                 445

Ala Phe Leu Lys Arg Asn Pro Gly Asn His Leu Tyr Lys Trp Lys Gln
    450                 455                 460

Ile Pro Asp Cys Glu Asn Val Lys Thr Thr Gln Cys Val Phe Pro Gln
465                 470                 475                 480

Asn Val Phe Gln Lys Gly Ile Tyr Leu Leu Arg Val Gln Ala Ser Asp
                485                 490                 495

Gly Asn Asn Thr Ser Phe Trp Ser Glu Glu Ile Lys Phe Asp Thr Glu
            500                 505                 510

Ile Gln Ala Phe Leu Leu Pro Pro Val Phe Asn Ile Arg Ser Leu Ser
        515                 520                 525

Asp Ser Phe His Ile Tyr Ile Gly Ala Pro Lys Gln Ser Gly Asn Thr
    530                 535                 540

Pro Val Ile Gln Asp Tyr Pro Leu Ile Tyr Glu Ile Ile Phe Trp Glu
545                 550                 555                 560

Asn Thr Ser Asn Ala Glu Arg Lys Ile Ile Glu Lys Lys Thr Asp Val
                565                 570                 575

Thr Val Pro Asn Leu Lys Pro Leu Thr Val Tyr Cys Val Lys Ala Arg
            580                 585                 590

Ala His Thr Met Asp Glu Lys Leu Asn Lys Ser Ser Val Phe Ser Asp
        595                 600                 605

Ala Val Cys Glu Lys Thr Lys Pro Gly Asn Thr Ser Lys Ile Trp Leu
```

610 615 620

Ile Val Gly Ile Cys Ile Ala Leu Phe Ala Leu Pro Phe Val Ile Tyr
625 630 635 640

Ala Ala Lys Val Phe Leu Arg Cys Ile Asn Tyr Val Phe Phe Pro Ser
645 650 655

Leu Lys Pro Ser Ser Ser Ile Asp Glu Tyr Phe Ser Glu Gln Pro Leu
660 665 670

Lys Asn Leu Leu Leu Ser Thr Ser Glu Glu Gln Ile Glu Lys Cys Phe
675 680 685

Ile Ile Glu Asn Ile Ser Thr Ile Ala Thr Val Glu Glu Thr Asn Gln
690 695 700

Thr Asp Glu Asp His Lys Lys Tyr Ser Ser Gln Thr Ser Gln Asp Ser
705 710 715 720

Gly Asn Tyr Ser Asn Glu Asp Glu Ser Glu Ser Lys Thr Ser Glu Glu
725 730 735

Leu Gln Gln Asp Phe Val
740

<210> 84
<211> 701
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 84
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Cys Asp Leu Pro Gln Thr His Ser Leu Gly Ser

```
            20                  25                  30

Arg Arg Thr Leu Met Leu Leu Ala Gln Met Arg Lys Ile Ser Leu Phe
        35                  40                  45

Ser Cys Leu Lys Asp Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe
    50                  55                  60

Gly Asn Gln Phe Gln Lys Ala Glu Thr Ile Pro Val Leu His Glu Met
65                  70                  75                  80

Ile Gln Gln Ile Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala
                85                  90                  95

Trp Asp Glu Thr Leu Leu Asp Lys Phe Tyr Thr Glu Leu Tyr Gln Gln
            100                 105                 110

Leu Asn Asp Leu Glu Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu
        115                 120                 125

Thr Pro Leu Met Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe
    130                 135                 140

Gln Arg Ile Thr Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala
145                 150                 155                 160

Trp Glu Val Val Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr
                165                 170                 175

Asn Leu Gln Glu Ser Leu Arg Ser Lys Glu Ser Gly Gly Gly Ser Gly
            180                 185                 190

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
        195                 200                 205

Gly Ser Leu Gln Ile Ser Tyr Asp Ser Pro Asp Tyr Thr Asp Glu Ser
    210                 215                 220
```

```
Cys Thr Phe Lys Ile Ser Leu Arg Asn Phe Arg Ser Ile Leu Ser Trp
225                 230                 235                 240


Glu Leu Lys Asn His Ser Ile Val Pro Thr His Tyr Thr Leu Leu Tyr
                245                 250                 255


Thr Ile Met Ser Lys Pro Glu Asp Leu Lys Val Val Lys Asn Cys Ala
            260                 265                 270


Asn Thr Thr Arg Ser Phe Cys Asp Leu Thr Asp Glu Trp Arg Ser Thr
        275                 280                 285


His Glu Ala Tyr Val Thr Val Leu Glu Gly Phe Ser Gly Asn Thr Thr
    290                 295                 300


Leu Phe Ser Cys Ser His Asn Phe Trp Leu Ala Ile Asp Met Ser Phe
305                 310                 315                 320


Glu Pro Pro Glu Phe Glu Ile Val Gly Phe Thr Asn His Ile Asn Val
                325                 330                 335


Met Val Lys Phe Pro Ser Ile Val Glu Glu Glu Leu Gln Phe Asp Leu
            340                 345                 350


Ser Leu Val Ile Glu Glu Gln Ser Glu Gly Ile Val Lys Lys His Lys
        355                 360                 365


Pro Glu Ile Lys Gly Asn Met Ser Gly Asn Phe Thr Tyr Ile Ile Asp
    370                 375                 380


Lys Leu Ile Pro Asn Thr Asn Tyr Cys Val Ser Val Tyr Leu Glu His
385                 390                 395                 400


Ser Asp Glu Gln Ala Val Ile Lys Ser Pro Leu Lys Cys Thr Leu Leu
                405                 410                 415


Pro Pro Gly Gln Glu Ser Glu Ser Ala Glu Ser Ala Lys Ile Gly Gly
```

```
            420                 425                 430

Ile Ile Thr Val Phe Leu Ile Ala Leu Val Leu Thr Ser Thr Ile Val
        435                 440                 445

Thr Leu Lys Trp Ile Gly Tyr Ile Cys Leu Arg Asn Ser Leu Pro Lys
    450                 455                 460

Val Leu Asn Phe His Asn Phe Leu Ala Trp Pro Phe Pro Asn Leu Pro
465                 470                 475                 480

Pro Leu Glu Ala Met Asp Met Val Glu Val Ile Tyr Ile Asn Arg Lys
                485                 490                 495

Lys Lys Val Trp Asp Tyr Asn Tyr Asp Asp Glu Ser Asp Ser Asp Thr
            500                 505                 510

Glu Ala Ala Pro Arg Thr Ser Gly Gly Gly Tyr Thr Met His Gly Leu
        515                 520                 525

Thr Val Arg Pro Leu Gly Gln Ala Ser Ala Thr Ser Thr Glu Ser Gln
    530                 535                 540

Leu Ile Asp Pro Glu Ser Glu Glu Glu Pro Asp Leu Pro Glu Val Asp
545                 550                 555                 560

Val Glu Leu Pro Thr Met Pro Lys Asp Ser Pro Gln Gln Leu Glu Leu
                565                 570                 575

Leu Ser Gly Pro Cys Glu Arg Arg Lys Ser Pro Leu Gln Asp Pro Phe
            580                 585                 590

Pro Glu Glu Asp Tyr Ser Ser Thr Glu Gly Ser Gly Gly Arg Ile Thr
        595                 600                 605

Phe Asn Val Asp Leu Asn Ser Val Phe Leu Arg Val Leu Asp Asp Glu
    610                 615                 620
```

Asp Ser Asp Asp Leu Glu Ala Pro Leu Met Leu Ser Ser His Leu Glu
625 630 635 640

Glu Met Val Asp Pro Glu Asp Pro Asp Asn Val Gln Ser Asn His Leu
645 650 655

Leu Ala Ser Gly Glu Gly Thr Gln Pro Thr Phe Pro Ser Pro Ser Ser
660 665 670

Glu Gly Leu Trp Ser Glu Asp Ala Pro Ser Asp Gln Ser Asp Thr Ser
675 680 685

Glu Ser Asp Val Asp Leu Gly Asp Gly Tyr Ile Met Arg
690 695 700

<210> 85
<211> 743
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 85
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Met Ser Tyr Asn Leu Leu Gly Phe Leu Gln Arg
20 25 30

Ser Ser Asn Phe Gln Cys Gln Lys Leu Leu Trp Gln Leu Asn Gly Arg
35 40 45

Leu Glu Tyr Cys Leu Lys Asp Arg Met Asn Phe Asp Ile Pro Glu Glu
50 55 60

Ile Lys Gln Leu Gln Gln Phe Gln Lys Glu Asp Ala Ala Leu Thr Ile
65 70 75 80

```
Tyr Glu Met Leu Gln Asn Ile Phe Ala Ile Phe Arg Gln Asp Ser Ser
                85                  90                  95

Ser Thr Gly Trp Asn Glu Thr Ile Val Glu Asn Leu Leu Ala Asn Val
            100                 105                 110

Tyr His Gln Ile Asn His Leu Lys Thr Val Leu Glu Glu Lys Leu Glu
        115                 120                 125

Lys Glu Asp Phe Thr Arg Gly Lys Leu Met Ser Ser Leu His Leu Lys
    130                 135                 140

Arg Tyr Tyr Gly Arg Ile Leu His Tyr Leu Lys Ala Lys Glu Tyr Ser
145                 150                 155                 160

His Cys Ala Trp Thr Ile Val Arg Val Glu Ile Leu Arg Asn Phe Tyr
                165                 170                 175

Phe Ile Asn Arg Leu Thr Gly Tyr Leu Arg Asn Ser Gly Gly Gly Ser
            180                 185                 190

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
        195                 200                 205

Gly Gly Ser Leu Gln Lys Asn Leu Lys Ser Pro Gln Lys Val Glu Val
    210                 215                 220

Asp Ile Ile Asp Asp Asn Phe Ile Leu Arg Trp Asn Arg Ser Asp Glu
225                 230                 235                 240

Ser Val Gly Asn Val Thr Phe Ser Phe Asp Tyr Gln Lys Thr Gly Met
                245                 250                 255

Asp Asn Trp Ile Lys Leu Ser Gly Cys Gln Asn Ile Thr Ser Thr Lys
            260                 265                 270

Cys Asn Phe Ser Ser Leu Lys Leu Asn Val Tyr Glu Glu Ile Lys Leu
```

```
        275                 280                 285

Arg Ile Arg Ala Glu Lys Glu Asn Thr Ser Ser Trp Tyr Glu Val Asp
    290                 295                 300

Ser Phe Thr Pro Phe Arg Lys Ala Gln Ile Gly Pro Pro Glu Val His
305                 310                 315                 320

Leu Glu Ala Glu Asp Lys Ala Ile Val Ile His Ile Ser Pro Gly Thr
                325                 330                 335

Lys Asp Ser Val Met Trp Ala Leu Asp Gly Leu Ser Phe Thr Tyr Ser
            340                 345                 350

Leu Val Ile Trp Lys Asn Ser Ser Gly Val Glu Glu Arg Ile Glu Asn
        355                 360                 365

Ile Tyr Ser Arg His Lys Ile Tyr Lys Leu Ser Pro Glu Thr Thr Tyr
    370                 375                 380

Cys Leu Lys Val Lys Ala Ala Leu Leu Thr Ser Trp Lys Ile Gly Val
385                 390                 395                 400

Tyr Ser Pro Val His Cys Ile Lys Thr Thr Val Glu Asn Glu Leu Pro
                405                 410                 415

Pro Pro Glu Asn Ile Glu Val Ser Val Gln Asn Gln Asn Tyr Val Leu
            420                 425                 430

Lys Trp Asp Tyr Thr Tyr Ala Asn Met Thr Phe Gln Val Gln Trp Leu
        435                 440                 445

His Ala Phe Leu Lys Arg Asn Pro Gly Asn His Leu Tyr Lys Trp Lys
    450                 455                 460

Gln Ile Pro Asp Cys Glu Asn Val Lys Thr Thr Gln Cys Val Phe Pro
465                 470                 475                 480
```

```
Gln Asn Val Phe Gln Lys Gly Ile Tyr Leu Leu Arg Val Gln Ala Ser
                485                 490                 495

Asp Gly Asn Asn Thr Ser Phe Trp Ser Glu Glu Ile Lys Phe Asp Thr
            500                 505                 510

Glu Ile Gln Ala Phe Leu Leu Pro Pro Val Phe Asn Ile Arg Ser Leu
        515                 520                 525

Ser Asp Ser Phe His Ile Tyr Ile Gly Ala Pro Lys Gln Ser Gly Asn
    530                 535                 540

Thr Pro Val Ile Gln Asp Tyr Pro Leu Ile Tyr Glu Ile Ile Phe Trp
545                 550                 555                 560

Glu Asn Thr Ser Asn Ala Glu Arg Lys Ile Ile Glu Lys Lys Thr Asp
                565                 570                 575

Val Thr Val Pro Asn Leu Lys Pro Leu Thr Val Tyr Cys Val Lys Ala
            580                 585                 590

Arg Ala His Thr Met Asp Glu Lys Leu Asn Lys Ser Ser Val Phe Ser
        595                 600                 605

Asp Ala Val Cys Glu Lys Thr Lys Pro Gly Asn Thr Ser Lys Ile Trp
    610                 615                 620

Leu Ile Val Gly Ile Cys Ile Ala Leu Phe Ala Leu Pro Phe Val Ile
625                 630                 635                 640

Tyr Ala Ala Lys Val Phe Leu Arg Cys Ile Asn Tyr Val Phe Phe Pro
                645                 650                 655

Ser Leu Lys Pro Ser Ser Ser Ile Asp Glu Tyr Phe Ser Glu Gln Pro
            660                 665                 670

Leu Lys Asn Leu Leu Leu Ser Thr Ser Glu Glu Gln Ile Glu Lys Cys
```

675 680 685

Phe Ile Ile Glu Asn Ile Ser Thr Ile Ala Thr Val Glu Glu Thr Asn
690 695 700

Gln Thr Asp Glu Asp His Lys Lys Tyr Ser Ser Gln Thr Ser Gln Asp
705 710 715 720

Ser Gly Asn Tyr Ser Asn Glu Asp Glu Ser Glu Ser Lys Thr Ser Glu
725 730 735

Glu Leu Gln Gln Asp Phe Val
740

<210> 86
<211> 702
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 86
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Met Ser Tyr Asn Leu Leu Gly Phe Leu Gln Arg
20 25 30

Ser Ser Asn Phe Gln Cys Gln Lys Leu Leu Trp Gln Leu Asn Gly Arg
35 40 45

Leu Glu Tyr Cys Leu Lys Asp Arg Met Asn Phe Asp Ile Pro Glu Glu
50 55 60

Ile Lys Gln Leu Gln Gln Phe Gln Lys Glu Asp Ala Ala Leu Thr Ile
65 70 75 80

Tyr Glu Met Leu Gln Asn Ile Phe Ala Ile Phe Arg Gln Asp Ser Ser

```
                85                  90                  95

Ser Thr Gly Trp Asn Glu Thr Ile Val Glu Asn Leu Leu Ala Asn Val
            100                 105                 110

Tyr His Gln Ile Asn His Leu Lys Thr Val Leu Glu Glu Lys Leu Glu
        115                 120                 125

Lys Glu Asp Phe Thr Arg Gly Lys Leu Met Ser Ser Leu His Leu Lys
    130                 135                 140

Arg Tyr Tyr Gly Arg Ile Leu His Tyr Leu Lys Ala Lys Glu Tyr Ser
145                 150                 155                 160

His Cys Ala Trp Thr Ile Val Arg Val Glu Ile Leu Arg Asn Phe Tyr
                165                 170                 175

Phe Ile Asn Arg Leu Thr Gly Tyr Leu Arg Asn Ser Gly Gly Gly Ser
            180                 185                 190

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
        195                 200                 205

Gly Gly Ser Leu Gln Ile Ser Tyr Asp Ser Pro Asp Tyr Thr Asp Glu
    210                 215                 220

Ser Cys Thr Phe Lys Ile Ser Leu Arg Asn Phe Arg Ser Ile Leu Ser
225                 230                 235                 240

Trp Glu Leu Lys Asn His Ser Ile Val Pro Thr His Tyr Thr Leu Leu
                245                 250                 255

Tyr Thr Ile Met Ser Lys Pro Glu Asp Leu Lys Val Val Lys Asn Cys
            260                 265                 270

Ala Asn Thr Thr Arg Ser Phe Cys Asp Leu Thr Asp Glu Trp Arg Ser
        275                 280                 285
```

```
Thr His Glu Ala Tyr Val Thr Val Leu Glu Gly Phe Ser Gly Asn Thr
    290                 295                 300

Thr Leu Phe Ser Cys Ser His Asn Phe Trp Leu Ala Ile Asp Met Ser
305                 310                 315                 320

Phe Glu Pro Pro Glu Phe Glu Ile Val Gly Phe Thr Asn His Ile Asn
                325                 330                 335

Val Met Val Lys Phe Pro Ser Ile Val Glu Glu Glu Leu Gln Phe Asp
            340                 345                 350

Leu Ser Leu Val Ile Glu Glu Gln Ser Glu Gly Ile Val Lys Lys His
        355                 360                 365

Lys Pro Glu Ile Lys Gly Asn Met Ser Gly Asn Phe Thr Tyr Ile Ile
    370                 375                 380

Asp Lys Leu Ile Pro Asn Thr Asn Tyr Cys Val Ser Val Tyr Leu Glu
385                 390                 395                 400

His Ser Asp Glu Gln Ala Val Ile Lys Ser Pro Leu Lys Cys Thr Leu
                405                 410                 415

Leu Pro Pro Gly Gln Glu Ser Glu Ser Ala Glu Ser Ala Lys Ile Gly
            420                 425                 430

Gly Ile Ile Thr Val Phe Leu Ile Ala Leu Val Leu Thr Ser Thr Ile
        435                 440                 445

Val Thr Leu Lys Trp Ile Gly Tyr Ile Cys Leu Arg Asn Ser Leu Pro
    450                 455                 460

Lys Val Leu Asn Phe His Asn Phe Leu Ala Trp Pro Phe Pro Asn Leu
465                 470                 475                 480

Pro Pro Leu Glu Ala Met Asp Met Val Glu Val Ile Tyr Ile Asn Arg
```

```
                485                 490                 495

Lys Lys Lys Val Trp Asp Tyr Asn Tyr Asp Asp Glu Ser Asp Ser Asp
            500                 505                 510

Thr Glu Ala Ala Pro Arg Thr Ser Gly Gly Gly Tyr Thr Met His Gly
        515                 520                 525

Leu Thr Val Arg Pro Leu Gly Gln Ala Ser Ala Thr Ser Thr Glu Ser
    530                 535                 540

Gln Leu Ile Asp Pro Glu Ser Glu Glu Glu Pro Asp Leu Pro Glu Val
545                 550                 555                 560

Asp Val Glu Leu Pro Thr Met Pro Lys Asp Ser Pro Gln Gln Leu Glu
                565                 570                 575

Leu Leu Ser Gly Pro Cys Glu Arg Arg Lys Ser Pro Leu Gln Asp Pro
            580                 585                 590

Phe Pro Glu Glu Asp Tyr Ser Ser Thr Glu Gly Ser Gly Gly Arg Ile
        595                 600                 605

Thr Phe Asn Val Asp Leu Asn Ser Val Phe Leu Arg Val Leu Asp Asp
    610                 615                 620

Glu Asp Ser Asp Asp Leu Glu Ala Pro Leu Met Leu Ser Ser His Leu
625                 630                 635                 640

Glu Glu Met Val Asp Pro Glu Asp Pro Asp Asn Val Gln Ser Asn His
                645                 650                 655

Leu Leu Ala Ser Gly Glu Gly Thr Gln Pro Thr Phe Pro Ser Pro Ser
            660                 665                 670

Ser Glu Gly Leu Trp Ser Glu Asp Ala Pro Ser Asp Gln Ser Asp Thr
        675                 680                 685
```

Ser Glu Ser Asp Val Asp Leu Gly Asp Gly Tyr Ile Met Arg
690 695 700

<210> 87
<211> 657
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 87
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

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

Lys Lys Tyr Phe Asn Ala Gly His Ser Asp Val Ala Asp Asn Gly Thr
35 40 45

Leu Phe Leu Gly Ile Leu Lys Asn Trp Lys Glu Glu Ser Asp Arg Lys
50 55 60

Ile Met Gln Ser Gln Ile Val Ser Phe Tyr Phe Lys Leu Phe Lys Asn
65 70 75 80

Phe Lys Asp Asp Gln Ser Ile Gln Lys Ser Val Glu Thr Ile Lys Glu
85 90 95

Asp Met Asn Val Lys Phe Phe Asn Ser Asn Lys Lys Lys Arg Asp Asp
100 105 110

Phe Glu Lys Leu Thr Asn Tyr Ser Val Thr Asp Leu Asn Val Gln Arg
115 120 125

Lys Ala Ile His Glu Leu Ile Gln Val Met Ala Glu Leu Ser Pro Ala
130 135 140

```
Ala Lys Thr Gly Lys Arg Lys Arg Ser Gln Met Leu Phe Arg Gly Ser
145                 150                 155                 160

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
                165                 170                 175

Gly Gly Ser Gly Gly Gly Ser Leu Gln Glu Met Gly Thr Ala Asp Leu
            180                 185                 190

Gly Pro Ser Ser Val Pro Thr Pro Thr Asn Val Thr Ile Glu Ser Tyr
        195                 200                 205

Asn Met Asn Pro Ile Val Tyr Trp Glu Tyr Gln Ile Met Pro Gln Val
    210                 215                 220

Pro Val Phe Thr Val Glu Val Lys Asn Tyr Gly Val Lys Asn Ser Glu
225                 230                 235                 240

Trp Ile Asp Ala Cys Ile Asn Ile Ser His His Tyr Cys Asn Ile Ser
                245                 250                 255

Asp His Val Gly Asp Pro Ser Asn Ser Leu Trp Val Arg Val Lys Ala
            260                 265                 270

Arg Val Gly Gln Lys Glu Ser Ala Tyr Ala Lys Ser Glu Glu Phe Ala
        275                 280                 285

Val Cys Arg Asp Gly Lys Ile Gly Pro Pro Lys Leu Asp Ile Arg Lys
    290                 295                 300

Glu Glu Lys Gln Ile Met Ile Asp Ile Phe His Pro Ser Val Phe Val
305                 310                 315                 320

Asn Gly Asp Glu Gln Glu Val Asp Tyr Asp Pro Glu Thr Thr Cys Tyr
                325                 330                 335

Ile Arg Val Tyr Asn Val Tyr Val Arg Met Asn Gly Ser Glu Ile Gln
```

```
            340                 345                 350

Tyr Lys Ile Leu Thr Gln Lys Glu Asp Asp Cys Asp Glu Ile Gln Cys
        355                 360                 365

Gln Leu Ala Ile Pro Val Ser Ser Leu Asn Ser Gln Tyr Cys Val Ser
    370                 375                 380

Ala Glu Gly Val Leu His Val Trp Gly Val Thr Thr Glu Lys Ser Lys
385                 390                 395                 400

Glu Val Cys Ile Thr Ile Phe Asn Ser Ser Ile Lys Gly Ser Leu Trp
                405                 410                 415

Ile Pro Val Val Ala Ala Leu Leu Leu Phe Leu Val Leu Ser Leu Val
            420                 425                 430

Phe Ile Cys Phe Tyr Ile Lys Lys Ile Asn Pro Leu Lys Glu Lys Ser
        435                 440                 445

Ile Ile Leu Pro Lys Ser Leu Ile Ser Val Val Arg Ser Ala Thr Leu
    450                 455                 460

Glu Thr Lys Pro Glu Ser Lys Tyr Val Ser Leu Ile Thr Ser Tyr Gln
465                 470                 475                 480

Pro Phe Ser Leu Glu Lys Glu Val Val Cys Glu Glu Pro Leu Ser Pro
                485                 490                 495

Ala Thr Val Pro Gly Met His Thr Glu Asp Asn Pro Gly Lys Val Glu
            500                 505                 510

His Thr Glu Glu Leu Ser Ser Ile Thr Glu Val Val Thr Thr Glu Glu
        515                 520                 525

Asn Ile Pro Asp Val Val Pro Gly Ser His Leu Thr Pro Ile Glu Arg
    530                 535                 540
```

Glu Ser Ser Ser Pro Leu Ser Ser Asn Gln Ser Glu Pro Gly Ser Ile
545 550 555 560

Ala Leu Asn Ser Tyr His Ser Arg Asn Cys Ser Glu Ser Asp His Ser
565 570 575

Arg Asn Gly Phe Asp Thr Asp Ser Ser Cys Leu Glu Ser His Ser Ser
580 585 590

Leu Ser Asp Ser Glu Phe Pro Pro Asn Asn Lys Gly Glu Ile Lys Thr
595 600 605

Glu Gly Gln Glu Leu Ile Thr Val Ile Lys Ala Pro Thr Ser Phe Gly
610 615 620

Tyr Asp Lys Pro His Val Leu Val Asp Leu Leu Val Asp Asp Ser Gly
625 630 635 640

Lys Glu Ser Leu Ile Gly Tyr Arg Pro Thr Glu Asp Ser Lys Glu Phe
645 650 655

Ser

<210> 88
<211> 501
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 88
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

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

```
Lys Lys Tyr Phe Asn Ala Gly His Ser Asp Val Ala Asp Asn Gly Thr
        35                  40                  45

Leu Phe Leu Gly Ile Leu Lys Asn Trp Lys Glu Glu Ser Asp Arg Lys
    50                  55                  60

Ile Met Gln Ser Gln Ile Val Ser Phe Tyr Phe Lys Leu Phe Lys Asn
65                  70                  75                  80

Phe Lys Asp Asp Gln Ser Ile Gln Lys Ser Val Glu Thr Ile Lys Glu
                85                  90                  95

Asp Met Asn Val Lys Phe Phe Asn Ser Asn Lys Lys Lys Arg Asp Asp
            100                 105                 110

Phe Glu Lys Leu Thr Asn Tyr Ser Val Thr Asp Leu Asn Val Gln Arg
        115                 120                 125

Lys Ala Ile His Glu Leu Ile Gln Val Met Ala Glu Leu Ser Pro Ala
    130                 135                 140

Ala Lys Thr Gly Lys Arg Lys Arg Ser Gln Met Leu Phe Arg Gly Ser
145                 150                 155                 160

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
                165                 170                 175

Gly Gly Ser Gly Gly Gly Ser Leu Gln Ala Pro Pro Asp Pro Leu Ser
            180                 185                 190

Gln Leu Pro Ala Pro Gln His Pro Lys Ile Arg Leu Tyr Asn Ala Glu
        195                 200                 205

Gln Val Leu Ser Trp Glu Pro Val Ala Leu Ser Asn Ser Thr Arg Pro
    210                 215                 220

Val Val Tyr Gln Val Gln Phe Lys Tyr Thr Asp Ser Lys Trp Phe Thr
```

```
225                 230                 235                 240

Ala Asp Ile Met Ser Ile Gly Val Asn Cys Thr Gln Ile Thr Ala Thr
                245                 250                 255

Glu Cys Asp Phe Thr Ala Ala Ser Pro Ser Ala Gly Phe Pro Met Asp
            260                 265                 270

Phe Asn Val Thr Leu Arg Leu Arg Ala Glu Leu Gly Ala Leu His Ser
        275                 280                 285

Ala Trp Val Thr Met Pro Trp Phe Gln His Tyr Arg Asn Val Thr Val
    290                 295                 300

Gly Pro Pro Glu Asn Ile Glu Val Thr Pro Gly Glu Gly Ser Leu Ile
305                 310                 315                 320

Ile Arg Phe Ser Ser Pro Phe Asp Ile Ala Asp Thr Ser Thr Ala Phe
                325                 330                 335

Phe Cys Tyr Tyr Val His Tyr Trp Glu Lys Gly Gly Ile Gln Gln Val
            340                 345                 350

Lys Gly Pro Phe Arg Ser Asn Ser Ile Ser Leu Asp Asn Leu Lys Pro
        355                 360                 365

Ser Arg Val Tyr Cys Leu Gln Val Gln Ala Gln Leu Leu Trp Asn Lys
    370                 375                 380

Ser Asn Ile Phe Arg Val Gly His Leu Ser Asn Ile Ser Cys Tyr Glu
385                 390                 395                 400

Thr Met Ala Asp Ala Ser Thr Glu Leu Gln Gln Val Ile Leu Ile Ser
                405                 410                 415

Val Gly Thr Phe Ser Leu Leu Ser Val Leu Ala Gly Ala Cys Phe Phe
            420                 425                 430
```

Leu Val Leu Lys Tyr Arg Gly Leu Ile Lys Tyr Trp Phe His Thr Pro
435 440 445

Pro Ser Ile Pro Leu Gln Ile Glu Glu Tyr Leu Lys Asp Pro Thr Gln
450 455 460

Pro Ile Leu Glu Ala Leu Asp Lys Asp Ser Ser Pro Lys Asp Asp Val
465 470 475 480

Trp Asp Ser Val Ser Ile Ile Ser Phe Pro Glu Lys Glu Gln Glu Asp
485 490 495

Val Leu Gln Thr Leu
500

<210> 89
<211> 781
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 89
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

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

Lys Lys Tyr Phe Asn Ala Gly His Ser Asp Val Ala Asp Asn Gly Thr
35 40 45

Leu Phe Leu Gly Ile Leu Lys Asn Trp Lys Glu Glu Ser Asp Arg Lys
50 55 60

Ile Met Gln Ser Gln Ile Val Ser Phe Tyr Phe Lys Leu Phe Lys Asn
65 70 75 80

```
Phe Lys Asp Asp Gln Ser Ile Gln Lys Ser Val Glu Thr Ile Lys Glu
               85                  90                  95

Asp Met Asn Val Lys Phe Phe Asn Ser Asn Lys Lys Lys Arg Asp Asp
            100                 105                 110

Phe Glu Lys Leu Thr Asn Tyr Ser Val Thr Asp Leu Asn Val Gln Arg
        115                 120                 125

Lys Ala Ile His Glu Leu Ile Gln Val Met Ala Glu Leu Gly Ala Asn
    130                 135                 140

Val Ser Gly Glu Phe Val Lys Glu Ala Glu Asn Leu Lys Lys Tyr Phe
145                 150                 155                 160

Asn Ala Gly His Ser Asp Val Ala Asp Asn Gly Thr Leu Phe Leu Gly
               165                 170                 175

Ile Leu Lys Asn Trp Lys Glu Glu Ser Asp Arg Lys Ile Met Gln Ser
            180                 185                 190

Gln Ile Val Ser Phe Tyr Phe Lys Leu Phe Lys Asn Phe Lys Asp Asp
        195                 200                 205

Gln Ser Ile Gln Lys Ser Val Glu Thr Ile Lys Glu Asp Met Asn Val
    210                 215                 220

Lys Phe Phe Asn Ser Asn Lys Lys Lys Arg Asp Asp Phe Glu Lys Leu
225                 230                 235                 240

Thr Asn Tyr Ser Val Thr Asp Leu Asn Val Gln Arg Lys Ala Ile His
               245                 250                 255

Glu Leu Ile Gln Val Met Ala Glu Leu Ser Pro Ala Ala Lys Thr Gly
            260                 265                 270

Lys Arg Lys Arg Ser Gln Met Leu Phe Arg Gly Ser Gly Gly Gly Ser
```

```
        275                 280                 285

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
    290                 295                 300

Gly Gly Ser Leu Gln Glu Met Gly Thr Ala Asp Leu Gly Pro Ser Ser
305                 310                 315                 320

Val Pro Thr Pro Thr Asn Val Thr Ile Glu Ser Tyr Asn Met Asn Pro
                325                 330                 335

Ile Val Tyr Trp Glu Tyr Gln Ile Met Pro Gln Val Pro Val Phe Thr
            340                 345                 350

Val Glu Val Lys Asn Tyr Gly Val Lys Asn Ser Glu Trp Ile Asp Ala
        355                 360                 365

Cys Ile Asn Ile Ser His His Tyr Cys Asn Ile Ser Asp His Val Gly
    370                 375                 380

Asp Pro Ser Asn Ser Leu Trp Val Arg Val Lys Ala Arg Val Gly Gln
385                 390                 395                 400

Lys Glu Ser Ala Tyr Ala Lys Ser Glu Glu Phe Ala Val Cys Arg Asp
                405                 410                 415

Gly Lys Ile Gly Pro Pro Lys Leu Asp Ile Arg Lys Glu Glu Lys Gln
            420                 425                 430

Ile Met Ile Asp Ile Phe His Pro Ser Val Phe Val Asn Gly Asp Glu
        435                 440                 445

Gln Glu Val Asp Tyr Asp Pro Glu Thr Thr Cys Tyr Ile Arg Val Tyr
    450                 455                 460

Asn Val Tyr Val Arg Met Asn Gly Ser Glu Ile Gln Tyr Lys Ile Leu
465                 470                 475                 480
```

```
Thr Gln Lys Glu Asp Asp Cys Asp Glu Ile Gln Cys Gln Leu Ala Ile
                485                 490                 495

Pro Val Ser Ser Leu Asn Ser Gln Tyr Cys Val Ser Ala Glu Gly Val
            500                 505                 510

Leu His Val Trp Gly Val Thr Thr Glu Lys Ser Lys Glu Val Cys Ile
        515                 520                 525

Thr Ile Phe Asn Ser Ser Ile Lys Gly Ser Leu Trp Ile Pro Val Val
    530                 535                 540

Ala Ala Leu Leu Leu Phe Leu Val Leu Ser Leu Val Phe Ile Cys Phe
545                 550                 555                 560

Tyr Ile Lys Lys Ile Asn Pro Leu Lys Glu Lys Ser Ile Ile Leu Pro
                565                 570                 575

Lys Ser Leu Ile Ser Val Val Arg Ser Ala Thr Leu Glu Thr Lys Pro
            580                 585                 590

Glu Ser Lys Tyr Val Ser Leu Ile Thr Ser Tyr Gln Pro Phe Ser Leu
        595                 600                 605

Glu Lys Glu Val Val Cys Glu Glu Pro Leu Ser Pro Ala Thr Val Pro
    610                 615                 620

Gly Met His Thr Glu Asp Asn Pro Gly Lys Val Glu His Thr Glu Glu
625                 630                 635                 640

Leu Ser Ser Ile Thr Glu Val Val Thr Thr Glu Glu Asn Ile Pro Asp
                645                 650                 655

Val Val Pro Gly Ser His Leu Thr Pro Ile Glu Arg Glu Ser Ser Ser
            660                 665                 670

Pro Leu Ser Ser Asn Gln Ser Glu Pro Gly Ser Ile Ala Leu Asn Ser
```

675 680 685

Tyr His Ser Arg Asn Cys Ser Glu Ser Asp His Ser Arg Asn Gly Phe
690 695 700

Asp Thr Asp Ser Ser Cys Leu Glu Ser His Ser Ser Leu Ser Asp Ser
705 710 715 720

Glu Phe Pro Pro Asn Asn Lys Gly Glu Ile Lys Thr Glu Gly Gln Glu
725 730 735

Leu Ile Thr Val Ile Lys Ala Pro Thr Ser Phe Gly Tyr Asp Lys Pro
740 745 750

His Val Leu Val Asp Leu Leu Val Asp Asp Ser Gly Lys Glu Ser Leu
755 760 765

Ile Gly Tyr Arg Pro Thr Glu Asp Ser Lys Glu Phe Ser
770 775 780

<210> 90
<211> 625
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 90
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

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

Lys Lys Tyr Phe Asn Ala Gly His Ser Asp Val Ala Asp Asn Gly Thr
35 40 45

Leu Phe Leu Gly Ile Leu Lys Asn Trp Lys Glu Glu Ser Asp Arg Lys

```
    50                  55                  60

Ile Met Gln Ser Gln Ile Val Ser Phe Tyr Phe Lys Leu Phe Lys Asn
65                  70                  75                  80

Phe Lys Asp Asp Gln Ser Ile Gln Lys Ser Val Glu Thr Ile Lys Glu
                85                  90                  95

Asp Met Asn Val Lys Phe Phe Asn Ser Asn Lys Lys Lys Arg Asp Asp
            100                 105                 110

Phe Glu Lys Leu Thr Asn Tyr Ser Val Thr Asp Leu Asn Val Gln Arg
        115                 120                 125

Lys Ala Ile His Glu Leu Ile Gln Val Met Ala Glu Leu Gly Ala Asn
    130                 135                 140

Val Ser Gly Glu Phe Val Lys Glu Ala Glu Asn Leu Lys Lys Tyr Phe
145                 150                 155                 160

Asn Ala Gly His Ser Asp Val Ala Asp Asn Gly Thr Leu Phe Leu Gly
                165                 170                 175

Ile Leu Lys Asn Trp Lys Glu Glu Ser Asp Arg Lys Ile Met Gln Ser
            180                 185                 190

Gln Ile Val Ser Phe Tyr Phe Lys Leu Phe Lys Asn Phe Lys Asp Asp
        195                 200                 205

Gln Ser Ile Gln Lys Ser Val Glu Thr Ile Lys Glu Asp Met Asn Val
    210                 215                 220

Lys Phe Phe Asn Ser Asn Lys Lys Lys Arg Asp Asp Phe Glu Lys Leu
225                 230                 235                 240

Thr Asn Tyr Ser Val Thr Asp Leu Asn Val Gln Arg Lys Ala Ile His
                245                 250                 255
```

```
Glu Leu Ile Gln Val Met Ala Glu Leu Ser Pro Ala Ala Lys Thr Gly
            260                 265                 270

Lys Arg Lys Arg Ser Gln Met Leu Phe Arg Gly Ser Gly Gly Gly Ser
        275                 280                 285

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
    290                 295                 300

Gly Gly Ser Leu Gln Ala Pro Pro Asp Pro Leu Ser Gln Leu Pro Ala
305                 310                 315                 320

Pro Gln His Pro Lys Ile Arg Leu Tyr Asn Ala Glu Gln Val Leu Ser
                325                 330                 335

Trp Glu Pro Val Ala Leu Ser Asn Ser Thr Arg Pro Val Val Tyr Gln
            340                 345                 350

Val Gln Phe Lys Tyr Thr Asp Ser Lys Trp Phe Thr Ala Asp Ile Met
        355                 360                 365

Ser Ile Gly Val Asn Cys Thr Gln Ile Thr Ala Thr Glu Cys Asp Phe
    370                 375                 380

Thr Ala Ala Ser Pro Ser Ala Gly Phe Pro Met Asp Phe Asn Val Thr
385                 390                 395                 400

Leu Arg Leu Arg Ala Glu Leu Gly Ala Leu His Ser Ala Trp Val Thr
                405                 410                 415

Met Pro Trp Phe Gln His Tyr Arg Asn Val Thr Val Gly Pro Pro Glu
            420                 425                 430

Asn Ile Glu Val Thr Pro Gly Glu Gly Ser Leu Ile Ile Arg Phe Ser
        435                 440                 445

Ser Pro Phe Asp Ile Ala Asp Thr Ser Thr Ala Phe Phe Cys Tyr Tyr
```

```
    450                 455                 460

Val His Tyr Trp Glu Lys Gly Gly Ile Gln Gln Val Lys Gly Pro Phe
465                 470                 475                 480

Arg Ser Asn Ser Ile Ser Leu Asp Asn Leu Lys Pro Ser Arg Val Tyr
                485                 490                 495

Cys Leu Gln Val Gln Ala Gln Leu Leu Trp Asn Lys Ser Asn Ile Phe
            500                 505                 510

Arg Val Gly His Leu Ser Asn Ile Ser Cys Tyr Glu Thr Met Ala Asp
        515                 520                 525

Ala Ser Thr Glu Leu Gln Gln Val Ile Leu Ile Ser Val Gly Thr Phe
    530                 535                 540

Ser Leu Leu Ser Val Leu Ala Gly Ala Cys Phe Phe Leu Val Leu Lys
545                 550                 555                 560

Tyr Arg Gly Leu Ile Lys Tyr Trp Phe His Thr Pro Pro Ser Ile Pro
                565                 570                 575

Leu Gln Ile Glu Glu Tyr Leu Lys Asp Pro Thr Gln Pro Ile Leu Glu
            580                 585                 590

Ala Leu Asp Lys Asp Ser Ser Pro Lys Asp Asp Val Trp Asp Ser Val
        595                 600                 605

Ser Ile Ile Ser Phe Pro Glu Lys Glu Gln Glu Asp Val Leu Gln Thr
    610                 615                 620

Leu
625
```

<210> 91
<211> 630
<212> PRT

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 91
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Lys
20 25 30

Pro Val Ala His Val Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln
35 40 45

Trp Leu Asn Arg Arg Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu
50 55 60

Arg Asp Asn Gln Leu Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr
65 70 75 80

Ser Gln Val Leu Phe Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu
85 90 95

Leu Thr His Thr Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val
100 105 110

Asn Leu Leu Ser Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu
115 120 125

Gly Ala Glu Ala Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val
130 135 140

Phe Gln Leu Glu Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro
145 150 155 160

Asp Tyr Leu Asp Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile
165 170 175

```
Ala Leu Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
            180                 185                 190

Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Leu Gln Leu Val Pro His
        195                 200                 205

Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro Gln Gly Lys Tyr
    210                 215                 220

Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys Gly
225                 230                 235                 240

Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp Cys
                245                 250                 255

Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu Arg
            260                 265                 270

His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val Glu
        275                 280                 285

Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg Lys
    290                 295                 300

Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe Asn
305                 310                 315                 320

Cys Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu Lys
                325                 330                 335

Gln Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu Asn
            340                 345                 350

Glu Cys Val Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr Lys
        355                 360                 365

Leu Cys Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser Gly
```

```
    370                 375                 380

Thr Thr Val Leu Leu Pro Leu Val Ile Phe Phe Gly Leu Cys Leu Leu
385                 390                 395                 400

Ser Leu Leu Phe Ile Gly Leu Met Tyr Arg Tyr Gln Arg Trp Lys Ser
                405                 410                 415

Lys Leu Tyr Ser Ile Val Cys Gly Lys Ser Thr Pro Glu Lys Glu Gly
            420                 425                 430

Glu Leu Glu Gly Thr Thr Thr Lys Pro Leu Ala Pro Asn Pro Ser Phe
        435                 440                 445

Ser Pro Thr Pro Gly Phe Thr Pro Thr Leu Gly Phe Ser Pro Val Pro
    450                 455                 460

Ser Ser Thr Phe Thr Ser Ser Ser Thr Tyr Thr Pro Gly Asp Cys Pro
465                 470                 475                 480

Asn Phe Ala Ala Pro Arg Arg Glu Val Ala Pro Pro Tyr Gln Gly Ala
                485                 490                 495

Asp Pro Ile Leu Ala Thr Ala Leu Ala Ser Asp Pro Ile Pro Asn Pro
            500                 505                 510

Leu Gln Lys Trp Glu Asp Ser Ala His Lys Pro Gln Ser Leu Asp Thr
        515                 520                 525

Asp Asp Pro Ala Thr Leu Tyr Ala Val Val Glu Asn Val Pro Pro Leu
    530                 535                 540

Arg Trp Lys Glu Phe Val Arg Arg Leu Gly Leu Ser Asp His Glu Ile
545                 550                 555                 560

Asp Arg Leu Glu Leu Gln Asn Gly Arg Cys Leu Arg Glu Ala Gln Tyr
                565                 570                 575
```

Ser Met Leu Ala Thr Trp Arg Arg Arg Thr Pro Arg Arg Glu Ala Thr
580 585 590

Leu Glu Leu Leu Gly Arg Val Leu Arg Asp Met Asp Leu Leu Gly Cys
595 600 605

Leu Glu Asp Ile Glu Glu Ala Leu Cys Gly Pro Ala Ala Leu Pro Pro
610 615 620

Ala Pro Ser Leu Leu Arg
625 630

<210> 92
<211> 643
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 92
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Lys
20 25 30

Pro Val Ala His Val Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln
35 40 45

Trp Leu Asn Arg Arg Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu
50 55 60

Arg Asp Asn Gln Leu Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr
65 70 75 80

Ser Gln Val Leu Phe Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu
85 90 95

```
Leu Thr His Thr Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val
            100                 105                 110

Asn Leu Leu Ser Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu
        115                 120                 125

Gly Ala Glu Ala Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val
    130                 135                 140

Phe Gln Leu Glu Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro
145                 150                 155                 160

Asp Tyr Leu Asp Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile
                165                 170                 175

Ala Leu Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
            180                 185                 190

Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Leu Gln Leu Pro Ala Gln
        195                 200                 205

Val Ala Phe Thr Pro Tyr Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu
    210                 215                 220

Arg Glu Tyr Tyr Asp Gln Thr Ala Gln Met Cys Cys Ser Lys Cys Ser
225                 230                 235                 240

Pro Gly Gln His Ala Lys Val Phe Cys Thr Lys Thr Ser Asp Thr Val
                245                 250                 255

Cys Asp Ser Cys Glu Asp Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val
            260                 265                 270

Pro Glu Cys Leu Ser Cys Gly Ser Arg Cys Ser Ser Asp Gln Val Glu
        275                 280                 285

Thr Gln Ala Cys Thr Arg Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro
```

```
    290                 295                 300

Gly Trp Tyr Cys Ala Leu Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala
305                 310                 315                 320

Pro Leu Arg Lys Cys Arg Pro Gly Phe Gly Val Ala Arg Pro Gly Thr
                325                 330                 335

Glu Thr Ser Asp Val Val Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser
            340                 345                 350

Asn Thr Thr Ser Ser Thr Asp Ile Cys Arg Pro His Gln Ile Cys Asn
        355                 360                 365

Val Val Ala Ile Pro Gly Asn Ala Ser Met Asp Ala Val Cys Thr Ser
    370                 375                 380

Thr Ser Pro Thr Arg Ser Met Ala Pro Gly Ala Val His Leu Pro Gln
385                 390                 395                 400

Pro Val Ser Thr Arg Ser Gln His Thr Gln Pro Thr Pro Glu Pro Ser
                405                 410                 415

Thr Ala Pro Ser Thr Ser Phe Leu Leu Pro Met Gly Pro Ser Pro Pro
            420                 425                 430

Ala Glu Gly Ser Thr Gly Asp Phe Ala Leu Pro Val Gly Leu Ile Val
        435                 440                 445

Gly Val Thr Ala Leu Gly Leu Leu Ile Ile Gly Val Val Asn Cys Val
    450                 455                 460

Ile Met Thr Gln Val Lys Lys Lys Pro Leu Cys Leu Gln Arg Glu Ala
465                 470                 475                 480

Lys Val Pro His Leu Pro Ala Asp Lys Ala Arg Gly Thr Gln Gly Pro
                485                 490                 495
```

```
Glu Gln Gln His Leu Leu Ile Thr Ala Pro Ser Ser Ser Ser Ser Ser
            500                 505                 510

Leu Glu Ser Ser Ala Ser Ala Leu Asp Arg Arg Ala Pro Thr Arg Asn
        515                 520                 525

Gln Pro Gln Ala Pro Gly Val Glu Ala Ser Gly Ala Gly Glu Ala Arg
    530                 535                 540

Ala Ser Thr Gly Ser Ser Asp Ser Ser Pro Gly Gly His Gly Thr Gln
545                 550                 555                 560

Val Asn Val Thr Cys Ile Val Asn Val Cys Ser Ser Ser Asp His Ser
                565                 570                 575

Ser Gln Cys Ser Ser Gln Ala Ser Ser Thr Met Gly Asp Thr Asp Ser
            580                 585                 590

Ser Pro Ser Glu Ser Pro Lys Asp Glu Gln Val Pro Phe Ser Lys Glu
        595                 600                 605

Glu Cys Ala Phe Arg Ser Gln Leu Glu Thr Pro Glu Thr Leu Leu Gly
    610                 615                 620

Ser Thr Glu Glu Lys Pro Leu Pro Leu Gly Val Pro Asp Ala Gly Met
625                 630                 635                 640

Lys Pro Ser
```

<210> 93
<211> 752
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 93
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1   5   10   15

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

Asp Ser Gln Gln Lys Ser Leu Val Met Ser Gly Pro Tyr Glu Leu Lys
        35   40   45

Ala Leu His Leu Gln Gly Gln Asp Met Glu Gln Gln Val Val Phe Ser
    50   55   60

Met Ser Phe Val Gln Gly Glu Glu Ser Asn Asp Lys Ile Pro Val Ala
65   70   75   80

Leu Gly Leu Lys Glu Lys Asn Leu Tyr Leu Ser Cys Val Leu Lys Asp
                85   90   95

Asp Lys Pro Thr Leu Gln Leu Glu Ser Val Asp Pro Lys Asn Tyr Pro
            100   105   110

Lys Lys Lys Met Glu Lys Arg Phe Val Phe Asn Lys Ile Glu Ile Asn
        115   120   125

Asn Lys Leu Glu Phe Glu Ser Ala Gln Phe Pro Asn Trp Tyr Ile Ser
    130   135   140

Thr Ser Gln Ala Glu Asn Met Pro Val Phe Leu Gly Gly Thr Lys Gly
145   150   155   160

Gly Gln Asp Ile Thr Asp Phe Thr Met Gln Phe Val Ser Ser Ser Gly
                165   170   175

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
            180   185   190

Gly Ser Gly Gly Gly Ser Leu Gln Leu Glu Ala Asp Lys Cys Lys Glu

```
        195                 200                 205

Arg Glu Glu Lys Ile Ile Leu Val Ser Ser Ala Asn Glu Ile Asp Val
    210                 215                 220

Arg Pro Cys Pro Leu Asn Pro Asn Glu His Lys Gly Thr Ile Thr Trp
225                 230                 235                 240

Tyr Lys Asp Asp Ser Lys Thr Pro Val Ser Thr Glu Gln Ala Ser Arg
                245                 250                 255

Ile His Gln His Lys Glu Lys Leu Trp Phe Val Pro Ala Lys Val Glu
            260                 265                 270

Asp Ser Gly His Tyr Tyr Cys Val Val Arg Asn Ser Ser Tyr Cys Leu
        275                 280                 285

Arg Ile Lys Ile Ser Ala Lys Phe Val Glu Asn Glu Pro Asn Leu Cys
    290                 295                 300

Tyr Asn Ala Gln Ala Ile Phe Lys Gln Lys Leu Pro Val Ala Gly Asp
305                 310                 315                 320

Gly Gly Leu Val Cys Pro Tyr Met Glu Phe Phe Lys Asn Glu Asn Asn
                325                 330                 335

Glu Leu Pro Lys Leu Gln Trp Tyr Lys Asp Cys Lys Pro Leu Leu Leu
            340                 345                 350

Asp Asn Ile His Phe Ser Gly Val Lys Asp Arg Leu Ile Val Met Asn
        355                 360                 365

Val Ala Glu Lys His Arg Gly Asn Tyr Thr Cys His Ala Ser Tyr Thr
    370                 375                 380

Tyr Leu Gly Lys Gln Tyr Pro Ile Thr Arg Val Ile Glu Phe Ile Thr
385                 390                 395                 400
```

```
Leu Glu Glu Asn Lys Pro Thr Arg Pro Val Ile Val Ser Pro Ala Asn
                405                 410                 415

Glu Thr Met Glu Val Asp Leu Gly Ser Gln Ile Gln Leu Ile Cys Asn
            420                 425                 430

Val Thr Gly Gln Leu Ser Asp Ile Ala Tyr Trp Lys Trp Asn Gly Ser
        435                 440                 445

Val Ile Asp Glu Asp Asp Pro Val Leu Gly Glu Asp Tyr Tyr Ser Val
    450                 455                 460

Glu Asn Pro Ala Asn Lys Arg Arg Ser Thr Leu Ile Thr Val Leu Asn
465                 470                 475                 480

Ile Ser Glu Ile Glu Ser Arg Phe Tyr Lys His Pro Phe Thr Cys Phe
                485                 490                 495

Ala Lys Asn Thr His Gly Ile Asp Ala Ala Tyr Ile Gln Leu Ile Tyr
            500                 505                 510

Pro Val Thr Asn Phe Gln Lys His Met Ile Gly Ile Cys Val Thr Leu
        515                 520                 525

Thr Val Ile Ile Val Cys Ser Val Phe Ile Tyr Lys Ile Phe Lys Ile
    530                 535                 540

Asp Ile Val Leu Trp Tyr Arg Asp Ser Cys Tyr Asp Phe Leu Pro Ile
545                 550                 555                 560

Lys Ala Ser Asp Gly Lys Thr Tyr Asp Ala Tyr Ile Leu Tyr Pro Lys
                565                 570                 575

Thr Val Gly Glu Gly Ser Thr Ser Asp Cys Asp Ile Phe Val Phe Lys
            580                 585                 590

Val Leu Pro Glu Val Leu Glu Lys Gln Cys Gly Tyr Lys Leu Phe Ile
```

595 600 605

Tyr Gly Arg Asp Asp Tyr Val Gly Glu Asp Ile Val Glu Val Ile Asn
610 615 620

Glu Asn Val Lys Lys Ser Arg Arg Leu Ile Ile Ile Leu Val Arg Glu
625 630 635 640

Thr Ser Gly Phe Ser Trp Leu Gly Gly Ser Ser Glu Glu Gln Ile Ala
645 650 655

Met Tyr Asn Ala Leu Val Gln Asp Gly Ile Lys Val Val Leu Leu Glu
660 665 670

Leu Glu Lys Ile Gln Asp Tyr Glu Lys Met Pro Glu Ser Ile Lys Phe
675 680 685

Ile Lys Gln Lys His Gly Ala Ile Arg Trp Ser Gly Asp Phe Thr Gln
690 695 700

Gly Pro Gln Ser Ala Lys Thr Arg Phe Trp Lys Asn Val Arg Tyr His
705 710 715 720

Met Pro Val Gln Arg Arg Ser Pro Ser Ser Lys His Gln Leu Leu Ser
725 730 735

Pro Ala Thr Lys Glu Lys Leu Gln Arg Glu Ala His Val Pro Leu Gly
740 745 750

<210> 94
<211> 750
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 94
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu

```
1               5                   10                  15

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

Asp Ser Gln Gln Lys Ser Leu Val Met Ser Gly Pro Tyr Glu Leu Lys
        35                  40                  45

Ala Leu His Leu Gln Gly Gln Asp Met Glu Gln Gln Val Val Phe Ser
    50                  55                  60

Met Ser Phe Val Gln Gly Glu Glu Ser Asn Asp Lys Ile Pro Val Ala
65                  70                  75                  80

Leu Gly Leu Lys Glu Lys Asn Leu Tyr Leu Ser Cys Val Leu Lys Asp
                85                  90                  95

Asp Lys Pro Thr Leu Gln Leu Glu Ser Val Asp Pro Lys Asn Tyr Pro
            100                 105                 110

Lys Lys Lys Met Glu Lys Arg Phe Val Phe Asn Lys Ile Glu Ile Asn
        115                 120                 125

Asn Lys Leu Glu Phe Glu Ser Ala Gln Phe Pro Asn Trp Tyr Ile Ser
    130                 135                 140

Thr Ser Gln Ala Glu Asn Met Pro Val Phe Leu Gly Gly Thr Lys Gly
145                 150                 155                 160

Gly Gln Asp Ile Thr Asp Phe Thr Met Gln Phe Val Ser Ser Ser Gly
                165                 170                 175

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
            180                 185                 190

Gly Ser Gly Gly Gly Ser Leu Gln Ser Glu Arg Cys Asp Asp Trp Gly
        195                 200                 205
```

```
Leu Asp Thr Met Arg Gln Ile Gln Val Phe Glu Asp Glu Pro Ala Arg
    210                 215                 220

Ile Lys Cys Pro Leu Phe Glu His Phe Leu Lys Phe Asn Tyr Ser Thr
225                 230                 235                 240

Ala His Ser Ala Gly Leu Thr Leu Ile Trp Tyr Trp Thr Arg Gln Asp
                245                 250                 255

Arg Asp Leu Glu Glu Pro Ile Asn Phe Arg Leu Pro Glu Asn Arg Ile
            260                 265                 270

Ser Lys Glu Lys Asp Val Leu Trp Phe Arg Pro Thr Leu Leu Asn Asp
        275                 280                 285

Thr Gly Asn Tyr Thr Cys Met Leu Arg Asn Thr Thr Tyr Cys Ser Lys
    290                 295                 300

Val Ala Phe Pro Leu Glu Val Val Gln Lys Asp Ser Cys Phe Asn Ser
305                 310                 315                 320

Pro Met Lys Leu Pro Val His Lys Leu Tyr Ile Glu Tyr Gly Ile Gln
                325                 330                 335

Arg Ile Thr Cys Pro Asn Val Asp Gly Tyr Phe Pro Ser Ser Val Lys
            340                 345                 350

Pro Thr Ile Thr Trp Tyr Met Gly Cys Tyr Lys Ile Gln Asn Phe Asn
        355                 360                 365

Asn Val Ile Pro Glu Gly Met Asn Leu Ser Phe Leu Ile Ala Leu Ile
    370                 375                 380

Ser Asn Asn Gly Asn Tyr Thr Cys Val Val Thr Tyr Pro Glu Asn Gly
385                 390                 395                 400

Arg Thr Phe His Leu Thr Arg Thr Leu Thr Val Lys Val Val Gly Ser
```

```
                405                 410                 415

Pro Lys Asn Ala Val Pro Pro Val Ile His Ser Pro Asn Asp His Val
            420                 425                 430

Val Tyr Glu Lys Glu Pro Gly Glu Glu Leu Leu Ile Pro Cys Thr Val
        435                 440                 445

Tyr Phe Ser Phe Leu Met Asp Ser Arg Asn Glu Val Trp Trp Thr Ile
    450                 455                 460

Asp Gly Lys Lys Pro Asp Asp Ile Thr Ile Asp Val Thr Ile Asn Glu
465                 470                 475                 480

Ser Ile Ser His Ser Arg Thr Glu Asp Glu Thr Arg Thr Gln Ile Leu
                485                 490                 495

Ser Ile Lys Lys Val Thr Ser Glu Asp Leu Lys Arg Ser Tyr Val Cys
            500                 505                 510

His Ala Arg Ser Ala Lys Gly Glu Val Ala Lys Ala Ala Lys Val Lys
        515                 520                 525

Gln Lys Val Pro Ala Pro Arg Tyr Thr Val Glu Leu Ala Cys Gly Phe
    530                 535                 540

Gly Ala Thr Val Leu Leu Val Val Ile Leu Ile Val Val Tyr His Val
545                 550                 555                 560

Tyr Trp Leu Glu Met Val Leu Phe Tyr Arg Ala His Phe Gly Thr Asp
                565                 570                 575

Glu Thr Ile Leu Asp Gly Lys Glu Tyr Asp Ile Tyr Val Ser Tyr Ala
            580                 585                 590

Arg Asn Ala Glu Glu Glu Glu Phe Val Leu Leu Thr Leu Arg Gly Val
        595                 600                 605
```

```
Leu Glu Asn Glu Phe Gly Tyr Lys Leu Cys Ile Phe Asp Arg Asp Ser
    610                 615                 620

Leu Pro Gly Gly Ile Val Thr Asp Glu Thr Leu Ser Phe Ile Gln Lys
625                 630                 635                 640

Ser Arg Arg Leu Leu Val Val Leu Ser Pro Asn Tyr Val Leu Gln Gly
                645                 650                 655

Thr Gln Ala Leu Leu Glu Leu Lys Ala Gly Leu Glu Asn Met Ala Ser
            660                 665                 670

Arg Gly Asn Ile Asn Val Ile Leu Val Gln Tyr Lys Ala Val Lys Glu
        675                 680                 685

Thr Lys Val Lys Glu Leu Lys Arg Ala Lys Thr Val Leu Thr Val Ile
    690                 695                 700

Lys Trp Lys Gly Glu Lys Ser Lys Tyr Pro Gln Gly Arg Phe Trp Lys
705                 710                 715                 720

Gln Leu Gln Val Ala Met Pro Val Lys Lys Ser Pro Arg Arg Ser Ser
                725                 730                 735

Ser Asp Glu Gln Gly Leu Ser Tyr Ser Ser Leu Lys Asn Val
            740                 745                 750
```

<210> 95
<211> 767
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 95

```
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1               5                   10                  15
```

```
His Ala Ala Arg Pro Asn Tyr Pro Lys Lys Lys Met Glu Lys Arg Phe
            20                  25                  30

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

Gln Phe Pro Asn Trp Tyr Ile Ser Thr Ser Gln Ala Glu Asn Met Pro
    50                  55                  60

Val Phe Leu Gly Gly Thr Lys Gly Gly Gln Asp Ile Thr Asp Phe Thr
65                  70                  75                  80

Met Gln Phe Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
                85                  90                  95

Gly Gly Gly Gly Ser Ala Pro Val Arg Ser Leu Asn Cys Thr Leu Arg
            100                 105                 110

Asp Ser Gln Gln Lys Ser Leu Val Met Ser Gly Pro Tyr Glu Leu Lys
        115                 120                 125

Ala Leu His Leu Gln Gly Gln Asp Met Glu Gln Gln Val Val Phe Ser
    130                 135                 140

Met Ser Phe Val Gln Gly Glu Glu Ser Asn Asp Lys Ile Pro Val Ala
145                 150                 155                 160

Leu Gly Leu Lys Glu Lys Asn Leu Tyr Leu Ser Cys Val Leu Lys Asp
                165                 170                 175

Asp Lys Pro Thr Leu Gln Leu Glu Ser Val Asp Pro Lys Ser Gly Gly
            180                 185                 190

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
        195                 200                 205

Ser Gly Gly Gly Ser Leu Gln Leu Glu Ala Asp Lys Cys Lys Glu Arg
```

```
    210                 215                 220

Glu Glu Lys Ile Ile Leu Val Ser Ser Ala Asn Glu Ile Asp Val Arg
225                 230                 235                 240

Pro Cys Pro Leu Asn Pro Asn Glu His Lys Gly Thr Ile Thr Trp Tyr
                245                 250                 255

Lys Asp Asp Ser Lys Thr Pro Val Ser Thr Glu Gln Ala Ser Arg Ile
            260                 265                 270

His Gln His Lys Glu Lys Leu Trp Phe Val Pro Ala Lys Val Glu Asp
        275                 280                 285

Ser Gly His Tyr Tyr Cys Val Val Arg Asn Ser Ser Tyr Cys Leu Arg
    290                 295                 300

Ile Lys Ile Ser Ala Lys Phe Val Glu Asn Glu Pro Asn Leu Cys Tyr
305                 310                 315                 320

Asn Ala Gln Ala Ile Phe Lys Gln Lys Leu Pro Val Ala Gly Asp Gly
                325                 330                 335

Gly Leu Val Cys Pro Tyr Met Glu Phe Phe Lys Asn Glu Asn Asn Glu
            340                 345                 350

Leu Pro Lys Leu Gln Trp Tyr Lys Asp Cys Lys Pro Leu Leu Leu Asp
        355                 360                 365

Asn Ile His Phe Ser Gly Val Lys Asp Arg Leu Ile Val Met Asn Val
    370                 375                 380

Ala Glu Lys His Arg Gly Asn Tyr Thr Cys His Ala Ser Tyr Thr Tyr
385                 390                 395                 400

Leu Gly Lys Gln Tyr Pro Ile Thr Arg Val Ile Glu Phe Ile Thr Leu
                405                 410                 415
```

```
Glu Glu Asn Lys Pro Thr Arg Pro Val Ile Val Ser Pro Ala Asn Glu
            420                 425                 430

Thr Met Glu Val Asp Leu Gly Ser Gln Ile Gln Leu Ile Cys Asn Val
        435                 440                 445

Thr Gly Gln Leu Ser Asp Ile Ala Tyr Trp Lys Trp Asn Gly Ser Val
    450                 455                 460

Ile Asp Glu Asp Asp Pro Val Leu Gly Glu Asp Tyr Tyr Ser Val Glu
465                 470                 475                 480

Asn Pro Ala Asn Lys Arg Arg Ser Thr Leu Ile Thr Val Leu Asn Ile
                485                 490                 495

Ser Glu Ile Glu Ser Arg Phe Tyr Lys His Pro Phe Thr Cys Phe Ala
            500                 505                 510

Lys Asn Thr His Gly Ile Asp Ala Ala Tyr Ile Gln Leu Ile Tyr Pro
        515                 520                 525

Val Thr Asn Phe Gln Lys His Met Ile Gly Ile Cys Val Thr Leu Thr
    530                 535                 540

Val Ile Ile Val Cys Ser Val Phe Ile Tyr Lys Ile Phe Lys Ile Asp
545                 550                 555                 560

Ile Val Leu Trp Tyr Arg Asp Ser Cys Tyr Asp Phe Leu Pro Ile Lys
                565                 570                 575

Ala Ser Asp Gly Lys Thr Tyr Asp Ala Tyr Ile Leu Tyr Pro Lys Thr
            580                 585                 590

Val Gly Glu Gly Ser Thr Ser Asp Cys Asp Ile Phe Val Phe Lys Val
        595                 600                 605

Leu Pro Glu Val Leu Glu Lys Gln Cys Gly Tyr Lys Leu Phe Ile Tyr
```

610 615 620

Gly Arg Asp Asp Tyr Val Gly Glu Asp Ile Val Glu Val Ile Asn Glu
625 630 635 640

Asn Val Lys Lys Ser Arg Arg Leu Ile Ile Ile Leu Val Arg Glu Thr
645 650 655

Ser Gly Phe Ser Trp Leu Gly Gly Ser Ser Glu Glu Gln Ile Ala Met
660 665 670

Tyr Asn Ala Leu Val Gln Asp Gly Ile Lys Val Val Leu Leu Glu Leu
675 680 685

Glu Lys Ile Gln Asp Tyr Glu Lys Met Pro Glu Ser Ile Lys Phe Ile
690 695 700

Lys Gln Lys His Gly Ala Ile Arg Trp Ser Gly Asp Phe Thr Gln Gly
705 710 715 720

Pro Gln Ser Ala Lys Thr Arg Phe Trp Lys Asn Val Arg Tyr His Met
725 730 735

Pro Val Gln Arg Arg Ser Pro Ser Ser Lys His Gln Leu Leu Ser Pro
740 745 750

Ala Thr Lys Glu Lys Leu Gln Arg Glu Ala His Val Pro Leu Gly
755 760 765

<210> 96
<211> 765
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 96
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu

```
1               5                   10                  15

His Ala Ala Arg Pro Asn Tyr Pro Lys Lys Lys Met Glu Lys Arg Phe
            20                  25                  30

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

Gln Phe Pro Asn Trp Tyr Ile Ser Thr Ser Gln Ala Glu Asn Met Pro
    50                  55                  60

Val Phe Leu Gly Gly Thr Lys Gly Gly Gln Asp Ile Thr Asp Phe Thr
65                  70                  75                  80

Met Gln Phe Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
                85                  90                  95

Gly Gly Gly Gly Ser Ala Pro Val Arg Ser Leu Asn Cys Thr Leu Arg
            100                 105                 110

Asp Ser Gln Gln Lys Ser Leu Val Met Ser Gly Pro Tyr Glu Leu Lys
        115                 120                 125

Ala Leu His Leu Gln Gly Gln Asp Met Glu Gln Gln Val Val Phe Ser
    130                 135                 140

Met Ser Phe Val Gln Gly Glu Glu Ser Asn Asp Lys Ile Pro Val Ala
145                 150                 155                 160

Leu Gly Leu Lys Glu Lys Asn Leu Tyr Leu Ser Cys Val Leu Lys Asp
                165                 170                 175

Asp Lys Pro Thr Leu Gln Leu Glu Ser Val Asp Pro Lys Ser Gly Gly
            180                 185                 190

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
        195                 200                 205
```

```
Ser Gly Gly Gly Ser Leu Gln Ser Glu Arg Cys Asp Asp Trp Gly Leu
    210                 215                 220

Asp Thr Met Arg Gln Ile Gln Val Phe Glu Asp Glu Pro Ala Arg Ile
225                 230                 235                 240

Lys Cys Pro Leu Phe Glu His Phe Leu Lys Phe Asn Tyr Ser Thr Ala
                245                 250                 255

His Ser Ala Gly Leu Thr Leu Ile Trp Tyr Trp Thr Arg Gln Asp Arg
            260                 265                 270

Asp Leu Glu Glu Pro Ile Asn Phe Arg Leu Pro Glu Asn Arg Ile Ser
        275                 280                 285

Lys Glu Lys Asp Val Leu Trp Phe Arg Pro Thr Leu Leu Asn Asp Thr
    290                 295                 300

Gly Asn Tyr Thr Cys Met Leu Arg Asn Thr Thr Tyr Cys Ser Lys Val
305                 310                 315                 320

Ala Phe Pro Leu Glu Val Val Gln Lys Asp Ser Cys Phe Asn Ser Pro
                325                 330                 335

Met Lys Leu Pro Val His Lys Leu Tyr Ile Glu Tyr Gly Ile Gln Arg
            340                 345                 350

Ile Thr Cys Pro Asn Val Asp Gly Tyr Phe Pro Ser Ser Val Lys Pro
        355                 360                 365

Thr Ile Thr Trp Tyr Met Gly Cys Tyr Lys Ile Gln Asn Phe Asn Asn
    370                 375                 380

Val Ile Pro Glu Gly Met Asn Leu Ser Phe Leu Ile Ala Leu Ile Ser
385                 390                 395                 400

Asn Asn Gly Asn Tyr Thr Cys Val Val Thr Tyr Pro Glu Asn Gly Arg
```

```
                405                 410                 415

Thr Phe His Leu Thr Arg Thr Leu Thr Val Lys Val Val Gly Ser Pro
            420                 425                 430

Lys Asn Ala Val Pro Pro Val Ile His Ser Pro Asn Asp His Val Val
        435                 440                 445

Tyr Glu Lys Glu Pro Gly Glu Glu Leu Leu Ile Pro Cys Thr Val Tyr
    450                 455                 460

Phe Ser Phe Leu Met Asp Ser Arg Asn Glu Val Trp Trp Thr Ile Asp
465                 470                 475                 480

Gly Lys Lys Pro Asp Asp Ile Thr Ile Asp Val Thr Ile Asn Glu Ser
                485                 490                 495

Ile Ser His Ser Arg Thr Glu Asp Glu Thr Arg Thr Gln Ile Leu Ser
            500                 505                 510

Ile Lys Lys Val Thr Ser Glu Asp Leu Lys Arg Ser Tyr Val Cys His
        515                 520                 525

Ala Arg Ser Ala Lys Gly Glu Val Ala Lys Ala Ala Lys Val Lys Gln
    530                 535                 540

Lys Val Pro Ala Pro Arg Tyr Thr Val Glu Leu Ala Cys Gly Phe Gly
545                 550                 555                 560

Ala Thr Val Leu Leu Val Val Ile Leu Ile Val Val Tyr His Val Tyr
                565                 570                 575

Trp Leu Glu Met Val Leu Phe Tyr Arg Ala His Phe Gly Thr Asp Glu
            580                 585                 590

Thr Ile Leu Asp Gly Lys Glu Tyr Asp Ile Tyr Val Ser Tyr Ala Arg
        595                 600                 605
```

```
Asn Ala Glu Glu Glu Glu Phe Val Leu Leu Thr Leu Arg Gly Val Leu
    610                 615                 620

Glu Asn Glu Phe Gly Tyr Lys Leu Cys Ile Phe Asp Arg Asp Ser Leu
625                 630                 635                 640

Pro Gly Gly Ile Val Thr Asp Glu Thr Leu Ser Phe Ile Gln Lys Ser
                645                 650                 655

Arg Arg Leu Leu Val Val Leu Ser Pro Asn Tyr Val Leu Gln Gly Thr
            660                 665                 670

Gln Ala Leu Leu Glu Leu Lys Ala Gly Leu Glu Asn Met Ala Ser Arg
        675                 680                 685

Gly Asn Ile Asn Val Ile Leu Val Gln Tyr Lys Ala Val Lys Glu Thr
    690                 695                 700

Lys Val Lys Glu Leu Lys Arg Ala Lys Thr Val Leu Thr Val Ile Lys
705                 710                 715                 720

Trp Lys Gly Glu Lys Ser Lys Tyr Pro Gln Gly Arg Phe Trp Lys Gln
                725                 730                 735

Leu Gln Val Ala Met Pro Val Lys Lys Ser Pro Arg Arg Ser Ser Ser
            740                 745                 750

Asp Glu Gln Gly Leu Ser Tyr Ser Ser Leu Lys Asn Val
        755                 760                 765
```

<210> 97
<211> 679
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 97
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1   5   10   15

His Ala Ala Arg Pro Val Pro Pro Gly Glu Asp Ser Lys Asp Val Ala
            20   25   30

Ala Pro His Arg Gln Pro Leu Thr Ser Ser Glu Arg Ile Asp Lys Gln
        35   40   45

Ile Arg Tyr Ile Leu Asp Gly Ile Ser Ala Leu Arg Lys Glu Thr Cys
    50   55   60

Asn Lys Ser Asn Met Cys Glu Ser Ser Lys Glu Ala Leu Ala Glu Asn
65   70   75   80

Asn Leu Asn Leu Pro Lys Met Ala Glu Lys Asp Gly Cys Phe Gln Ser
                85   90   95

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

Glu Phe Glu Val Tyr Leu Glu Tyr Leu Gln Asn Arg Phe Glu Ser Ser
        115   120   125

Glu Glu Gln Ala Arg Ala Val Gln Met Ser Thr Lys Val Leu Ile Gln
    130   135   140

Phe Leu Gln Lys Lys Ala Lys Asn Leu Asp Ala Ile Thr Thr Pro Asp
145   150   155   160

Pro Thr Thr Asn Ala Ser Leu Leu Thr Lys Leu Gln Ala Gln Asn Gln
                165   170   175

Trp Leu Gln Asp Met Thr Thr His Leu Ile Leu Arg Ser Phe Lys Glu
            180   185   190

Phe Leu Gln Ser Ser Leu Arg Ala Leu Arg Gln Met Ser Gly Gly Gly

```
        195                 200                 205

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
    210                 215                 220

Gly Gly Gly Ser Leu Gln Leu Ala Pro Arg Arg Cys Pro Ala Gln Glu
225                 230                 235                 240

Val Ala Arg Gly Val Leu Thr Ser Leu Pro Gly Asp Ser Val Thr Leu
                245                 250                 255

Thr Cys Pro Gly Val Glu Pro Glu Asp Asn Ala Thr Val His Trp Val
            260                 265                 270

Leu Arg Lys Pro Ala Ala Gly Ser His Pro Ser Arg Trp Ala Gly Met
        275                 280                 285

Gly Arg Arg Leu Leu Leu Arg Ser Val Gln Leu His Asp Ser Gly Asn
    290                 295                 300

Tyr Ser Cys Tyr Arg Ala Gly Arg Pro Ala Gly Thr Val His Leu Leu
305                 310                 315                 320

Val Asp Val Pro Pro Glu Glu Pro Gln Leu Ser Cys Phe Arg Lys Ser
                325                 330                 335

Pro Leu Ser Asn Val Val Cys Glu Trp Gly Pro Arg Ser Thr Pro Ser
            340                 345                 350

Leu Thr Thr Lys Ala Val Leu Leu Val Arg Lys Phe Gln Asn Ser Pro
        355                 360                 365

Ala Glu Asp Phe Gln Glu Pro Cys Gln Tyr Ser Gln Glu Ser Gln Lys
    370                 375                 380

Phe Ser Cys Gln Leu Ala Val Pro Glu Gly Asp Ser Ser Phe Tyr Ile
385                 390                 395                 400
```

```
Val Ser Met Cys Val Ala Ser Ser Val Gly Ser Lys Phe Ser Lys Thr
                405                 410                 415

Gln Thr Phe Gln Gly Cys Gly Ile Leu Gln Pro Asp Pro Pro Ala Asn
            420                 425                 430

Ile Thr Val Thr Ala Val Ala Arg Asn Pro Arg Trp Leu Ser Val Thr
        435                 440                 445

Trp Gln Asp Pro His Ser Trp Asn Ser Ser Phe Tyr Arg Leu Arg Phe
    450                 455                 460

Glu Leu Arg Tyr Arg Ala Glu Arg Ser Lys Thr Phe Thr Thr Trp Met
465                 470                 475                 480

Val Lys Asp Leu Gln His His Cys Val Ile His Asp Ala Trp Ser Gly
                485                 490                 495

Leu Arg His Val Val Gln Leu Arg Ala Gln Glu Glu Phe Gly Gln Gly
            500                 505                 510

Glu Trp Ser Glu Trp Ser Pro Glu Ala Met Gly Thr Pro Trp Thr Glu
        515                 520                 525

Ser Arg Ser Pro Pro Ala Glu Asn Glu Val Ser Thr Pro Met Gln Ala
    530                 535                 540

Leu Thr Thr Asn Lys Asp Asp Asp Asn Ile Leu Phe Arg Asp Ser Ala
545                 550                 555                 560

Asn Ala Thr Ser Leu Pro Val Gln Asp Ser Ser Ser Val Pro Leu Pro
                565                 570                 575

Thr Phe Leu Val Ala Gly Gly Ser Leu Ala Phe Gly Thr Leu Leu Cys
            580                 585                 590

Ile Ala Ile Val Leu Arg Phe Lys Lys Thr Trp Lys Leu Arg Ala Leu
```

595 600 605

Lys Glu Gly Lys Thr Ser Met His Pro Pro Tyr Ser Leu Gly Gln Leu
610 615 620

Val Pro Glu Arg Pro Arg Pro Thr Pro Val Leu Val Pro Leu Ile Ser
625 630 635 640

Pro Pro Val Ser Pro Ser Ser Leu Gly Ser Asp Asn Thr Ser Ser His
645 650 655

Asn Arg Pro Asp Ala Arg Asp Pro Arg Ser Pro Tyr Asp Ile Ser Asn
660 665 670

Thr Asp Tyr Phe Phe Pro Arg
675

<210> 98
<211> 1126
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 98
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Val Pro Pro Gly Glu Asp Ser Lys Asp Val Ala
20 25 30

Ala Pro His Arg Gln Pro Leu Thr Ser Ser Glu Arg Ile Asp Lys Gln
35 40 45

Ile Arg Tyr Ile Leu Asp Gly Ile Ser Ala Leu Arg Lys Glu Thr Cys
50 55 60

Asn Lys Ser Asn Met Cys Glu Ser Ser Lys Glu Ala Leu Ala Glu Asn

```
65                  70                  75                  80

Asn Leu Asn Leu Pro Lys Met Ala Glu Lys Asp Gly Cys Phe Gln Ser
                85                  90                  95

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

Glu Phe Glu Val Tyr Leu Glu Tyr Leu Gln Asn Arg Phe Glu Ser Ser
        115                 120                 125

Glu Glu Gln Ala Arg Ala Val Gln Met Ser Thr Lys Val Leu Ile Gln
    130                 135                 140

Phe Leu Gln Lys Lys Ala Lys Asn Leu Asp Ala Ile Thr Thr Pro Asp
145                 150                 155                 160

Pro Thr Thr Asn Ala Ser Leu Leu Thr Lys Leu Gln Ala Gln Asn Gln
                165                 170                 175

Trp Leu Gln Asp Met Thr Thr His Leu Ile Leu Arg Ser Phe Lys Glu
            180                 185                 190

Phe Leu Gln Ser Ser Leu Arg Ala Leu Arg Gln Met Ser Gly Gly Gly
        195                 200                 205

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
    210                 215                 220

Gly Gly Gly Ser Leu Gln Glu Leu Leu Asp Pro Cys Gly Tyr Ile Ser
225                 230                 235                 240

Pro Glu Ser Pro Val Val Gln Leu His Ser Asn Phe Thr Ala Val Cys
                245                 250                 255

Val Leu Lys Glu Lys Cys Met Asp Tyr Phe His Val Asn Ala Asn Tyr
            260                 265                 270
```

```
Ile Val Trp Lys Thr Asn His Phe Thr Ile Pro Lys Glu Gln Tyr Thr
        275                 280                 285

Ile Ile Asn Arg Thr Ala Ser Ser Val Thr Phe Thr Asp Ile Ala Ser
    290                 295                 300

Leu Asn Ile Gln Leu Thr Cys Asn Ile Leu Thr Phe Gly Gln Leu Glu
305                 310                 315                 320

Gln Asn Val Tyr Gly Ile Thr Ile Ile Ser Gly Leu Pro Pro Glu Lys
                325                 330                 335

Pro Lys Asn Leu Ser Cys Ile Val Asn Glu Gly Lys Lys Met Arg Cys
            340                 345                 350

Glu Trp Asp Gly Gly Arg Glu Thr His Leu Glu Thr Asn Phe Thr Leu
        355                 360                 365

Lys Ser Glu Trp Ala Thr His Lys Phe Ala Asp Cys Lys Ala Lys Arg
    370                 375                 380

Asp Thr Pro Thr Ser Cys Thr Val Asp Tyr Ser Thr Val Tyr Phe Val
385                 390                 395                 400

Asn Ile Glu Val Trp Val Glu Ala Glu Asn Ala Leu Gly Lys Val Thr
                405                 410                 415

Ser Asp His Ile Asn Phe Asp Pro Val Tyr Lys Val Lys Pro Asn Pro
            420                 425                 430

Pro His Asn Leu Ser Val Ile Asn Ser Glu Glu Leu Ser Ser Ile Leu
        435                 440                 445

Lys Leu Thr Trp Thr Asn Pro Ser Ile Lys Ser Val Ile Ile Leu Lys
    450                 455                 460

Tyr Asn Ile Gln Tyr Arg Thr Lys Asp Ala Ser Thr Trp Ser Gln Ile
```

```
465                 470                 475                 480

Pro Pro Glu Asp Thr Ala Ser Thr Arg Ser Ser Phe Thr Val Gln Asp
                485                 490                 495

Leu Lys Pro Phe Thr Glu Tyr Val Phe Arg Ile Arg Cys Met Lys Glu
            500                 505                 510

Asp Gly Lys Gly Tyr Trp Ser Asp Trp Ser Glu Glu Ala Ser Gly Ile
        515                 520                 525

Thr Tyr Glu Asp Arg Pro Ser Lys Ala Pro Ser Phe Trp Tyr Lys Ile
    530                 535                 540

Asp Pro Ser His Thr Gln Gly Tyr Arg Thr Val Gln Leu Val Trp Lys
545                 550                 555                 560

Thr Leu Pro Pro Phe Glu Ala Asn Gly Lys Ile Leu Asp Tyr Glu Val
                565                 570                 575

Thr Leu Thr Arg Trp Lys Ser His Leu Gln Asn Tyr Thr Val Asn Ala
            580                 585                 590

Thr Lys Leu Thr Val Asn Leu Thr Asn Asp Arg Tyr Leu Ala Thr Leu
        595                 600                 605

Thr Val Arg Asn Leu Val Gly Lys Ser Asp Ala Ala Val Leu Thr Ile
    610                 615                 620

Pro Ala Cys Asp Phe Gln Ala Thr His Pro Val Met Asp Leu Lys Ala
625                 630                 635                 640

Phe Pro Lys Asp Asn Met Leu Trp Val Glu Trp Thr Thr Pro Arg Glu
                645                 650                 655

Ser Val Lys Lys Tyr Ile Leu Glu Trp Cys Val Leu Ser Asp Lys Ala
            660                 665                 670
```

```
Pro Cys Ile Thr Asp Trp Gln Gln Glu Asp Gly Thr Val His Arg Thr
        675                 680                 685

Tyr Leu Arg Gly Asn Leu Ala Glu Ser Lys Cys Tyr Leu Ile Thr Val
    690                 695                 700

Thr Pro Val Tyr Ala Asp Gly Pro Gly Ser Pro Glu Ser Ile Lys Ala
705                 710                 715                 720

Tyr Leu Lys Gln Ala Pro Pro Ser Lys Gly Pro Thr Val Arg Thr Lys
                725                 730                 735

Lys Val Gly Lys Asn Glu Ala Val Leu Glu Trp Asp Gln Leu Pro Val
            740                 745                 750

Asp Val Gln Asn Gly Phe Ile Arg Asn Tyr Thr Ile Phe Tyr Arg Thr
        755                 760                 765

Ile Ile Gly Asn Glu Thr Ala Val Asn Val Asp Ser Ser His Thr Glu
    770                 775                 780

Tyr Thr Leu Ser Ser Leu Thr Ser Asp Thr Leu Tyr Met Val Arg Met
785                 790                 795                 800

Ala Ala Tyr Thr Asp Glu Gly Gly Lys Asp Gly Pro Glu Phe Thr Phe
                805                 810                 815

Thr Thr Pro Lys Phe Ala Gln Gly Glu Ile Glu Ala Ile Val Val Pro
            820                 825                 830

Val Cys Leu Ala Phe Leu Leu Thr Thr Leu Leu Gly Val Leu Phe Cys
        835                 840                 845

Phe Asn Lys Arg Asp Leu Ile Lys Lys His Ile Trp Pro Asn Val Pro
    850                 855                 860

Asp Pro Ser Lys Ser His Ile Ala Gln Trp Ser Pro His Thr Pro Pro
```

```
865                 870                 875                 880

Arg His Asn Phe Asn Ser Lys Asp Gln Met Tyr Ser Asp Gly Asn Phe
                885                 890                 895

Thr Asp Val Ser Val Val Glu Ile Glu Ala Asn Asp Lys Lys Pro Phe
            900                 905                 910

Pro Glu Asp Leu Lys Ser Leu Asp Leu Phe Lys Lys Glu Lys Ile Asn
        915                 920                 925

Thr Glu Gly His Ser Ser Gly Ile Gly Gly Ser Ser Cys Met Ser Ser
    930                 935                 940

Ser Arg Pro Ser Ile Ser Ser Ser Asp Glu Asn Glu Ser Ser Gln Asn
945                 950                 955                 960

Thr Ser Ser Thr Val Gln Tyr Ser Thr Val Val His Ser Gly Tyr Arg
                965                 970                 975

His Gln Val Pro Ser Val Gln Val Phe Ser Arg Ser Glu Ser Thr Gln
            980                 985                 990

Pro Leu Leu Asp Ser Glu Glu Arg  Pro Glu Asp Leu Gln  Leu Val Asp
        995                 1000                1005

His Val  Asp Gly Gly Asp Gly  Ile Leu Pro Arg Gln  Gln Tyr Phe
    1010                1015                1020

Lys Gln  Asn Cys Ser Gln His  Glu Ser Ser Pro Asp  Ile Ser His
    1025                1030                1035

Phe Glu  Arg Ser Lys Gln Val  Ser Ser Val Asn Glu  Glu Asp Phe
    1040                1045                1050

Val Arg  Leu Lys Gln Gln Ile  Ser Asp His Ile Ser  Gln Ser Cys
    1055                1060                1065
```

Gly Ser Gly Gln Met Lys Met Phe Gln Glu Val Ser Ala Ala Asp
    1070   1075   1080

Ala Phe Gly Pro Gly Thr Glu Gly Gln Val Glu Arg Phe Glu Thr
    1085   1090   1095

Val Gly Met Glu Ala Ala Thr Asp Glu Gly Met Pro Lys Ser Tyr
    1100   1105   1110

Leu Pro Gln Thr Val Arg Gln Gly Gly Tyr Met Pro Gln
    1115   1120   1125

<210> 99
<211> 1207
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 99
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1   5   10   15

His Ala Ala Arg Pro Ile Trp Glu Leu Lys Lys Asp Val Tyr Val Val
            20   25   30

Glu Leu Asp Trp Tyr Pro Asp Ala Pro Gly Glu Met Val Val Leu Thr
        35   40   45

Cys Asp Thr Pro Glu Glu Asp Gly Ile Thr Trp Thr Leu Asp Gln Ser
    50   55   60

Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys Glu
65   70   75   80

Phe Gly Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Glu Val Leu
                85   90   95

```
Ser His Ser Leu Leu Leu Leu His Lys Lys Glu Asp Gly Ile Trp Ser
            100                 105                 110

Thr Asp Ile Leu Lys Asp Gln Lys Glu Pro Lys Asn Lys Thr Phe Leu
        115                 120                 125

Arg Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp Leu
    130                 135                 140

Thr Thr Ile Ser Thr Asp Leu Thr Phe Ser Val Lys Ser Ser Arg Gly
145                 150                 155                 160

Ser Ser Asp Pro Gln Gly Val Thr Cys Gly Ala Ala Thr Leu Ser Ala
                165                 170                 175

Glu Arg Val Arg Gly Asp Asn Lys Glu Tyr Glu Tyr Ser Val Glu Cys
            180                 185                 190

Gln Glu Asp Ser Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro Ile Glu
        195                 200                 205

Val Met Val Asp Ala Val His Lys Leu Lys Tyr Glu Asn Tyr Thr Ser
    210                 215                 220

Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys Asn Leu
225                 230                 235                 240

Gln Leu Lys Pro Leu Lys Asn Ser Arg Gln Val Glu Val Ser Trp Glu
                245                 250                 255

Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu Thr Phe
            260                 265                 270

Cys Val Gln Val Gln Gly Lys Ser Lys Arg Glu Lys Lys Asp Arg Val
        275                 280                 285

Phe Thr Asp Lys Thr Ser Ala Thr Val Ile Cys Arg Lys Asn Ala Ser
```

```
    290                 295                 300

Ile Ser Val Arg Ala Gln Asp Arg Tyr Tyr Ser Ser Ser Trp Ser Glu
305                 310                 315                 320

Trp Ala Ser Val Pro Cys Ser Gly Ser Thr Ser Gly Ser Gly Lys Pro
                325                 330                 335

Gly Ser Gly Glu Gly Ser Thr Lys Gly Arg Asn Leu Pro Val Ala Thr
            340                 345                 350

Pro Asp Pro Gly Met Phe Pro Cys Leu His His Ser Gln Asn Leu Leu
        355                 360                 365

Arg Ala Val Ser Asn Met Leu Gln Lys Ala Arg Gln Thr Leu Glu Phe
    370                 375                 380

Tyr Pro Cys Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys Asp
385                 390                 395                 400

Lys Thr Ser Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Lys Asn
                405                 410                 415

Glu Ser Cys Leu Asn Ser Arg Glu Thr Ser Phe Ile Thr Asn Gly Ser
            420                 425                 430

Cys Leu Ala Ser Arg Lys Thr Ser Phe Met Met Ala Leu Cys Leu Ser
        435                 440                 445

Ser Ile Tyr Glu Asp Leu Lys Met Tyr Gln Val Glu Phe Lys Thr Met
    450                 455                 460

Asn Ala Lys Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp Gln
465                 470                 475                 480

Asn Met Leu Ala Val Ile Asp Glu Leu Met Gln Ala Leu Asn Phe Asn
                485                 490                 495
```

```
Ser Glu Thr Val Pro Gln Lys Ser Ser Leu Glu Glu Pro Asp Phe Tyr
            500                 505                 510

Lys Thr Lys Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile Arg
        515                 520                 525

Ala Val Thr Ile Asp Arg Val Met Ser Tyr Leu Asn Ala Ser Ser Gly
    530                 535                 540

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
545                 550                 555                 560

Gly Ser Gly Gly Gly Ser Leu Gln Cys Arg Thr Ser Glu Cys Cys Phe
                565                 570                 575

Gln Asp Pro Pro Tyr Pro Asp Ala Asp Ser Gly Ser Ala Ser Gly Pro
            580                 585                 590

Arg Asp Leu Arg Cys Tyr Arg Ile Ser Ser Asp Arg Tyr Glu Cys Ser
        595                 600                 605

Trp Gln Tyr Glu Gly Pro Thr Ala Gly Val Ser His Phe Leu Arg Cys
    610                 615                 620

Cys Leu Ser Ser Gly Arg Cys Cys Tyr Phe Ala Ala Gly Ser Ala Thr
625                 630                 635                 640

Arg Leu Gln Phe Ser Asp Gln Ala Gly Val Ser Val Leu Tyr Thr Val
                645                 650                 655

Thr Leu Trp Val Glu Ser Trp Ala Arg Asn Gln Thr Glu Lys Ser Pro
            660                 665                 670

Glu Val Thr Leu Gln Leu Tyr Asn Ser Val Lys Tyr Glu Pro Pro Leu
        675                 680                 685

Gly Asp Ile Lys Val Ser Lys Leu Ala Gly Gln Leu Arg Met Glu Trp
```

```
    690                 695                 700

Glu Thr Pro Asp Asn Gln Val Gly Ala Glu Val Gln Phe Arg His Arg
705                 710                 715                 720

Thr Pro Ser Ser Pro Trp Lys Leu Gly Asp Cys Gly Pro Gln Asp Asp
                725                 730                 735

Asp Thr Glu Ser Cys Leu Cys Pro Leu Glu Met Asn Val Ala Gln Glu
            740                 745                 750

Phe Gln Leu Arg Arg Arg Gln Leu Gly Ser Gln Gly Ser Ser Trp Ser
        755                 760                 765

Lys Trp Ser Ser Pro Val Cys Val Pro Pro Glu Asn Pro Pro Gln Pro
    770                 775                 780

Gln Val Arg Phe Ser Val Glu Gln Leu Gly Gln Asp Gly Arg Arg Arg
785                 790                 795                 800

Leu Thr Leu Lys Glu Gln Pro Thr Gln Leu Glu Leu Pro Glu Gly Cys
                805                 810                 815

Gln Gly Leu Ala Pro Gly Thr Glu Val Thr Tyr Arg Leu Gln Leu His
            820                 825                 830

Met Leu Ser Cys Pro Cys Lys Ala Lys Ala Thr Arg Thr Leu His Leu
        835                 840                 845

Gly Lys Met Pro Tyr Leu Ser Gly Ala Ala Tyr Asn Val Ala Val Ile
    850                 855                 860

Ser Ser Asn Gln Phe Gly Pro Gly Leu Asn Gln Thr Trp His Ile Pro
865                 870                 875                 880

Ala Asp Thr His Thr Glu Pro Val Ala Leu Asn Ile Ser Val Gly Thr
                885                 890                 895
```

```
Asn Gly Thr Thr Met Tyr Trp Pro Ala Arg Ala Gln Ser Met Thr Tyr
            900                 905                 910

Cys Ile Glu Trp Gln Pro Val Gly Gln Asp Gly Gly Leu Ala Thr Cys
        915                 920                 925

Ser Leu Thr Ala Pro Gln Asp Pro Asp Pro Ala Gly Met Ala Thr Tyr
    930                 935                 940

Ser Trp Ser Arg Glu Ser Gly Ala Met Gly Gln Glu Lys Cys Tyr Tyr
945                 950                 955                 960

Ile Thr Ile Phe Ala Ser Ala His Pro Glu Lys Leu Thr Leu Trp Ser
                965                 970                 975

Thr Val Leu Ser Thr Tyr His Phe Gly Gly Asn Ala Ser Ala Ala Gly
            980                 985                 990

Thr Pro His His Val Ser Val Lys  Asn His Ser Leu Asp  Ser Val Ser
        995                 1000                1005

Val Asp  Trp Ala Pro Ser Leu  Leu Ser Thr Cys Pro  Gly Val Leu
    1010                1015                1020

Lys Glu  Tyr Val Val Arg Cys  Arg Asp Glu Asp Ser  Lys Gln Val
    1025                1030                1035

Ser Glu  His Pro Val Gln Pro  Thr Glu Thr Gln Val  Thr Leu Ser
    1040                1045                1050

Gly Leu  Arg Ala Gly Val Ala  Tyr Thr Val Gln Val  Arg Ala Asp
    1055                1060                1065

Thr Ala  Trp Leu Arg Gly Val  Trp Ser Gln Pro Gln  Arg Phe Ser
    1070                1075                1080

Ile Glu  Val Gln Val Ser Asp  Trp Leu Ile Phe Phe  Ala Ser Leu
```

```
    1085                1090                1095

Gly Ser  Phe Leu Ser Ile Leu  Leu Val Gly Val Leu  Gly Tyr Leu
    1100                1105                1110

Gly Leu  Asn Arg Ala Ala Arg  His Leu Cys Pro Pro  Leu Pro Thr
    1115                1120                1125

Pro Cys  Ala Ser Ser Ala Ile  Glu Phe Pro Gly Gly  Lys Glu Thr
    1130                1135                1140

Trp Gln  Trp Ile Asn Pro Val  Asp Phe Gln Glu Glu  Ala Ser Leu
    1145                1150                1155

Gln Glu  Ala Leu Val Val Glu  Met Ser Trp Asp Lys  Gly Glu Arg
    1160                1165                1170

Thr Glu  Pro Leu Glu Lys Thr  Glu Leu Pro Glu Gly  Ala Pro Glu
    1175                1180                1185

Leu Ala  Leu Asp Thr Glu Leu  Ser Leu Glu Asp Gly  Asp Arg Cys
    1190                1195                1200

Lys Ala  Lys Met
    1205


<210> 100
<211> 1407
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 100
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1               5                  10                  15

His Ala Ala Arg Pro Ile Trp Glu Leu Lys Lys Asp Val Tyr Val Val
```

```
            20                  25                  30

Glu Leu Asp Trp Tyr Pro Asp Ala Pro Gly Glu Met Val Val Leu Thr
        35                  40                  45

Cys Asp Thr Pro Glu Glu Asp Gly Ile Thr Trp Thr Leu Asp Gln Ser
    50                  55                  60

Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys Glu
65                  70                  75                  80

Phe Gly Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Glu Val Leu
                85                  90                  95

Ser His Ser Leu Leu Leu Leu His Lys Lys Glu Asp Gly Ile Trp Ser
            100                 105                 110

Thr Asp Ile Leu Lys Asp Gln Lys Glu Pro Lys Asn Lys Thr Phe Leu
        115                 120                 125

Arg Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp Leu
    130                 135                 140

Thr Thr Ile Ser Thr Asp Leu Thr Phe Ser Val Lys Ser Ser Arg Gly
145                 150                 155                 160

Ser Ser Asp Pro Gln Gly Val Thr Cys Gly Ala Ala Thr Leu Ser Ala
                165                 170                 175

Glu Arg Val Arg Gly Asp Asn Lys Glu Tyr Glu Tyr Ser Val Glu Cys
            180                 185                 190

Gln Glu Asp Ser Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro Ile Glu
        195                 200                 205

Val Met Val Asp Ala Val His Lys Leu Lys Tyr Glu Asn Tyr Thr Ser
    210                 215                 220
```

```
Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys Asn Leu
225                 230                 235                 240

Gln Leu Lys Pro Leu Lys Asn Ser Arg Gln Val Glu Val Ser Trp Glu
                245                 250                 255

Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu Thr Phe
            260                 265                 270

Cys Val Gln Val Gln Gly Lys Ser Lys Arg Glu Lys Lys Asp Arg Val
        275                 280                 285

Phe Thr Asp Lys Thr Ser Ala Thr Val Ile Cys Arg Lys Asn Ala Ser
    290                 295                 300

Ile Ser Val Arg Ala Gln Asp Arg Tyr Tyr Ser Ser Ser Trp Ser Glu
305                 310                 315                 320

Trp Ala Ser Val Pro Cys Ser Gly Ser Thr Ser Gly Ser Gly Lys Pro
                325                 330                 335

Gly Ser Gly Glu Gly Ser Thr Lys Gly Arg Asn Leu Pro Val Ala Thr
            340                 345                 350

Pro Asp Pro Gly Met Phe Pro Cys Leu His His Ser Gln Asn Leu Leu
        355                 360                 365

Arg Ala Val Ser Asn Met Leu Gln Lys Ala Arg Gln Thr Leu Glu Phe
    370                 375                 380

Tyr Pro Cys Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys Asp
385                 390                 395                 400

Lys Thr Ser Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Lys Asn
                405                 410                 415

Glu Ser Cys Leu Asn Ser Arg Glu Thr Ser Phe Ile Thr Asn Gly Ser
```

```
            420                 425                 430

Cys Leu Ala Ser Arg Lys Thr Ser Phe Met Met Ala Leu Cys Leu Ser
        435                 440                 445

Ser Ile Tyr Glu Asp Leu Lys Met Tyr Gln Val Glu Phe Lys Thr Met
    450                 455                 460

Asn Ala Lys Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp Gln
465                 470                 475                 480

Asn Met Leu Ala Val Ile Asp Glu Leu Met Gln Ala Leu Asn Phe Asn
                485                 490                 495

Ser Glu Thr Val Pro Gln Lys Ser Ser Leu Glu Glu Pro Asp Phe Tyr
            500                 505                 510

Lys Thr Lys Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile Arg
        515                 520                 525

Ala Val Thr Ile Asp Arg Val Met Ser Tyr Leu Asn Ala Ser Ser Gly
    530                 535                 540

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
545                 550                 555                 560

Gly Ser Gly Gly Gly Ser Leu Gln Lys Ile Asp Ala Cys Lys Arg Gly
                565                 570                 575

Asp Val Thr Val Lys Pro Ser His Val Ile Leu Leu Gly Ser Thr Val
            580                 585                 590

Asn Ile Thr Cys Ser Leu Lys Pro Arg Gln Gly Cys Phe His Tyr Ser
        595                 600                 605

Arg Arg Asn Lys Leu Ile Leu Tyr Lys Phe Asp Arg Arg Ile Asn Phe
    610                 615                 620
```

```
His His Gly His Ser Leu Asn Ser Gln Val Thr Gly Leu Pro Leu Gly
625                 630                 635                 640

Thr Thr Leu Phe Val Cys Lys Leu Ala Cys Ile Asn Ser Asp Glu Ile
                645                 650                 655

Gln Ile Cys Gly Ala Glu Ile Phe Val Gly Val Ala Pro Glu Gln Pro
            660                 665                 670

Gln Asn Leu Ser Cys Ile Gln Lys Gly Glu Gln Gly Thr Val Ala Cys
        675                 680                 685

Thr Trp Glu Arg Gly Arg Asp Thr His Leu Tyr Thr Glu Tyr Thr Leu
    690                 695                 700

Gln Leu Ser Gly Pro Lys Asn Leu Thr Trp Gln Lys Gln Cys Lys Asp
705                 710                 715                 720

Ile Tyr Cys Asp Tyr Leu Asp Phe Gly Ile Asn Leu Thr Pro Glu Ser
                725                 730                 735

Pro Glu Ser Asn Phe Thr Ala Lys Val Thr Ala Val Asn Ser Leu Gly
            740                 745                 750

Ser Ser Ser Ser Leu Pro Ser Thr Phe Thr Phe Leu Asp Ile Val Arg
        755                 760                 765

Pro Leu Pro Pro Trp Asp Ile Arg Ile Lys Phe Gln Lys Ala Ser Val
    770                 775                 780

Ser Arg Cys Thr Leu Tyr Trp Arg Asp Glu Gly Leu Val Leu Leu Asn
785                 790                 795                 800

Arg Leu Arg Tyr Arg Pro Ser Asn Ser Arg Leu Trp Asn Met Val Asn
                805                 810                 815

Val Thr Lys Ala Lys Gly Arg His Asp Leu Leu Asp Leu Lys Pro Phe
```

```
            820                 825                 830

Thr Glu Tyr Glu Phe Gln Ile Ser Ser Lys Leu His Leu Tyr Lys Gly
        835                 840                 845

Ser Trp Ser Asp Trp Ser Glu Ser Leu Arg Ala Gln Thr Pro Glu Glu
    850                 855                 860

Glu Pro Thr Gly Met Leu Asp Val Trp Tyr Met Lys Arg His Ile Asp
865                 870                 875                 880

Tyr Ser Arg Gln Gln Ile Ser Leu Phe Trp Lys Asn Leu Ser Val Ser
                885                 890                 895

Glu Ala Arg Gly Lys Ile Leu His Tyr Gln Val Thr Leu Gln Glu Leu
            900                 905                 910

Thr Gly Gly Lys Ala Met Thr Gln Asn Ile Thr Gly His Thr Ser Trp
        915                 920                 925

Thr Thr Val Ile Pro Arg Thr Gly Asn Trp Ala Val Ala Val Ser Ala
    930                 935                 940

Ala Asn Ser Lys Gly Ser Ser Leu Pro Thr Arg Ile Asn Ile Met Asn
945                 950                 955                 960

Leu Cys Glu Ala Gly Leu Leu Ala Pro Arg Gln Val Ser Ala Asn Ser
                965                 970                 975

Glu Gly Met Asp Asn Ile Leu Val Thr Trp Gln Pro Pro Arg Lys Asp
            980                 985                 990

Pro Ser Ala Val Gln Glu Tyr Val  Val Glu Trp Arg Glu  Leu His Pro
        995                 1000                1005

Gly Gly  Asp Thr Gln Val Pro  Leu Asn Trp Leu Arg  Ser Arg Pro
    1010                1015                1020
```

```
Tyr Asn  Val Ser Ala Leu Ile  Ser Glu Asn Ile Lys  Ser Tyr Ile
    1025                1030                1035

Cys Tyr  Glu Ile Arg Val Tyr  Ala Leu Ser Gly Asp  Gln Gly Gly
    1040                1045                1050

Cys Ser  Ser Ile Leu Gly Asn  Ser Lys His Lys Ala  Pro Leu Ser
    1055                1060                1065

Gly Pro  His Ile Asn Ala Ile  Thr Glu Glu Lys Gly  Ser Ile Leu
    1070                1075                1080

Ile Ser  Trp Asn Ser Ile Pro  Val Gln Glu Gln Met  Gly Cys Leu
    1085                1090                1095

Leu His  Tyr Arg Ile Tyr Trp  Lys Glu Arg Asp Ser  Asn Ser Gln
    1100                1105                1110

Pro Gln  Leu Cys Glu Ile Pro  Tyr Arg Val Ser Gln  Asn Ser His
    1115                1120                1125

Pro Ile  Asn Ser Leu Gln Pro  Arg Val Thr Tyr Val  Leu Trp Met
    1130                1135                1140

Thr Ala  Leu Thr Ala Ala Gly  Glu Ser Ser His Gly  Asn Glu Arg
    1145                1150                1155

Glu Phe  Cys Leu Gln Gly Lys  Ala Asn Trp Met Ala  Phe Val Ala
    1160                1165                1170

Pro Ser  Ile Cys Ile Ala Ile  Ile Met Val Gly Ile  Phe Ser Thr
    1175                1180                1185

His Tyr  Phe Gln Gln Lys Val  Phe Val Leu Leu Ala  Ala Leu Arg
    1190                1195                1200

Pro Gln  Trp Cys Ser Arg Glu  Ile Pro Asp Pro Ala  Asn Ser Thr
```

```
    1205                1210                1215

Cys Ala  Lys Lys Tyr Pro Ile  Ala Glu Glu Lys Thr  Gln Leu Pro
    1220                1225                1230

Leu Asp  Arg Leu Leu Ile Asp  Trp Pro Thr Pro Glu  Asp Pro Glu
    1235                1240                1245

Pro Leu  Val Ile Ser Glu Val  Leu His Gln Val Thr  Pro Val Phe
    1250                1255                1260

Arg His  Pro Pro Cys Ser Asn  Trp Pro Gln Arg Glu  Lys Gly Ile
    1265                1270                1275

Gln Gly  His Gln Ala Ser Glu  Lys Asp Met Met His  Ser Ala Ser
    1280                1285                1290

Ser Pro  Pro Pro Pro Arg Ala  Leu Gln Ala Glu Ser  Arg Gln Leu
    1295                1300                1305

Val Asp  Leu Tyr Lys Val Leu  Glu Ser Arg Gly Ser  Asp Pro Lys
    1310                1315                1320

Pro Glu  Asn Pro Ala Cys Pro  Trp Thr Val Leu Pro  Ala Gly Asp
    1325                1330                1335

Leu Pro  Thr His Asp Gly Tyr  Leu Pro Ser Asn Ile  Asp Asp Leu
    1340                1345                1350

Pro Ser  His Glu Ala Pro Leu  Ala Asp Ser Leu Glu  Glu Leu Glu
    1355                1360                1365

Pro Gln  His Ile Ser Leu Ser  Val Phe Pro Ser Ser  Ser Leu His
    1370                1375                1380

Pro Leu  Thr Phe Ser Cys Gly  Asp Lys Leu Thr Leu  Asp Gln Leu
    1385                1390                1395
```

Lys Met Arg Cys Asp Ser Leu Met Leu
    1400   1405

<210> 101
<211> 976
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 101
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1   5   10   15

His Ala Ala Arg Pro His Lys Cys Asp Ile Thr Leu Gln Glu Ile Ile
            20   25   30

Lys Thr Leu Asn Ser Leu Thr Glu Gln Lys Thr Leu Cys Thr Glu Leu
        35   40   45

Thr Val Thr Asp Ile Phe Ala Ala Ser Lys Asn Thr Thr Glu Lys Glu
    50   55   60

Thr Phe Cys Arg Ala Ala Thr Val Leu Arg Gln Phe Tyr Ser His His
65   70   75   80

Glu Lys Asp Thr Arg Cys Leu Gly Ala Thr Ala Gln Gln Phe His Arg
                85   90   95

His Lys Gln Leu Ile Arg Phe Leu Lys Arg Leu Asp Arg Asn Leu Trp
            100   105   110

Gly Leu Ala Gly Leu Asn Ser Cys Pro Val Lys Glu Ala Asn Gln Ser
        115   120   125

Thr Leu Glu Asn Phe Leu Glu Arg Leu Lys Thr Ile Met Arg Glu Lys
    130   135   140

```
Tyr Ser Lys Cys Ser Ser Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser
145                 150                 155                 160

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Leu Gln
                165                 170                 175

Met Lys Val Leu Gln Glu Pro Thr Cys Val Ser Asp Tyr Met Ser Ile
            180                 185                 190

Ser Thr Cys Glu Trp Lys Met Asn Gly Pro Thr Asn Cys Ser Thr Glu
        195                 200                 205

Leu Arg Leu Leu Tyr Gln Leu Val Phe Leu Leu Ser Glu Ala His Thr
    210                 215                 220

Cys Ile Pro Glu Asn Asn Gly Gly Ala Gly Cys Val Cys His Leu Leu
225                 230                 235                 240

Met Asp Asp Val Val Ser Ala Asp Asn Tyr Thr Leu Asp Leu Trp Ala
                245                 250                 255

Gly Gln Gln Leu Leu Trp Lys Gly Ser Phe Lys Pro Ser Glu His Val
            260                 265                 270

Lys Pro Arg Ala Pro Gly Asn Leu Thr Val His Thr Asn Val Ser Asp
        275                 280                 285

Thr Leu Leu Leu Thr Trp Ser Asn Pro Tyr Pro Pro Asp Asn Tyr Leu
    290                 295                 300

Tyr Asn His Leu Thr Tyr Ala Val Asn Ile Trp Ser Glu Asn Asp Pro
305                 310                 315                 320

Ala Asp Phe Arg Ile Tyr Asn Val Thr Tyr Leu Glu Pro Ser Leu Arg
                325                 330                 335

Ile Ala Ala Ser Thr Leu Lys Ser Gly Ile Ser Tyr Arg Ala Arg Val
```

```
            340                 345                 350

Arg Ala Trp Ala Gln Cys Tyr Asn Thr Thr Trp Ser Glu Trp Ser Pro
        355                 360                 365

Ser Thr Lys Trp His Asn Ser Tyr Arg Glu Pro Phe Glu Gln His Leu
    370                 375                 380

Leu Leu Gly Val Ser Val Ser Cys Ile Val Ile Leu Ala Val Cys Leu
385                 390                 395                 400

Leu Cys Tyr Val Ser Ile Thr Lys Ile Lys Lys Glu Trp Trp Asp Gln
                405                 410                 415

Ile Pro Asn Pro Ala Arg Ser Arg Leu Val Ala Ile Ile Ile Gln Asp
            420                 425                 430

Ala Gln Gly Ser Gln Trp Glu Lys Arg Ser Arg Gly Gln Glu Pro Ala
        435                 440                 445

Lys Cys Pro His Trp Lys Asn Cys Leu Thr Lys Leu Leu Pro Cys Phe
    450                 455                 460

Leu Glu His Asn Met Lys Arg Asp Glu Asp Pro His Lys Ala Ala Lys
465                 470                 475                 480

Glu Met Pro Phe Gln Gly Ser Gly Lys Ser Ala Trp Cys Pro Val Glu
                485                 490                 495

Ile Ser Lys Thr Val Leu Trp Pro Glu Ser Ile Ser Val Val Arg Cys
            500                 505                 510

Val Glu Leu Phe Glu Ala Pro Val Glu Cys Glu Glu Glu Glu Glu Val
        515                 520                 525

Glu Glu Glu Lys Gly Ser Phe Cys Ala Ser Pro Glu Ser Ser Arg Asp
    530                 535                 540
```

```
Asp Phe Gln Glu Gly Arg Glu Gly Ile Val Ala Arg Leu Thr Glu Ser
545                 550                 555                 560

Leu Phe Leu Asp Leu Leu Gly Glu Glu Asn Gly Gly Phe Cys Gln Gln
                565                 570                 575

Asp Met Gly Glu Ser Cys Leu Leu Pro Pro Ser Gly Ser Thr Ser Ala
            580                 585                 590

His Met Pro Trp Asp Glu Phe Pro Ser Ala Gly Pro Lys Glu Ala Pro
        595                 600                 605

Pro Trp Gly Lys Glu Gln Pro Leu His Leu Glu Pro Ser Pro Pro Ala
    610                 615                 620

Ser Pro Thr Gln Ser Pro Asp Asn Leu Thr Cys Thr Glu Thr Pro Leu
625                 630                 635                 640

Val Ile Ala Gly Asn Pro Ala Tyr Arg Ser Phe Ser Asn Ser Leu Ser
                645                 650                 655

Gln Ser Pro Cys Pro Arg Glu Leu Gly Pro Asp Pro Leu Leu Ala Arg
            660                 665                 670

His Leu Glu Glu Val Glu Pro Glu Met Pro Cys Val Pro Gln Leu Ser
        675                 680                 685

Glu Pro Thr Thr Val Pro Gln Pro Glu Pro Glu Thr Trp Glu Gln Ile
    690                 695                 700

Leu Arg Arg Asn Val Leu Gln His Gly Ala Ala Ala Ala Pro Val Ser
705                 710                 715                 720

Ala Pro Thr Ser Gly Tyr Gln Glu Phe Val His Ala Val Glu Gln Gly
                725                 730                 735

Gly Thr Gln Ala Ser Ala Val Val Gly Leu Gly Pro Pro Gly Glu Ala
```

```
            740                 745                 750

Gly Tyr Lys Ala Phe Ser Ser Leu Leu Ala Ser Ser Ala Val Ser Pro
        755                 760                 765

Glu Lys Cys Gly Phe Gly Ala Ser Ser Gly Glu Glu Gly Tyr Lys Pro
    770                 775                 780

Phe Gln Asp Leu Ile Pro Gly Cys Pro Gly Asp Pro Ala Pro Val Pro
785                 790                 795                 800

Val Pro Leu Phe Thr Phe Gly Leu Asp Arg Glu Pro Pro Arg Ser Pro
                805                 810                 815

Gln Ser Ser His Leu Pro Ser Ser Ser Pro Glu His Leu Gly Leu Glu
            820                 825                 830

Pro Gly Glu Lys Val Glu Asp Met Pro Lys Pro Pro Leu Pro Gln Glu
        835                 840                 845

Gln Ala Thr Asp Pro Leu Val Asp Ser Leu Gly Ser Gly Ile Val Tyr
    850                 855                 860

Ser Ala Leu Thr Cys His Leu Cys Gly His Leu Lys Gln Cys His Gly
865                 870                 875                 880

Gln Glu Asp Gly Gly Gln Thr Pro Val Met Ala Ser Pro Cys Cys Gly
                885                 890                 895

Cys Cys Cys Gly Asp Arg Ser Ser Pro Pro Thr Thr Pro Leu Arg Ala
            900                 905                 910

Pro Asp Pro Ser Pro Gly Gly Val Pro Leu Glu Ala Ser Leu Cys Pro
        915                 920                 925

Ala Ser Leu Ala Pro Ser Gly Ile Ser Glu Lys Ser Lys Ser Ser Ser
    930                 935                 940
```

Ser Phe His Pro Ala Pro Gly Asn Ala Gln Ser Ser Ser Gln Thr Pro
945 950 955 960

Lys Ile Val Asn Phe Val Ser Val Gly Pro Thr Tyr Met Arg Val Ser
965 970 975

<210> 102
<211> 523
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 102
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro His Lys Cys Asp Ile Thr Leu Gln Glu Ile Ile
20 25 30

Lys Thr Leu Asn Ser Leu Thr Glu Gln Lys Thr Leu Cys Thr Glu Leu
35 40 45

Thr Val Thr Asp Ile Phe Ala Ala Ser Lys Asn Thr Thr Glu Lys Glu
50 55 60

Thr Phe Cys Arg Ala Ala Thr Val Leu Arg Gln Phe Tyr Ser His His
65 70 75 80

Glu Lys Asp Thr Arg Cys Leu Gly Ala Thr Ala Gln Gln Phe His Arg
85 90 95

His Lys Gln Leu Ile Arg Phe Leu Lys Arg Leu Asp Arg Asn Leu Trp
100 105 110

Gly Leu Ala Gly Leu Asn Ser Cys Pro Val Lys Glu Ala Asn Gln Ser
115 120 125

```
Thr Leu Glu Asn Phe Leu Glu Arg Leu Lys Thr Ile Met Arg Glu Lys
    130                 135                 140

Tyr Ser Lys Cys Ser Ser Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser
145                 150                 155                 160

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Leu Gln
                165                 170                 175

Leu Asn Thr Thr Ile Leu Thr Pro Asn Gly Asn Glu Asp Thr Thr Ala
            180                 185                 190

Asp Phe Phe Leu Thr Thr Met Pro Thr Asp Ser Leu Ser Val Ser Thr
        195                 200                 205

Leu Pro Leu Pro Glu Val Gln Cys Phe Val Phe Asn Val Glu Tyr Met
    210                 215                 220

Asn Cys Thr Trp Asn Ser Ser Ser Glu Pro Gln Pro Thr Asn Leu Thr
225                 230                 235                 240

Leu His Tyr Trp Tyr Lys Asn Ser Asp Asn Asp Lys Val Gln Lys Cys
                245                 250                 255

Ser His Tyr Leu Phe Ser Glu Glu Ile Thr Ser Gly Cys Gln Leu Gln
            260                 265                 270

Lys Lys Glu Ile His Leu Tyr Gln Thr Phe Val Val Gln Leu Gln Asp
        275                 280                 285

Pro Arg Glu Pro Arg Arg Gln Ala Thr Gln Met Leu Lys Leu Gln Asn
    290                 295                 300

Leu Val Ile Pro Trp Ala Pro Glu Asn Leu Thr Leu His Lys Leu Ser
305                 310                 315                 320

Glu Ser Gln Leu Glu Leu Asn Trp Asn Asn Arg Phe Leu Asn His Cys
```

```
                325                 330                 335

Leu Glu His Leu Val Gln Tyr Arg Thr Asp Trp Asp His Ser Trp Thr
            340                 345                 350

Glu Gln Ser Val Asp Tyr Arg His Lys Phe Ser Leu Pro Ser Val Asp
        355                 360                 365

Gly Gln Lys Arg Tyr Thr Phe Arg Val Arg Ser Arg Phe Asn Pro Leu
    370                 375                 380

Cys Gly Ser Ala Gln His Trp Ser Glu Trp Ser His Pro Ile His Trp
385                 390                 395                 400

Gly Ser Asn Thr Ser Lys Glu Asn Pro Phe Leu Phe Ala Leu Glu Ala
                405                 410                 415

Val Val Ile Ser Val Gly Ser Met Gly Leu Ile Ile Ser Leu Leu Cys
            420                 425                 430

Val Tyr Phe Trp Leu Glu Arg Thr Met Pro Arg Ile Pro Thr Leu Lys
        435                 440                 445

Asn Leu Glu Asp Leu Val Thr Glu Tyr His Gly Asn Phe Ser Ala Trp
    450                 455                 460

Ser Gly Val Ser Lys Gly Leu Ala Glu Ser Leu Gln Pro Asp Tyr Ser
465                 470                 475                 480

Glu Arg Leu Cys Leu Val Ser Glu Ile Pro Pro Lys Gly Gly Ala Leu
                485                 490                 495

Gly Glu Gly Pro Gly Ala Ser Pro Cys Asn Gln His Ser Pro Tyr Trp
            500                 505                 510

Ala Pro Pro Cys Tyr Thr Leu Lys Pro Glu Thr
        515                 520
```

<210> 103
<211> 582
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 103
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro His Lys Cys Asp Ile Thr Leu Gln Glu Ile Ile
20 25 30

Lys Thr Leu Asn Ser Leu Thr Glu Gln Lys Thr Leu Cys Thr Glu Leu
35 40 45

Thr Val Thr Asp Ile Phe Ala Ala Ser Lys Asn Thr Thr Glu Lys Glu
50 55 60

Thr Phe Cys Arg Ala Ala Thr Val Leu Arg Gln Phe Tyr Ser His His
65 70 75 80

Glu Lys Asp Thr Arg Cys Leu Gly Ala Thr Ala Gln Gln Phe His Arg
85 90 95

His Lys Gln Leu Ile Arg Phe Leu Lys Arg Leu Asp Arg Asn Leu Trp
100 105 110

Gly Leu Ala Gly Leu Asn Ser Cys Pro Val Lys Glu Ala Asn Gln Ser
115 120 125

Thr Leu Glu Asn Phe Leu Glu Arg Leu Lys Thr Ile Met Arg Glu Lys
130 135 140

Tyr Ser Lys Cys Ser Ser Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser
145 150 155 160

```
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Leu Gln
                165                 170                 175

Gly Gly Gly Gly Ala Ala Pro Thr Glu Thr Gln Pro Pro Val Thr Asn
            180                 185                 190

Leu Ser Val Ser Val Glu Asn Leu Cys Thr Val Ile Trp Thr Trp Asn
        195                 200                 205

Pro Pro Glu Gly Ala Ser Ser Asn Cys Ser Leu Trp Tyr Phe Ser His
    210                 215                 220

Phe Gly Asp Lys Gln Asp Lys Lys Ile Ala Pro Glu Thr Arg Arg Ser
225                 230                 235                 240

Ile Glu Val Pro Leu Asn Glu Arg Ile Cys Leu Gln Val Gly Ser Gln
                245                 250                 255

Cys Ser Thr Asn Glu Ser Glu Lys Pro Ser Ile Leu Val Glu Lys Cys
            260                 265                 270

Ile Ser Pro Pro Glu Gly Asp Pro Glu Ser Ala Val Thr Glu Leu Gln
        275                 280                 285

Cys Ile Trp His Asn Leu Ser Tyr Met Lys Cys Ser Trp Leu Pro Gly
    290                 295                 300

Arg Asn Thr Ser Pro Asp Thr Asn Tyr Thr Leu Tyr Tyr Trp His Arg
305                 310                 315                 320

Ser Leu Glu Lys Ile His Gln Cys Glu Asn Ile Phe Arg Glu Gly Gln
                325                 330                 335

Tyr Phe Gly Cys Ser Phe Asp Leu Thr Lys Val Lys Asp Ser Ser Phe
            340                 345                 350

Glu Gln His Ser Val Gln Ile Met Val Lys Asp Asn Ala Gly Lys Ile
```

```
        355                 360                 365

Lys Pro Ser Phe Asn Ile Val Pro Leu Thr Ser Arg Val Lys Pro Asp
    370                 375                 380

Pro Pro His Ile Lys Asn Leu Ser Phe His Asn Asp Asp Leu Tyr Val
385                 390                 395                 400

Gln Trp Glu Asn Pro Gln Asn Phe Ile Ser Arg Cys Leu Phe Tyr Glu
                405                 410                 415

Val Glu Val Asn Asn Ser Gln Thr Glu Thr His Asn Val Phe Tyr Val
            420                 425                 430

Gln Glu Ala Lys Cys Glu Asn Pro Glu Phe Glu Arg Asn Val Glu Asn
        435                 440                 445

Thr Ser Cys Phe Met Val Pro Gly Val Leu Pro Asp Thr Leu Asn Thr
    450                 455                 460

Val Arg Ile Arg Val Lys Thr Asn Lys Leu Cys Tyr Glu Asp Asp Lys
465                 470                 475                 480

Leu Trp Ser Asn Trp Ser Gln Glu Met Ser Ile Gly Lys Lys Arg Asn
                485                 490                 495

Ser Thr Leu Tyr Ile Thr Met Leu Leu Ile Val Pro Val Ile Val Ala
            500                 505                 510

Gly Ala Ile Ile Val Leu Leu Leu Tyr Leu Lys Arg Leu Lys Ile Ile
        515                 520                 525

Ile Phe Pro Pro Ile Pro Asp Pro Gly Lys Ile Phe Lys Glu Met Phe
    530                 535                 540

Gly Asp Gln Asn Asp Asp Thr Leu His Trp Lys Lys Tyr Asp Ile Tyr
545                 550                 555                 560
```

Glu Lys Gln Thr Lys Glu Glu Thr Asp Ser Val Val Leu Ile Glu Asn
565 570 575

Leu Lys Lys Ala Ser Gln
580

<210> 104
<211> 981
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 104
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Asn Thr Thr Glu Lys Glu Thr Phe Cys Arg Ala
20 25 30

Ala Thr Val Leu Arg Gln Phe Tyr Ser His His Glu Lys Asp Thr Arg
35 40 45

Cys Leu Gly Ala Thr Ala Gln Gln Phe His Arg His Lys Gln Leu Ile
50 55 60

Arg Phe Leu Lys Arg Leu Asp Arg Asn Leu Trp Gly Leu Ala Gly Leu
65 70 75 80

Asn Ser Cys Pro Val Lys Glu Ala Asn Gln Ser Thr Leu Glu Asn Phe
85 90 95

Leu Glu Arg Leu Lys Thr Ile Met Arg Glu Lys Tyr Ser Lys Cys Ser
100 105 110

Ser Gly Gly Asn Gly Gly His Lys Cys Asp Ile Thr Leu Gln Glu Ile
115 120 125

```
Ile Lys Thr Leu Asn Ser Leu Thr Glu Gln Lys Thr Leu Cys Thr Glu
    130                 135                 140

Leu Thr Val Thr Asp Ile Phe Ala Ala Ser Lys Ser Gly Gly Gly Ser
145                 150                 155                 160

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
                165                 170                 175

Gly Gly Ser Leu Gln Met Lys Val Leu Gln Glu Pro Thr Cys Val Ser
            180                 185                 190

Asp Tyr Met Ser Ile Ser Thr Cys Glu Trp Lys Met Asn Gly Pro Thr
        195                 200                 205

Asn Cys Ser Thr Glu Leu Arg Leu Leu Tyr Gln Leu Val Phe Leu Leu
    210                 215                 220

Ser Glu Ala His Thr Cys Ile Pro Glu Asn Asn Gly Gly Ala Gly Cys
225                 230                 235                 240

Val Cys His Leu Leu Met Asp Asp Val Val Ser Ala Asp Asn Tyr Thr
                245                 250                 255

Leu Asp Leu Trp Ala Gly Gln Gln Leu Leu Trp Lys Gly Ser Phe Lys
            260                 265                 270

Pro Ser Glu His Val Lys Pro Arg Ala Pro Gly Asn Leu Thr Val His
        275                 280                 285

Thr Asn Val Ser Asp Thr Leu Leu Leu Thr Trp Ser Asn Pro Tyr Pro
    290                 295                 300

Pro Asp Asn Tyr Leu Tyr Asn His Leu Thr Tyr Ala Val Asn Ile Trp
305                 310                 315                 320

Ser Glu Asn Asp Pro Ala Asp Phe Arg Ile Tyr Asn Val Thr Tyr Leu
```

```
                325                 330                 335

Glu Pro Ser Leu Arg Ile Ala Ala Ser Thr Leu Lys Ser Gly Ile Ser
            340                 345                 350

Tyr Arg Ala Arg Val Arg Ala Trp Ala Gln Cys Tyr Asn Thr Thr Trp
        355                 360                 365

Ser Glu Trp Ser Pro Ser Thr Lys Trp His Asn Ser Tyr Arg Glu Pro
    370                 375                 380

Phe Glu Gln His Leu Leu Leu Gly Val Ser Val Ser Cys Ile Val Ile
385                 390                 395                 400

Leu Ala Val Cys Leu Leu Cys Tyr Val Ser Ile Thr Lys Ile Lys Lys
                405                 410                 415

Glu Trp Trp Asp Gln Ile Pro Asn Pro Ala Arg Ser Arg Leu Val Ala
            420                 425                 430

Ile Ile Ile Gln Asp Ala Gln Gly Ser Gln Trp Glu Lys Arg Ser Arg
        435                 440                 445

Gly Gln Glu Pro Ala Lys Cys Pro His Trp Lys Asn Cys Leu Thr Lys
    450                 455                 460

Leu Leu Pro Cys Phe Leu Glu His Asn Met Lys Arg Asp Glu Asp Pro
465                 470                 475                 480

His Lys Ala Ala Lys Glu Met Pro Phe Gln Gly Ser Gly Lys Ser Ala
                485                 490                 495

Trp Cys Pro Val Glu Ile Ser Lys Thr Val Leu Trp Pro Glu Ser Ile
            500                 505                 510

Ser Val Val Arg Cys Val Glu Leu Phe Glu Ala Pro Val Glu Cys Glu
        515                 520                 525
```

```
Glu Glu Glu Glu Val Glu Glu Glu Lys Gly Ser Phe Cys Ala Ser Pro
    530                 535                 540

Glu Ser Ser Arg Asp Asp Phe Gln Glu Gly Arg Glu Gly Ile Val Ala
545                 550                 555                 560

Arg Leu Thr Glu Ser Leu Phe Leu Asp Leu Leu Gly Glu Glu Asn Gly
                565                 570                 575

Gly Phe Cys Gln Gln Asp Met Gly Glu Ser Cys Leu Leu Pro Pro Ser
            580                 585                 590

Gly Ser Thr Ser Ala His Met Pro Trp Asp Glu Phe Pro Ser Ala Gly
        595                 600                 605

Pro Lys Glu Ala Pro Pro Trp Gly Lys Glu Gln Pro Leu His Leu Glu
    610                 615                 620

Pro Ser Pro Pro Ala Ser Pro Thr Gln Ser Pro Asp Asn Leu Thr Cys
625                 630                 635                 640

Thr Glu Thr Pro Leu Val Ile Ala Gly Asn Pro Ala Tyr Arg Ser Phe
                645                 650                 655

Ser Asn Ser Leu Ser Gln Ser Pro Cys Pro Arg Glu Leu Gly Pro Asp
            660                 665                 670

Pro Leu Leu Ala Arg His Leu Glu Glu Val Glu Pro Glu Met Pro Cys
        675                 680                 685

Val Pro Gln Leu Ser Glu Pro Thr Thr Val Pro Gln Pro Glu Pro Glu
    690                 695                 700

Thr Trp Glu Gln Ile Leu Arg Arg Asn Val Leu Gln His Gly Ala Ala
705                 710                 715                 720

Ala Ala Pro Val Ser Ala Pro Thr Ser Gly Tyr Gln Glu Phe Val His
```

```
                725                 730                 735

Ala Val Glu Gln Gly Gly Thr Gln Ala Ser Ala Val Val Gly Leu Gly
            740                 745                 750

Pro Pro Gly Glu Ala Gly Tyr Lys Ala Phe Ser Ser Leu Leu Ala Ser
        755                 760                 765

Ser Ala Val Ser Pro Glu Lys Cys Gly Phe Gly Ala Ser Ser Gly Glu
    770                 775                 780

Glu Gly Tyr Lys Pro Phe Gln Asp Leu Ile Pro Gly Cys Pro Gly Asp
785                 790                 795                 800

Pro Ala Pro Val Pro Val Pro Leu Phe Thr Phe Gly Leu Asp Arg Glu
                805                 810                 815

Pro Pro Arg Ser Pro Gln Ser Ser His Leu Pro Ser Ser Ser Pro Glu
            820                 825                 830

His Leu Gly Leu Glu Pro Gly Glu Lys Val Glu Asp Met Pro Lys Pro
        835                 840                 845

Pro Leu Pro Gln Glu Gln Ala Thr Asp Pro Leu Val Asp Ser Leu Gly
    850                 855                 860

Ser Gly Ile Val Tyr Ser Ala Leu Thr Cys His Leu Cys Gly His Leu
865                 870                 875                 880

Lys Gln Cys His Gly Gln Glu Asp Gly Gly Gln Thr Pro Val Met Ala
                885                 890                 895

Ser Pro Cys Cys Gly Cys Cys Cys Gly Asp Arg Ser Ser Pro Pro Thr
            900                 905                 910

Thr Pro Leu Arg Ala Pro Asp Pro Ser Pro Gly Gly Val Pro Leu Glu
        915                 920                 925
```

Ala Ser Leu Cys Pro Ala Ser Leu Ala Pro Ser Gly Ile Ser Glu Lys
930 935 940

Ser Lys Ser Ser Ser Ser Phe His Pro Ala Pro Gly Asn Ala Gln Ser
945 950 955 960

Ser Ser Gln Thr Pro Lys Ile Val Asn Phe Val Ser Val Gly Pro Thr
965 970 975

Tyr Met Arg Val Ser
980

<210> 105
<211> 528
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 105
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Asn Thr Thr Glu Lys Glu Thr Phe Cys Arg Ala
20 25 30

Ala Thr Val Leu Arg Gln Phe Tyr Ser His His Glu Lys Asp Thr Arg
35 40 45

Cys Leu Gly Ala Thr Ala Gln Gln Phe His Arg His Lys Gln Leu Ile
50 55 60

Arg Phe Leu Lys Arg Leu Asp Arg Asn Leu Trp Gly Leu Ala Gly Leu
65 70 75 80

Asn Ser Cys Pro Val Lys Glu Ala Asn Gln Ser Thr Leu Glu Asn Phe
85 90 95

```
Leu Glu Arg Leu Lys Thr Ile Met Arg Glu Lys Tyr Ser Lys Cys Ser
            100                 105                 110

Ser Gly Gly Asn Gly Gly His Lys Cys Asp Ile Thr Leu Gln Glu Ile
        115                 120                 125

Ile Lys Thr Leu Asn Ser Leu Thr Glu Gln Lys Thr Leu Cys Thr Glu
    130                 135                 140

Leu Thr Val Thr Asp Ile Phe Ala Ala Ser Lys Ser Gly Gly Gly Ser
145                 150                 155                 160

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
                165                 170                 175

Gly Gly Ser Leu Gln Leu Asn Thr Thr Ile Leu Thr Pro Asn Gly Asn
            180                 185                 190

Glu Asp Thr Thr Ala Asp Phe Phe Leu Thr Thr Met Pro Thr Asp Ser
        195                 200                 205

Leu Ser Val Ser Thr Leu Pro Leu Pro Glu Val Gln Cys Phe Val Phe
    210                 215                 220

Asn Val Glu Tyr Met Asn Cys Thr Trp Asn Ser Ser Ser Glu Pro Gln
225                 230                 235                 240

Pro Thr Asn Leu Thr Leu His Tyr Trp Tyr Lys Asn Ser Asp Asn Asp
                245                 250                 255

Lys Val Gln Lys Cys Ser His Tyr Leu Phe Ser Glu Glu Ile Thr Ser
            260                 265                 270

Gly Cys Gln Leu Gln Lys Lys Glu Ile His Leu Tyr Gln Thr Phe Val
        275                 280                 285

Val Gln Leu Gln Asp Pro Arg Glu Pro Arg Arg Gln Ala Thr Gln Met
```

```
    290                 295                 300

Leu Lys Leu Gln Asn Leu Val Ile Pro Trp Ala Pro Glu Asn Leu Thr
305                 310                 315                 320

Leu His Lys Leu Ser Glu Ser Gln Leu Glu Leu Asn Trp Asn Asn Arg
                325                 330                 335

Phe Leu Asn His Cys Leu Glu His Leu Val Gln Tyr Arg Thr Asp Trp
            340                 345                 350

Asp His Ser Trp Thr Glu Gln Ser Val Asp Tyr Arg His Lys Phe Ser
        355                 360                 365

Leu Pro Ser Val Asp Gly Gln Lys Arg Tyr Thr Phe Arg Val Arg Ser
    370                 375                 380

Arg Phe Asn Pro Leu Cys Gly Ser Ala Gln His Trp Ser Glu Trp Ser
385                 390                 395                 400

His Pro Ile His Trp Gly Ser Asn Thr Ser Lys Glu Asn Pro Phe Leu
                405                 410                 415

Phe Ala Leu Glu Ala Val Val Ile Ser Val Gly Ser Met Gly Leu Ile
            420                 425                 430

Ile Ser Leu Leu Cys Val Tyr Phe Trp Leu Glu Arg Thr Met Pro Arg
        435                 440                 445

Ile Pro Thr Leu Lys Asn Leu Glu Asp Leu Val Thr Glu Tyr His Gly
    450                 455                 460

Asn Phe Ser Ala Trp Ser Gly Val Ser Lys Gly Leu Ala Glu Ser Leu
465                 470                 475                 480

Gln Pro Asp Tyr Ser Glu Arg Leu Cys Leu Val Ser Glu Ile Pro Pro
                485                 490                 495
```

Lys Gly Gly Ala Leu Gly Glu Gly Pro Gly Ala Ser Pro Cys Asn Gln
500 505 510

His Ser Pro Tyr Trp Ala Pro Pro Cys Tyr Thr Leu Lys Pro Glu Thr
515 520 525

<210> 106
<211> 587
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 106
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Asn Thr Thr Glu Lys Glu Thr Phe Cys Arg Ala
20 25 30

Ala Thr Val Leu Arg Gln Phe Tyr Ser His His Glu Lys Asp Thr Arg
35 40 45

Cys Leu Gly Ala Thr Ala Gln Gln Phe His Arg His Lys Gln Leu Ile
50 55 60

Arg Phe Leu Lys Arg Leu Asp Arg Asn Leu Trp Gly Leu Ala Gly Leu
65 70 75 80

Asn Ser Cys Pro Val Lys Glu Ala Asn Gln Ser Thr Leu Glu Asn Phe
85 90 95

Leu Glu Arg Leu Lys Thr Ile Met Arg Glu Lys Tyr Ser Lys Cys Ser
100 105 110

Ser Gly Gly Asn Gly Gly His Lys Cys Asp Ile Thr Leu Gln Glu Ile
115 120 125

```
Ile Lys Thr Leu Asn Ser Leu Thr Glu Gln Lys Thr Leu Cys Thr Glu
    130                 135                 140

Leu Thr Val Thr Asp Ile Phe Ala Ala Ser Lys Ser Gly Gly Gly Ser
145                 150                 155                 160

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
                165                 170                 175

Gly Gly Ser Leu Gln Gly Gly Gly Gly Ala Ala Pro Thr Glu Thr Gln
            180                 185                 190

Pro Pro Val Thr Asn Leu Ser Val Ser Val Glu Asn Leu Cys Thr Val
        195                 200                 205

Ile Trp Thr Trp Asn Pro Pro Glu Gly Ala Ser Ser Asn Cys Ser Leu
    210                 215                 220

Trp Tyr Phe Ser His Phe Gly Asp Lys Gln Asp Lys Lys Ile Ala Pro
225                 230                 235                 240

Glu Thr Arg Arg Ser Ile Glu Val Pro Leu Asn Glu Arg Ile Cys Leu
                245                 250                 255

Gln Val Gly Ser Gln Cys Ser Thr Asn Glu Ser Glu Lys Pro Ser Ile
            260                 265                 270

Leu Val Glu Lys Cys Ile Ser Pro Pro Glu Gly Asp Pro Glu Ser Ala
        275                 280                 285

Val Thr Glu Leu Gln Cys Ile Trp His Asn Leu Ser Tyr Met Lys Cys
    290                 295                 300

Ser Trp Leu Pro Gly Arg Asn Thr Ser Pro Asp Thr Asn Tyr Thr Leu
305                 310                 315                 320

Tyr Tyr Trp His Arg Ser Leu Glu Lys Ile His Gln Cys Glu Asn Ile
```

```
                325                 330                 335

Phe Arg Glu Gly Gln Tyr Phe Gly Cys Ser Phe Asp Leu Thr Lys Val
            340                 345                 350

Lys Asp Ser Ser Phe Glu Gln His Ser Val Gln Ile Met Val Lys Asp
        355                 360                 365

Asn Ala Gly Lys Ile Lys Pro Ser Phe Asn Ile Val Pro Leu Thr Ser
    370                 375                 380

Arg Val Lys Pro Asp Pro Pro His Ile Lys Asn Leu Ser Phe His Asn
385                 390                 395                 400

Asp Asp Leu Tyr Val Gln Trp Glu Asn Pro Gln Asn Phe Ile Ser Arg
                405                 410                 415

Cys Leu Phe Tyr Glu Val Glu Val Asn Asn Ser Gln Thr Glu Thr His
            420                 425                 430

Asn Val Phe Tyr Val Gln Glu Ala Lys Cys Glu Asn Pro Glu Phe Glu
        435                 440                 445

Arg Asn Val Glu Asn Thr Ser Cys Phe Met Val Pro Gly Val Leu Pro
    450                 455                 460

Asp Thr Leu Asn Thr Val Arg Ile Arg Val Lys Thr Asn Lys Leu Cys
465                 470                 475                 480

Tyr Glu Asp Asp Lys Leu Trp Ser Asn Trp Ser Gln Glu Met Ser Ile
                485                 490                 495

Gly Lys Lys Arg Asn Ser Thr Leu Tyr Ile Thr Met Leu Leu Ile Val
            500                 505                 510

Pro Val Ile Val Ala Gly Ala Ile Ile Val Leu Leu Leu Tyr Leu Lys
        515                 520                 525
```

Arg Leu Lys Ile Ile Ile Phe Pro Pro Ile Pro Asp Pro Gly Lys Ile
530 535 540

Phe Lys Glu Met Phe Gly Asp Gln Asn Asp Asp Thr Leu His Trp Lys
545 550 555 560

Lys Tyr Asp Ile Tyr Glu Lys Gln Thr Lys Glu Glu Thr Asp Ser Val
565 570 575

Val Leu Ile Glu Asn Leu Lys Lys Ala Ser Gln
580 585

<210> 107
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 107
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Ser Pro Gly Gln Gly Thr Gln Ser Glu Asn Ser
20 25 30

Cys Thr His Phe Pro Gly Asn Leu Pro Asn Met Leu Arg Asp Leu Arg
35 40 45

Asp Ala Phe Ser Arg Val Lys Thr Phe Phe Gln Met Lys Asp Gln Leu
50 55 60

Asp Asn Leu Leu Leu Lys Glu Ser Leu Leu Glu Asp Phe Lys Gly Tyr
65 70 75 80

Leu Gly Cys Gln Ala Leu Ser Glu Met Ile Gln Phe Tyr Leu Glu Glu
85 90 95

```
Val Met Pro Gln Ala Glu Asn Gln Asp Pro Asp Ile Lys Ala His Val
            100                 105                 110

Asn Ser Leu Gly Glu Asn Leu Lys Thr Leu Arg Leu Arg Leu Arg Arg
        115                 120                 125

Cys His Arg Phe Leu Pro Cys Glu Asn Lys Ser Lys Ala Val Glu Gln
    130                 135                 140

Val Lys Asn Ala Phe Asn Lys Leu Gln Glu Lys Gly Ile Tyr Lys Ala
145                 150                 155                 160

Met Ser Glu Phe Asp Ile Phe Ile Asn Tyr Ile Glu Ala Tyr Met Thr
                165                 170                 175

Met Lys Ile Arg Asn Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
            180                 185                 190

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Leu Gln His
        195                 200                 205

Gly Thr Glu Leu Pro Ser Pro Pro Ser Val Trp Phe Glu Ala Glu Phe
    210                 215                 220

Phe His His Ile Leu His Trp Thr Pro Ile Pro Asn Gln Ser Glu Ser
225                 230                 235                 240

Thr Cys Tyr Glu Val Ala Leu Leu Arg Tyr Gly Ile Glu Ser Trp Asn
                245                 250                 255

Ser Ile Ser Asn Cys Ser Gln Thr Leu Ser Tyr Asp Leu Thr Ala Val
            260                 265                 270

Thr Leu Asp Leu Tyr His Ser Asn Gly Tyr Arg Ala Arg Val Arg Ala
        275                 280                 285

Val Asp Gly Ser Arg His Ser Asn Trp Thr Val Thr Asn Thr Arg Phe
```

```
    290                 295                 300

Ser Val Asp Glu Val Thr Leu Thr Val Gly Ser Val Asn Leu Glu Ile
305                 310                 315                 320

His Asn Gly Phe Ile Leu Gly Lys Ile Gln Leu Pro Arg Pro Lys Met
                325                 330                 335

Ala Pro Ala Asn Asp Thr Tyr Glu Ser Ile Phe Ser His Phe Arg Glu
            340                 345                 350

Tyr Glu Ile Ala Ile Arg Lys Val Pro Gly Asn Phe Thr Phe Thr His
        355                 360                 365

Lys Lys Val Lys His Glu Asn Phe Ser Leu Leu Thr Ser Gly Glu Val
    370                 375                 380

Gly Glu Phe Cys Val Gln Val Lys Pro Ser Val Ala Ser Arg Ser Asn
385                 390                 395                 400

Lys Gly Met Trp Ser Lys Glu Glu Cys Ile Ser Leu Thr Arg Gln Tyr
                405                 410                 415

Phe Thr Val Thr Asn Val Ile Ile Phe Phe Ala Phe Val Leu Leu Leu
            420                 425                 430

Ser Gly Ala Leu Ala Tyr Cys Leu Ala Leu Gln Leu Tyr Val Arg Arg
        435                 440                 445

Arg Lys Lys Leu Pro Ser Val Leu Leu Phe Lys Lys Pro Ser Pro Phe
    450                 455                 460

Ile Phe Ile Ser Gln Arg Pro Ser Pro Glu Thr Gln Asp Thr Ile His
465                 470                 475                 480

Pro Leu Asp Glu Glu Ala Phe Leu Lys Val Ser Pro Glu Leu Lys Asn
                485                 490                 495
```

```
Leu Asp Leu His Gly Ser Thr Asp Ser Gly Phe Gly Ser Thr Lys Pro
            500                 505                 510

Ser Leu Gln Thr Glu Glu Pro Gln Phe Leu Leu Pro Asp Pro His Pro
        515                 520                 525

Gln Ala Asp Arg Thr Leu Gly Asn Arg Glu Pro Pro Val Leu Gly Asp
    530                 535                 540

Ser Cys Ser Ser Gly Ser Ser Asn Ser Thr Asp Ser Gly Ile Cys Leu
545                 550                 555                 560

Gln Glu Pro Ser Leu Ser Pro Ser Thr Gly Pro Thr Trp Glu Gln Gln
                565                 570                 575

Val Gly Ser Asn Ser Arg Gly Gln Asp Asp Ser Gly Ile Asp Leu Val
            580                 585                 590

Gln Asn Ser Glu Gly Arg Ala Gly Asp Thr Gln Gly Gly Ser Ala Leu
        595                 600                 605

Gly His His Ser Pro Pro Glu Pro Glu Val Pro Gly Glu Glu Asp Pro
    610                 615                 620

Ala Ala Val Ala Phe Gln Gly Tyr Leu Arg Gln Thr Arg Cys Ala Glu
625                 630                 635                 640

Glu Lys Ala Thr Lys Thr Gly Cys Leu Glu Glu Glu Ser Pro Leu Thr
                645                 650                 655

Asp Gly Leu Gly Pro Lys Phe Gly Arg Cys Leu Val Asp Glu Ala Gly
            660                 665                 670

Leu His Pro Pro Ala Leu Ala Lys Gly Tyr Leu Lys Gln Asp Pro Leu
        675                 680                 685

Glu Met Thr Leu Ala Ser Ser Gly Ala Pro Thr Gly Gln Trp Asn Gln
```

690 695 700

Pro Thr Glu Glu Trp Ser Leu Leu Ala Leu Ser Ser Cys Ser Asp Leu
705 710 715 720

Gly Ile Ser Asp Trp Ser Phe Ala His Asp Leu Ala Pro Leu Gly Cys
725 730 735

Val Ala Ala Pro Gly Gly Leu Leu Gly Ser Phe Asn Ser Asp Leu Val
740 745 750

Thr Leu Pro Leu Ile Ser Ser Leu Gln Ser Ser Glu
755 760

<210> 108
<211> 513
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 108
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Ser Pro Gly Gln Gly Thr Gln Ser Glu Asn Ser
20 25 30

Cys Thr His Phe Pro Gly Asn Leu Pro Asn Met Leu Arg Asp Leu Arg
35 40 45

Asp Ala Phe Ser Arg Val Lys Thr Phe Phe Gln Met Lys Asp Gln Leu
50 55 60

Asp Asn Leu Leu Leu Lys Glu Ser Leu Leu Glu Asp Phe Lys Gly Tyr
65 70 75 80

Leu Gly Cys Gln Ala Leu Ser Glu Met Ile Gln Phe Tyr Leu Glu Glu

```
                85                  90                  95

Val Met Pro Gln Ala Glu Asn Gln Asp Pro Asp Ile Lys Ala His Val
            100                 105                 110

Asn Ser Leu Gly Glu Asn Leu Lys Thr Leu Arg Leu Arg Leu Arg Arg
        115                 120                 125

Cys His Arg Phe Leu Pro Cys Glu Asn Lys Ser Lys Ala Val Glu Gln
    130                 135                 140

Val Lys Asn Ala Phe Asn Lys Leu Gln Glu Lys Gly Ile Tyr Lys Ala
145                 150                 155                 160

Met Ser Glu Phe Asp Ile Phe Ile Asn Tyr Ile Glu Ala Tyr Met Thr
                165                 170                 175

Met Lys Ile Arg Asn Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
            180                 185                 190

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Leu Gln Met
        195                 200                 205

Val Pro Pro Pro Glu Asn Val Arg Met Asn Ser Val Asn Phe Lys Asn
    210                 215                 220

Ile Leu Gln Trp Glu Ser Pro Ala Phe Ala Lys Gly Asn Leu Thr Phe
225                 230                 235                 240

Thr Ala Gln Tyr Leu Ser Tyr Arg Ile Phe Gln Asp Lys Cys Met Asn
                245                 250                 255

Thr Thr Leu Thr Glu Cys Asp Phe Ser Ser Leu Ser Lys Tyr Gly Asp
            260                 265                 270

His Thr Leu Arg Val Arg Ala Glu Phe Ala Asp Glu His Ser Asp Trp
        275                 280                 285
```

```
Val Asn Ile Thr Phe Cys Pro Val Asp Asp Thr Ile Ile Gly Pro Pro
    290                 295                 300

Gly Met Gln Val Glu Val Leu Ala Asp Ser Leu His Met Arg Phe Leu
305                 310                 315                 320

Ala Pro Lys Ile Glu Asn Glu Tyr Glu Thr Trp Thr Met Lys Asn Val
                325                 330                 335

Tyr Asn Ser Trp Thr Tyr Asn Val Gln Tyr Trp Lys Asn Gly Thr Asp
            340                 345                 350

Glu Lys Phe Gln Ile Thr Pro Gln Tyr Asp Phe Glu Val Leu Arg Asn
        355                 360                 365

Leu Glu Pro Trp Thr Thr Tyr Cys Val Gln Val Arg Gly Phe Leu Pro
    370                 375                 380

Asp Arg Asn Lys Ala Gly Glu Trp Ser Glu Pro Val Cys Glu Gln Thr
385                 390                 395                 400

Thr His Asp Glu Thr Val Pro Ser Trp Met Val Ala Val Ile Leu Met
                405                 410                 415

Ala Ser Val Phe Met Val Cys Leu Ala Leu Leu Gly Cys Phe Ala Leu
            420                 425                 430

Leu Trp Cys Val Tyr Lys Lys Thr Lys Tyr Ala Phe Ser Pro Arg Asn
        435                 440                 445

Ser Leu Pro Gln His Leu Lys Glu Phe Leu Gly His Pro His His Asn
    450                 455                 460

Thr Leu Leu Phe Phe Ser Phe Pro Leu Ser Asp Glu Asn Asp Val Phe
465                 470                 475                 480

Asp Lys Leu Ser Val Ile Ala Glu Asp Ser Glu Ser Gly Lys Gln Asn
```

485 490 495

Pro Gly Asp Ser Cys Ser Leu Gly Thr Pro Pro Gly Gln Gly Pro Gln
500 505 510

Ser

<210> 109
<211> 770
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 109
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Ser Pro Gly Gln Gly Thr Gln Ser Glu Asn Ser
20 25 30

Cys Thr His Phe Pro Gly Asn Leu Pro Asn Met Leu Arg Asp Leu Arg
35 40 45

Asp Ala Phe Ser Arg Val Lys Thr Phe Phe Gln Met Lys Asp Gln Leu
50 55 60

Asp Asn Leu Leu Leu Lys Glu Ser Leu Leu Glu Asp Phe Lys Gly Tyr
65 70 75 80

Leu Gly Cys Gln Ala Leu Ser Glu Met Ile Gln Phe Tyr Leu Glu Glu
85 90 95

Val Met Pro Gln Ala Glu Asn Gln Asp Pro Asp Ile Lys Ala His Val
100 105 110

Asn Ser Leu Gly Glu Asn Leu Lys Thr Leu Arg Leu Arg Leu Arg Arg

```
        115                 120                 125

Cys His Arg Phe Leu Pro Cys Glu Asn Gly Gly Gly Ser Gly Gly Lys
    130                 135                 140

Ser Lys Ala Val Glu Gln Val Lys Asn Ala Phe Asn Lys Leu Gln Glu
145                 150                 155                 160

Lys Gly Ile Tyr Lys Ala Met Ser Glu Phe Asp Ile Phe Ile Asn Tyr
                165                 170                 175

Ile Glu Ala Tyr Met Thr Met Lys Ile Arg Asn Ser Gly Gly Gly Ser
            180                 185                 190

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
        195                 200                 205

Gly Gly Ser Leu Gln His Gly Thr Glu Leu Pro Ser Pro Pro Ser Val
    210                 215                 220

Trp Phe Glu Ala Glu Phe Phe His His Ile Leu His Trp Thr Pro Ile
225                 230                 235                 240

Pro Asn Gln Ser Glu Ser Thr Cys Tyr Glu Val Ala Leu Leu Arg Tyr
                245                 250                 255

Gly Ile Glu Ser Trp Asn Ser Ile Ser Asn Cys Ser Gln Thr Leu Ser
            260                 265                 270

Tyr Asp Leu Thr Ala Val Thr Leu Asp Leu Tyr His Ser Asn Gly Tyr
        275                 280                 285

Arg Ala Arg Val Arg Ala Val Asp Gly Ser Arg His Ser Asn Trp Thr
    290                 295                 300

Val Thr Asn Thr Arg Phe Ser Val Asp Glu Val Thr Leu Thr Val Gly
305                 310                 315                 320
```

```
Ser Val Asn Leu Glu Ile His Asn Gly Phe Ile Leu Gly Lys Ile Gln
                325                 330                 335

Leu Pro Arg Pro Lys Met Ala Pro Ala Asn Asp Thr Tyr Glu Ser Ile
            340                 345                 350

Phe Ser His Phe Arg Glu Tyr Glu Ile Ala Ile Arg Lys Val Pro Gly
        355                 360                 365

Asn Phe Thr Phe Thr His Lys Lys Val Lys His Glu Asn Phe Ser Leu
    370                 375                 380

Leu Thr Ser Gly Glu Val Gly Glu Phe Cys Val Gln Val Lys Pro Ser
385                 390                 395                 400

Val Ala Ser Arg Ser Asn Lys Gly Met Trp Ser Lys Glu Glu Cys Ile
                405                 410                 415

Ser Leu Thr Arg Gln Tyr Phe Thr Val Thr Asn Val Ile Ile Phe Phe
            420                 425                 430

Ala Phe Val Leu Leu Leu Ser Gly Ala Leu Ala Tyr Cys Leu Ala Leu
        435                 440                 445

Gln Leu Tyr Val Arg Arg Arg Lys Lys Leu Pro Ser Val Leu Leu Phe
    450                 455                 460

Lys Lys Pro Ser Pro Phe Ile Phe Ile Ser Gln Arg Pro Ser Pro Glu
465                 470                 475                 480

Thr Gln Asp Thr Ile His Pro Leu Asp Glu Glu Ala Phe Leu Lys Val
                485                 490                 495

Ser Pro Glu Leu Lys Asn Leu Asp Leu His Gly Ser Thr Asp Ser Gly
            500                 505                 510

Phe Gly Ser Thr Lys Pro Ser Leu Gln Thr Glu Glu Pro Gln Phe Leu
```

```
        515                 520                 525

Leu Pro Asp Pro His Pro Gln Ala Asp Arg Thr Leu Gly Asn Arg Glu
    530                 535                 540

Pro Pro Val Leu Gly Asp Ser Cys Ser Ser Gly Ser Ser Asn Ser Thr
545                 550                 555                 560

Asp Ser Gly Ile Cys Leu Gln Glu Pro Ser Leu Ser Pro Ser Thr Gly
                565                 570                 575

Pro Thr Trp Glu Gln Gln Val Gly Ser Asn Ser Arg Gly Gln Asp Asp
            580                 585                 590

Ser Gly Ile Asp Leu Val Gln Asn Ser Glu Gly Arg Ala Gly Asp Thr
        595                 600                 605

Gln Gly Gly Ser Ala Leu Gly His His Ser Pro Pro Glu Pro Glu Val
    610                 615                 620

Pro Gly Glu Glu Asp Pro Ala Ala Val Ala Phe Gln Gly Tyr Leu Arg
625                 630                 635                 640

Gln Thr Arg Cys Ala Glu Glu Lys Ala Thr Lys Thr Gly Cys Leu Glu
                645                 650                 655

Glu Glu Ser Pro Leu Thr Asp Gly Leu Gly Pro Lys Phe Gly Arg Cys
            660                 665                 670

Leu Val Asp Glu Ala Gly Leu His Pro Pro Ala Leu Ala Lys Gly Tyr
        675                 680                 685

Leu Lys Gln Asp Pro Leu Glu Met Thr Leu Ala Ser Ser Gly Ala Pro
    690                 695                 700

Thr Gly Gln Trp Asn Gln Pro Thr Glu Glu Trp Ser Leu Leu Ala Leu
705                 710                 715                 720
```

Ser Ser Cys Ser Asp Leu Gly Ile Ser Asp Trp Ser Phe Ala His Asp
725 730 735

Leu Ala Pro Leu Gly Cys Val Ala Ala Pro Gly Gly Leu Leu Gly Ser
740 745 750

Phe Asn Ser Asp Leu Val Thr Leu Pro Leu Ile Ser Ser Leu Gln Ser
755 760 765

Ser Glu
770

<210> 110
<211> 519
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 110
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Ser Pro Gly Gln Gly Thr Gln Ser Glu Asn Ser
20 25 30

Cys Thr His Phe Pro Gly Asn Leu Pro Asn Met Leu Arg Asp Leu Arg
35 40 45

Asp Ala Phe Ser Arg Val Lys Thr Phe Phe Gln Met Lys Asp Gln Leu
50 55 60

Asp Asn Leu Leu Leu Lys Glu Ser Leu Leu Glu Asp Phe Lys Gly Tyr
65 70 75 80

Leu Gly Cys Gln Ala Leu Ser Glu Met Ile Gln Phe Tyr Leu Glu Glu
85 90 95

```
Val Met Pro Gln Ala Glu Asn Gln Asp Pro Asp Ile Lys Ala His Val
            100                 105                 110

Asn Ser Leu Gly Glu Asn Leu Lys Thr Leu Arg Leu Arg Leu Arg Arg
        115                 120                 125

Cys His Arg Phe Leu Pro Cys Glu Asn Gly Gly Gly Ser Gly Gly Lys
    130                 135                 140

Ser Lys Ala Val Glu Gln Val Lys Asn Ala Phe Asn Lys Leu Gln Glu
145                 150                 155                 160

Lys Gly Ile Tyr Lys Ala Met Ser Glu Phe Asp Ile Phe Ile Asn Tyr
                165                 170                 175

Ile Glu Ala Tyr Met Thr Met Lys Ile Arg Asn Ser Gly Gly Gly Ser
            180                 185                 190

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
        195                 200                 205

Gly Gly Ser Leu Gln Met Val Pro Pro Pro Glu Asn Val Arg Met Asn
    210                 215                 220

Ser Val Asn Phe Lys Asn Ile Leu Gln Trp Glu Ser Pro Ala Phe Ala
225                 230                 235                 240

Lys Gly Asn Leu Thr Phe Thr Ala Gln Tyr Leu Ser Tyr Arg Ile Phe
                245                 250                 255

Gln Asp Lys Cys Met Asn Thr Thr Leu Thr Glu Cys Asp Phe Ser Ser
            260                 265                 270

Leu Ser Lys Tyr Gly Asp His Thr Leu Arg Val Arg Ala Glu Phe Ala
        275                 280                 285

Asp Glu His Ser Asp Trp Val Asn Ile Thr Phe Cys Pro Val Asp Asp
```

```
    290                 295                 300

Thr Ile Ile Gly Pro Pro Gly Met Gln Val Glu Val Leu Ala Asp Ser
305                 310                 315                 320

Leu His Met Arg Phe Leu Ala Pro Lys Ile Glu Asn Glu Tyr Glu Thr
                325                 330                 335

Trp Thr Met Lys Asn Val Tyr Asn Ser Trp Thr Tyr Asn Val Gln Tyr
            340                 345                 350

Trp Lys Asn Gly Thr Asp Glu Lys Phe Gln Ile Thr Pro Gln Tyr Asp
        355                 360                 365

Phe Glu Val Leu Arg Asn Leu Glu Pro Trp Thr Thr Tyr Cys Val Gln
    370                 375                 380

Val Arg Gly Phe Leu Pro Asp Arg Asn Lys Ala Gly Glu Trp Ser Glu
385                 390                 395                 400

Pro Val Cys Glu Gln Thr Thr His Asp Glu Thr Val Pro Ser Trp Met
                405                 410                 415

Val Ala Val Ile Leu Met Ala Ser Val Phe Met Val Cys Leu Ala Leu
            420                 425                 430

Leu Gly Cys Phe Ala Leu Leu Trp Cys Val Tyr Lys Lys Thr Lys Tyr
        435                 440                 445

Ala Phe Ser Pro Arg Asn Ser Leu Pro Gln His Leu Lys Glu Phe Leu
    450                 455                 460

Gly His Pro His His Asn Thr Leu Leu Phe Phe Ser Phe Pro Leu Ser
465                 470                 475                 480

Asp Glu Asn Asp Val Phe Asp Lys Leu Ser Val Ile Ala Glu Asp Ser
                485                 490                 495
```

Glu Ser Gly Lys Gln Asn Pro Gly Asp Ser Cys Ser Leu Gly Thr Pro
500 505 510

Pro Gly Gln Gly Pro Gln Ser
515

<210> 111
<211> 779
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 111
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Gly Tyr Leu Gly Cys Gln Ala Leu Ser Glu Met
20 25 30

Ile Gln Phe Tyr Leu Glu Glu Val Met Pro Gln Ala Glu Asn Gln Asp
35 40 45

Pro Asp Ile Lys Ala His Val Asn Ser Leu Gly Glu Asn Leu Lys Thr
50 55 60

Leu Arg Leu Arg Leu Arg Arg Cys His Arg Phe Leu Pro Cys Glu Asn
65 70 75 80

Lys Ser Lys Ala Val Glu Gln Val Lys Asn Ala Phe Asn Lys Leu Gln
85 90 95

Glu Lys Gly Ile Tyr Lys Ala Met Ser Glu Phe Asp Ile Phe Ile Asn
100 105 110

Tyr Ile Glu Ala Tyr Met Thr Met Lys Ile Arg Asn Gly Gly Gly Gly
115 120 125

```
Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser Pro Gly Gln Gly
    130                 135                 140

Thr Gln Ser Glu Asn Ser Cys Thr His Phe Pro Gly Asn Leu Pro Asn
145                 150                 155                 160

Met Leu Arg Asp Leu Arg Asp Ala Phe Ser Arg Val Lys Thr Phe Phe
                165                 170                 175

Gln Met Lys Asp Gln Leu Asp Asn Leu Leu Leu Lys Glu Ser Leu Leu
            180                 185                 190

Glu Asp Phe Lys Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
        195                 200                 205

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Leu Gln His Gly
    210                 215                 220

Thr Glu Leu Pro Ser Pro Pro Ser Val Trp Phe Glu Ala Glu Phe Phe
225                 230                 235                 240

His His Ile Leu His Trp Thr Pro Ile Pro Asn Gln Ser Glu Ser Thr
                245                 250                 255

Cys Tyr Glu Val Ala Leu Leu Arg Tyr Gly Ile Glu Ser Trp Asn Ser
            260                 265                 270

Ile Ser Asn Cys Ser Gln Thr Leu Ser Tyr Asp Leu Thr Ala Val Thr
        275                 280                 285

Leu Asp Leu Tyr His Ser Asn Gly Tyr Arg Ala Arg Val Arg Ala Val
    290                 295                 300

Asp Gly Ser Arg His Ser Asn Trp Thr Val Thr Asn Thr Arg Phe Ser
305                 310                 315                 320

Val Asp Glu Val Thr Leu Thr Val Gly Ser Val Asn Leu Glu Ile His
```

```
                325                 330                 335

Asn Gly Phe Ile Leu Gly Lys Ile Gln Leu Pro Arg Pro Lys Met Ala
            340                 345                 350

Pro Ala Asn Asp Thr Tyr Glu Ser Ile Phe Ser His Phe Arg Glu Tyr
        355                 360                 365

Glu Ile Ala Ile Arg Lys Val Pro Gly Asn Phe Thr Phe Thr His Lys
    370                 375                 380

Lys Val Lys His Glu Asn Phe Ser Leu Leu Thr Ser Gly Glu Val Gly
385                 390                 395                 400

Glu Phe Cys Val Gln Val Lys Pro Ser Val Ala Ser Arg Ser Asn Lys
                405                 410                 415

Gly Met Trp Ser Lys Glu Glu Cys Ile Ser Leu Thr Arg Gln Tyr Phe
            420                 425                 430

Thr Val Thr Asn Val Ile Ile Phe Phe Ala Phe Val Leu Leu Leu Ser
        435                 440                 445

Gly Ala Leu Ala Tyr Cys Leu Ala Leu Gln Leu Tyr Val Arg Arg Arg
    450                 455                 460

Lys Lys Leu Pro Ser Val Leu Leu Phe Lys Lys Pro Ser Pro Phe Ile
465                 470                 475                 480

Phe Ile Ser Gln Arg Pro Ser Pro Glu Thr Gln Asp Thr Ile His Pro
                485                 490                 495

Leu Asp Glu Glu Ala Phe Leu Lys Val Ser Pro Glu Leu Lys Asn Leu
            500                 505                 510

Asp Leu His Gly Ser Thr Asp Ser Gly Phe Gly Ser Thr Lys Pro Ser
        515                 520                 525
```

```
Leu Gln Thr Glu Glu Pro Gln Phe Leu Leu Pro Asp Pro His Pro Gln
    530                 535                 540

Ala Asp Arg Thr Leu Gly Asn Arg Glu Pro Pro Val Leu Gly Asp Ser
545                 550                 555                 560

Cys Ser Ser Gly Ser Ser Asn Ser Thr Asp Ser Gly Ile Cys Leu Gln
                565                 570                 575

Glu Pro Ser Leu Ser Pro Ser Thr Gly Pro Thr Trp Glu Gln Gln Val
            580                 585                 590

Gly Ser Asn Ser Arg Gly Gln Asp Asp Ser Gly Ile Asp Leu Val Gln
        595                 600                 605

Asn Ser Glu Gly Arg Ala Gly Asp Thr Gln Gly Gly Ser Ala Leu Gly
    610                 615                 620

His His Ser Pro Pro Glu Pro Glu Val Pro Gly Glu Glu Asp Pro Ala
625                 630                 635                 640

Ala Val Ala Phe Gln Gly Tyr Leu Arg Gln Thr Arg Cys Ala Glu Glu
                645                 650                 655

Lys Ala Thr Lys Thr Gly Cys Leu Glu Glu Glu Ser Pro Leu Thr Asp
            660                 665                 670

Gly Leu Gly Pro Lys Phe Gly Arg Cys Leu Val Asp Glu Ala Gly Leu
        675                 680                 685

His Pro Pro Ala Leu Ala Lys Gly Tyr Leu Lys Gln Asp Pro Leu Glu
    690                 695                 700

Met Thr Leu Ala Ser Ser Gly Ala Pro Thr Gly Gln Trp Asn Gln Pro
705                 710                 715                 720

Thr Glu Glu Trp Ser Leu Leu Ala Leu Ser Ser Cys Ser Asp Leu Gly
```

725 730 735

Ile Ser Asp Trp Ser Phe Ala His Asp Leu Ala Pro Leu Gly Cys Val
740 745 750

Ala Ala Pro Gly Gly Leu Leu Gly Ser Phe Asn Ser Asp Leu Val Thr
755 760 765

Leu Pro Leu Ile Ser Ser Leu Gln Ser Ser Glu
770 775

<210> 112
<211> 528
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 112
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Gly Tyr Leu Gly Cys Gln Ala Leu Ser Glu Met
20 25 30

Ile Gln Phe Tyr Leu Glu Glu Val Met Pro Gln Ala Glu Asn Gln Asp
35 40 45

Pro Asp Ile Lys Ala His Val Asn Ser Leu Gly Glu Asn Leu Lys Thr
50 55 60

Leu Arg Leu Arg Leu Arg Arg Cys His Arg Phe Leu Pro Cys Glu Asn
65 70 75 80

Lys Ser Lys Ala Val Glu Gln Val Lys Asn Ala Phe Asn Lys Leu Gln
85 90 95

Glu Lys Gly Ile Tyr Lys Ala Met Ser Glu Phe Asp Ile Phe Ile Asn

```
            100                 105                 110

Tyr Ile Glu Ala Tyr Met Thr Met Lys Ile Arg Asn Gly Gly Gly Gly
        115                 120                 125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser Pro Gly Gln Gly
    130                 135                 140

Thr Gln Ser Glu Asn Ser Cys Thr His Phe Pro Gly Asn Leu Pro Asn
145                 150                 155                 160

Met Leu Arg Asp Leu Arg Asp Ala Phe Ser Arg Val Lys Thr Phe Phe
                165                 170                 175

Gln Met Lys Asp Gln Leu Asp Asn Leu Leu Leu Lys Glu Ser Leu Leu
            180                 185                 190

Glu Asp Phe Lys Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
        195                 200                 205

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Leu Gln Met Val
    210                 215                 220

Pro Pro Pro Glu Asn Val Arg Met Asn Ser Val Asn Phe Lys Asn Ile
225                 230                 235                 240

Leu Gln Trp Glu Ser Pro Ala Phe Ala Lys Gly Asn Leu Thr Phe Thr
                245                 250                 255

Ala Gln Tyr Leu Ser Tyr Arg Ile Phe Gln Asp Lys Cys Met Asn Thr
            260                 265                 270

Thr Leu Thr Glu Cys Asp Phe Ser Ser Leu Ser Lys Tyr Gly Asp His
        275                 280                 285

Thr Leu Arg Val Arg Ala Glu Phe Ala Asp Glu His Ser Asp Trp Val
    290                 295                 300
```

```
Asn Ile Thr Phe Cys Pro Val Asp Asp Thr Ile Ile Gly Pro Pro Gly
305                 310                 315                 320

Met Gln Val Glu Val Leu Ala Asp Ser Leu His Met Arg Phe Leu Ala
                325                 330                 335

Pro Lys Ile Glu Asn Glu Tyr Glu Thr Trp Thr Met Lys Asn Val Tyr
            340                 345                 350

Asn Ser Trp Thr Tyr Asn Val Gln Tyr Trp Lys Asn Gly Thr Asp Glu
        355                 360                 365

Lys Phe Gln Ile Thr Pro Gln Tyr Asp Phe Glu Val Leu Arg Asn Leu
    370                 375                 380

Glu Pro Trp Thr Thr Tyr Cys Val Gln Val Arg Gly Phe Leu Pro Asp
385                 390                 395                 400

Arg Asn Lys Ala Gly Glu Trp Ser Glu Pro Val Cys Glu Gln Thr Thr
                405                 410                 415

His Asp Glu Thr Val Pro Ser Trp Met Val Ala Val Ile Leu Met Ala
            420                 425                 430

Ser Val Phe Met Val Cys Leu Ala Leu Leu Gly Cys Phe Ala Leu Leu
        435                 440                 445

Trp Cys Val Tyr Lys Lys Thr Lys Tyr Ala Phe Ser Pro Arg Asn Ser
    450                 455                 460

Leu Pro Gln His Leu Lys Glu Phe Leu Gly His Pro His His Asn Thr
465                 470                 475                 480

Leu Leu Phe Phe Ser Phe Pro Leu Ser Asp Glu Asn Asp Val Phe Asp
                485                 490                 495

Lys Leu Ser Val Ile Ala Glu Asp Ser Glu Ser Gly Lys Gln Asn Pro
```

500 505 510

Gly Asp Ser Cys Ser Leu Gly Thr Pro Pro Gly Gln Gly Pro Gln Ser
515 520 525

<210> 113
<211> 939
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 113
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Ser Pro Gly Gln Gly Thr Gln Ser Glu Asn Ser
20 25 30

Cys Thr His Phe Pro Gly Asn Leu Pro Asn Met Leu Arg Asp Leu Arg
35 40 45

Asp Ala Phe Ser Arg Val Lys Thr Phe Phe Gln Met Lys Asp Gln Leu
50 55 60

Asp Asn Leu Leu Leu Lys Glu Ser Leu Leu Glu Asp Phe Lys Gly Tyr
65 70 75 80

Leu Gly Cys Gln Ala Leu Ser Glu Met Ile Gln Phe Tyr Leu Glu Glu
85 90 95

Val Met Pro Gln Ala Glu Asn Gln Asp Pro Asp Ile Lys Ala His Val
100 105 110

Asn Ser Leu Gly Glu Asn Leu Lys Thr Leu Arg Leu Arg Leu Arg Arg
115 120 125

Cys His Arg Phe Leu Pro Cys Glu Asn Lys Ser Lys Ala Val Glu Gln

```
    130                 135                 140

Val Lys Asn Ala Phe Asn Lys Leu Gln Glu Lys Gly Ile Tyr Lys Ala
145                 150                 155                 160

Met Ser Glu Phe Asp Ile Phe Ile Asn Tyr Ile Glu Ala Tyr Met Thr
                165                 170                 175

Met Lys Ile Arg Asn Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
            180                 185                 190

Gly Gly Gly Ser Ser Pro Gly Gln Gly Thr Gln Ser Glu Asn Ser Cys
        195                 200                 205

Thr His Phe Pro Gly Asn Leu Pro Asn Met Leu Arg Asp Leu Arg Asp
    210                 215                 220

Ala Phe Ser Arg Val Lys Thr Phe Phe Gln Met Lys Asp Gln Leu Asp
225                 230                 235                 240

Asn Leu Leu Leu Lys Glu Ser Leu Leu Glu Asp Phe Lys Gly Tyr Leu
                245                 250                 255

Gly Cys Gln Ala Leu Ser Glu Met Ile Gln Phe Tyr Leu Glu Glu Val
            260                 265                 270

Met Pro Gln Ala Glu Asn Gln Asp Pro Asp Ile Lys Ala His Val Asn
        275                 280                 285

Ser Leu Gly Glu Asn Leu Lys Thr Leu Arg Leu Arg Leu Arg Arg Cys
    290                 295                 300

His Arg Phe Leu Pro Cys Glu Asn Lys Ser Lys Ala Val Glu Gln Val
305                 310                 315                 320

Lys Asn Ala Phe Asn Lys Leu Gln Glu Lys Gly Ile Tyr Lys Ala Met
                325                 330                 335
```

```
Ser Glu Phe Asp Ile Phe Ile Asn Tyr Ile Glu Ala Tyr Met Thr Met
            340                 345                 350

Lys Ile Arg Asn Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
        355                 360                 365

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Leu Gln His Gly
    370                 375                 380

Thr Glu Leu Pro Ser Pro Pro Ser Val Trp Phe Glu Ala Glu Phe Phe
385                 390                 395                 400

His His Ile Leu His Trp Thr Pro Ile Pro Asn Gln Ser Glu Ser Thr
                405                 410                 415

Cys Tyr Glu Val Ala Leu Leu Arg Tyr Gly Ile Glu Ser Trp Asn Ser
            420                 425                 430

Ile Ser Asn Cys Ser Gln Thr Leu Ser Tyr Asp Leu Thr Ala Val Thr
        435                 440                 445

Leu Asp Leu Tyr His Ser Asn Gly Tyr Arg Ala Arg Val Arg Ala Val
    450                 455                 460

Asp Gly Ser Arg His Ser Asn Trp Thr Val Thr Asn Thr Arg Phe Ser
465                 470                 475                 480

Val Asp Glu Val Thr Leu Thr Val Gly Ser Val Asn Leu Glu Ile His
                485                 490                 495

Asn Gly Phe Ile Leu Gly Lys Ile Gln Leu Pro Arg Pro Lys Met Ala
            500                 505                 510

Pro Ala Asn Asp Thr Tyr Glu Ser Ile Phe Ser His Phe Arg Glu Tyr
        515                 520                 525

Glu Ile Ala Ile Arg Lys Val Pro Gly Asn Phe Thr Phe Thr His Lys
```

```
    530                 535                 540

Lys Val Lys His Glu Asn Phe Ser Leu Leu Thr Ser Gly Glu Val Gly
545                 550                 555                 560

Glu Phe Cys Val Gln Val Lys Pro Ser Val Ala Ser Arg Ser Asn Lys
                565                 570                 575

Gly Met Trp Ser Lys Glu Glu Cys Ile Ser Leu Thr Arg Gln Tyr Phe
            580                 585                 590

Thr Val Thr Asn Val Ile Ile Phe Phe Ala Phe Val Leu Leu Leu Ser
        595                 600                 605

Gly Ala Leu Ala Tyr Cys Leu Ala Leu Gln Leu Tyr Val Arg Arg Arg
    610                 615                 620

Lys Lys Leu Pro Ser Val Leu Leu Phe Lys Lys Pro Ser Pro Phe Ile
625                 630                 635                 640

Phe Ile Ser Gln Arg Pro Ser Pro Glu Thr Gln Asp Thr Ile His Pro
                645                 650                 655

Leu Asp Glu Glu Ala Phe Leu Lys Val Ser Pro Glu Leu Lys Asn Leu
            660                 665                 670

Asp Leu His Gly Ser Thr Asp Ser Gly Phe Gly Ser Thr Lys Pro Ser
        675                 680                 685

Leu Gln Thr Glu Glu Pro Gln Phe Leu Leu Pro Asp Pro His Pro Gln
    690                 695                 700

Ala Asp Arg Thr Leu Gly Asn Arg Glu Pro Pro Val Leu Gly Asp Ser
705                 710                 715                 720

Cys Ser Ser Gly Ser Ser Asn Ser Thr Asp Ser Gly Ile Cys Leu Gln
                725                 730                 735
```

```
Glu Pro Ser Leu Ser Pro Ser Thr Gly Pro Thr Trp Glu Gln Gln Val
            740                 745                 750

Gly Ser Asn Ser Arg Gly Gln Asp Asp Ser Gly Ile Asp Leu Val Gln
        755                 760                 765

Asn Ser Glu Gly Arg Ala Gly Asp Thr Gln Gly Gly Ser Ala Leu Gly
    770                 775                 780

His His Ser Pro Pro Glu Pro Glu Val Pro Gly Glu Glu Asp Pro Ala
785                 790                 795                 800

Ala Val Ala Phe Gln Gly Tyr Leu Arg Gln Thr Arg Cys Ala Glu Glu
                805                 810                 815

Lys Ala Thr Lys Thr Gly Cys Leu Glu Glu Glu Ser Pro Leu Thr Asp
            820                 825                 830

Gly Leu Gly Pro Lys Phe Gly Arg Cys Leu Val Asp Glu Ala Gly Leu
        835                 840                 845

His Pro Pro Ala Leu Ala Lys Gly Tyr Leu Lys Gln Asp Pro Leu Glu
    850                 855                 860

Met Thr Leu Ala Ser Ser Gly Ala Pro Thr Gly Gln Trp Asn Gln Pro
865                 870                 875                 880

Thr Glu Glu Trp Ser Leu Leu Ala Leu Ser Ser Cys Ser Asp Leu Gly
                885                 890                 895

Ile Ser Asp Trp Ser Phe Ala His Asp Leu Ala Pro Leu Gly Cys Val
            900                 905                 910

Ala Ala Pro Gly Gly Leu Leu Gly Ser Phe Asn Ser Asp Leu Val Thr
        915                 920                 925

Leu Pro Leu Ile Ser Ser Leu Gln Ser Ser Glu
```

930 935

<210> 114
<211> 688
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 114
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Ser Pro Gly Gln Gly Thr Gln Ser Glu Asn Ser
20 25 30

Cys Thr His Phe Pro Gly Asn Leu Pro Asn Met Leu Arg Asp Leu Arg
35 40 45

Asp Ala Phe Ser Arg Val Lys Thr Phe Phe Gln Met Lys Asp Gln Leu
50 55 60

Asp Asn Leu Leu Leu Lys Glu Ser Leu Leu Glu Asp Phe Lys Gly Tyr
65 70 75 80

Leu Gly Cys Gln Ala Leu Ser Glu Met Ile Gln Phe Tyr Leu Glu Glu
85 90 95

Val Met Pro Gln Ala Glu Asn Gln Asp Pro Asp Ile Lys Ala His Val
100 105 110

Asn Ser Leu Gly Glu Asn Leu Lys Thr Leu Arg Leu Arg Leu Arg Arg
115 120 125

Cys His Arg Phe Leu Pro Cys Glu Asn Lys Ser Lys Ala Val Glu Gln
130 135 140

Val Lys Asn Ala Phe Asn Lys Leu Gln Glu Lys Gly Ile Tyr Lys Ala

```
145                 150                 155                 160

Met Ser Glu Phe Asp Ile Phe Ile Asn Tyr Ile Glu Ala Tyr Met Thr
                165                 170                 175

Met Lys Ile Arg Asn Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
            180                 185                 190

Gly Gly Gly Ser Ser Pro Gly Gln Gly Thr Gln Ser Glu Asn Ser Cys
        195                 200                 205

Thr His Phe Pro Gly Asn Leu Pro Asn Met Leu Arg Asp Leu Arg Asp
    210                 215                 220

Ala Phe Ser Arg Val Lys Thr Phe Phe Gln Met Lys Asp Gln Leu Asp
225                 230                 235                 240

Asn Leu Leu Leu Lys Glu Ser Leu Leu Glu Asp Phe Lys Gly Tyr Leu
                245                 250                 255

Gly Cys Gln Ala Leu Ser Glu Met Ile Gln Phe Tyr Leu Glu Glu Val
            260                 265                 270

Met Pro Gln Ala Glu Asn Gln Asp Pro Asp Ile Lys Ala His Val Asn
        275                 280                 285

Ser Leu Gly Glu Asn Leu Lys Thr Leu Arg Leu Arg Leu Arg Arg Cys
    290                 295                 300

His Arg Phe Leu Pro Cys Glu Asn Lys Ser Lys Ala Val Glu Gln Val
305                 310                 315                 320

Lys Asn Ala Phe Asn Lys Leu Gln Glu Lys Gly Ile Tyr Lys Ala Met
                325                 330                 335

Ser Glu Phe Asp Ile Phe Ile Asn Tyr Ile Glu Ala Tyr Met Thr Met
            340                 345                 350
```

```
Lys Ile Arg Asn Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
        355                 360                 365

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Leu Gln Met Val
    370                 375                 380

Pro Pro Pro Glu Asn Val Arg Met Asn Ser Val Asn Phe Lys Asn Ile
385                 390                 395                 400

Leu Gln Trp Glu Ser Pro Ala Phe Ala Lys Gly Asn Leu Thr Phe Thr
                405                 410                 415

Ala Gln Tyr Leu Ser Tyr Arg Ile Phe Gln Asp Lys Cys Met Asn Thr
            420                 425                 430

Thr Leu Thr Glu Cys Asp Phe Ser Ser Leu Ser Lys Tyr Gly Asp His
        435                 440                 445

Thr Leu Arg Val Arg Ala Glu Phe Ala Asp Glu His Ser Asp Trp Val
    450                 455                 460

Asn Ile Thr Phe Cys Pro Val Asp Asp Thr Ile Ile Gly Pro Pro Gly
465                 470                 475                 480

Met Gln Val Glu Val Leu Ala Asp Ser Leu His Met Arg Phe Leu Ala
                485                 490                 495

Pro Lys Ile Glu Asn Glu Tyr Glu Thr Trp Thr Met Lys Asn Val Tyr
            500                 505                 510

Asn Ser Trp Thr Tyr Asn Val Gln Tyr Trp Lys Asn Gly Thr Asp Glu
        515                 520                 525

Lys Phe Gln Ile Thr Pro Gln Tyr Asp Phe Glu Val Leu Arg Asn Leu
    530                 535                 540

Glu Pro Trp Thr Thr Tyr Cys Val Gln Val Arg Gly Phe Leu Pro Asp
```

545 550 555 560

Arg Asn Lys Ala Gly Glu Trp Ser Glu Pro Val Cys Glu Gln Thr Thr
565 570 575

His Asp Glu Thr Val Pro Ser Trp Met Val Ala Val Ile Leu Met Ala
580 585 590

Ser Val Phe Met Val Cys Leu Ala Leu Leu Gly Cys Phe Ala Leu Leu
595 600 605

Trp Cys Val Tyr Lys Lys Thr Lys Tyr Ala Phe Ser Pro Arg Asn Ser
610 615 620

Leu Pro Gln His Leu Lys Glu Phe Leu Gly His Pro His His Asn Thr
625 630 635 640

Leu Leu Phe Phe Ser Phe Pro Leu Ser Asp Glu Asn Asp Val Phe Asp
645 650 655

Lys Leu Ser Val Ile Ala Glu Asp Ser Glu Ser Gly Lys Gln Asn Pro
660 665 670

Gly Asp Ser Cys Ser Leu Gly Thr Pro Pro Gly Gln Gly Pro Gln Ser
675 680 685

<210> 115
<211> 575
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 115
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Leu Thr Cys Leu Gly Gly Phe Ala Ser Pro Gly

```
            20                  25                  30

Pro Val Pro Pro Ser Thr Ala Leu Arg Glu Leu Ile Glu Glu Leu Val
        35                  40                  45

Asn Ile Thr Gln Asn Gln Lys Ala Pro Leu Cys Asn Gly Ser Met Val
    50                  55                  60

Trp Ser Ile Asn Leu Thr Ala Gly Met Tyr Cys Ala Ala Leu Glu Ser
65                  70                  75                  80

Leu Ile Asn Val Ser Gly Cys Ser Ala Ile Glu Lys Thr Gln Arg Met
                85                  90                  95

Leu Ser Gly Phe Cys Pro His Lys Val Ser Ala Gly Gln Phe Ser Ser
            100                 105                 110

Leu His Val Arg Asp Thr Lys Ile Glu Val Ala Gln Phe Val Lys Asp
        115                 120                 125

Leu Leu Leu His Leu Lys Lys Leu Phe Arg Glu Gly Arg Phe Asn Ser
    130                 135                 140

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
145                 150                 155                 160

Gly Gly Ser Gly Gly Gly Ser Leu Gln Gly Gly Gly Gly Ala Ala Pro
                165                 170                 175

Thr Glu Thr Gln Pro Pro Val Thr Asn Leu Ser Val Ser Val Glu Asn
            180                 185                 190

Leu Cys Thr Val Ile Trp Thr Trp Asn Pro Pro Glu Gly Ala Ser Ser
        195                 200                 205

Asn Cys Ser Leu Trp Tyr Phe Ser His Phe Gly Asp Lys Gln Asp Lys
    210                 215                 220
```

```
Lys Ile Ala Pro Glu Thr Arg Arg Ser Ile Glu Val Pro Leu Asn Glu
225                 230                 235                 240


Arg Ile Cys Leu Gln Val Gly Ser Gln Cys Ser Thr Asn Glu Ser Glu
                245                 250                 255


Lys Pro Ser Ile Leu Val Glu Lys Cys Ile Ser Pro Pro Glu Gly Asp
            260                 265                 270


Pro Glu Ser Ala Val Thr Glu Leu Gln Cys Ile Trp His Asn Leu Ser
        275                 280                 285


Tyr Met Lys Cys Ser Trp Leu Pro Gly Arg Asn Thr Ser Pro Asp Thr
    290                 295                 300


Asn Tyr Thr Leu Tyr Tyr Trp His Arg Ser Leu Glu Lys Ile His Gln
305                 310                 315                 320


Cys Glu Asn Ile Phe Arg Glu Gly Gln Tyr Phe Gly Cys Ser Phe Asp
                325                 330                 335


Leu Thr Lys Val Lys Asp Ser Ser Phe Glu Gln His Ser Val Gln Ile
            340                 345                 350


Met Val Lys Asp Asn Ala Gly Lys Ile Lys Pro Ser Phe Asn Ile Val
        355                 360                 365


Pro Leu Thr Ser Arg Val Lys Pro Asp Pro Pro His Ile Lys Asn Leu
    370                 375                 380


Ser Phe His Asn Asp Asp Leu Tyr Val Gln Trp Glu Asn Pro Gln Asn
385                 390                 395                 400


Phe Ile Ser Arg Cys Leu Phe Tyr Glu Val Glu Val Asn Asn Ser Gln
                405                 410                 415


Thr Glu Thr His Asn Val Phe Tyr Val Gln Glu Ala Lys Cys Glu Asn
```

```
            420                 425                 430

Pro Glu Phe Glu Arg Asn Val Glu Asn Thr Ser Cys Phe Met Val Pro
        435                 440                 445

Gly Val Leu Pro Asp Thr Leu Asn Thr Val Arg Ile Arg Val Lys Thr
    450                 455                 460

Asn Lys Leu Cys Tyr Glu Asp Asp Lys Leu Trp Ser Asn Trp Ser Gln
465                 470                 475                 480

Glu Met Ser Ile Gly Lys Lys Arg Asn Ser Thr Leu Tyr Ile Thr Met
                485                 490                 495

Leu Leu Ile Val Pro Val Ile Val Ala Gly Ala Ile Ile Val Leu Leu
            500                 505                 510

Leu Tyr Leu Lys Arg Leu Lys Ile Ile Ile Phe Pro Pro Ile Pro Asp
        515                 520                 525

Pro Gly Lys Ile Phe Lys Glu Met Phe Gly Asp Gln Asn Asp Asp Thr
    530                 535                 540

Leu His Trp Lys Lys Tyr Asp Ile Tyr Glu Lys Gln Thr Lys Glu Glu
545                 550                 555                 560

Thr Asp Ser Val Val Leu Ile Glu Asn Leu Lys Lys Ala Ser Gln
                565                 570                 575


<210> 116
<211> 969
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 116
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
```

```
1               5                   10                  15

His Ala Ala Arg Pro Leu Thr Cys Leu Gly Gly Phe Ala Ser Pro Gly
            20                  25                  30

Pro Val Pro Pro Ser Thr Ala Leu Arg Glu Leu Ile Glu Glu Leu Val
        35                  40                  45

Asn Ile Thr Gln Asn Gln Lys Ala Pro Leu Cys Asn Gly Ser Met Val
    50                  55                  60

Trp Ser Ile Asn Leu Thr Ala Gly Met Tyr Cys Ala Ala Leu Glu Ser
65                  70                  75                  80

Leu Ile Asn Val Ser Gly Cys Ser Ala Ile Glu Lys Thr Gln Arg Met
                85                  90                  95

Leu Ser Gly Phe Cys Pro His Lys Val Ser Ala Gly Gln Phe Ser Ser
            100                 105                 110

Leu His Val Arg Asp Thr Lys Ile Glu Val Ala Gln Phe Val Lys Asp
        115                 120                 125

Leu Leu Leu His Leu Lys Lys Leu Phe Arg Glu Gly Arg Phe Asn Ser
    130                 135                 140

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
145                 150                 155                 160

Gly Gly Ser Gly Gly Gly Ser Leu Gln Met Lys Val Leu Gln Glu Pro
                165                 170                 175

Thr Cys Val Ser Asp Tyr Met Ser Ile Ser Thr Cys Glu Trp Lys Met
            180                 185                 190

Asn Gly Pro Thr Asn Cys Ser Thr Glu Leu Arg Leu Leu Tyr Gln Leu
        195                 200                 205
```

```
Val Phe Leu Leu Ser Glu Ala His Thr Cys Ile Pro Glu Asn Asn Gly
    210                 215                 220

Gly Ala Gly Cys Val Cys His Leu Leu Met Asp Asp Val Val Ser Ala
225                 230                 235                 240

Asp Asn Tyr Thr Leu Asp Leu Trp Ala Gly Gln Gln Leu Leu Trp Lys
                245                 250                 255

Gly Ser Phe Lys Pro Ser Glu His Val Lys Pro Arg Ala Pro Gly Asn
            260                 265                 270

Leu Thr Val His Thr Asn Val Ser Asp Thr Leu Leu Leu Thr Trp Ser
        275                 280                 285

Asn Pro Tyr Pro Pro Asp Asn Tyr Leu Tyr Asn His Leu Thr Tyr Ala
    290                 295                 300

Val Asn Ile Trp Ser Glu Asn Asp Pro Ala Asp Phe Arg Ile Tyr Asn
305                 310                 315                 320

Val Thr Tyr Leu Glu Pro Ser Leu Arg Ile Ala Ala Ser Thr Leu Lys
                325                 330                 335

Ser Gly Ile Ser Tyr Arg Ala Arg Val Arg Ala Trp Ala Gln Cys Tyr
            340                 345                 350

Asn Thr Thr Trp Ser Glu Trp Ser Pro Ser Thr Lys Trp His Asn Ser
        355                 360                 365

Tyr Arg Glu Pro Phe Glu Gln His Leu Leu Leu Gly Val Ser Val Ser
    370                 375                 380

Cys Ile Val Ile Leu Ala Val Cys Leu Leu Cys Tyr Val Ser Ile Thr
385                 390                 395                 400

Lys Ile Lys Lys Glu Trp Trp Asp Gln Ile Pro Asn Pro Ala Arg Ser
```

```
                405                 410                 415

Arg Leu Val Ala Ile Ile Ile Gln Asp Ala Gln Gly Ser Gln Trp Glu
            420                 425                 430

Lys Arg Ser Arg Gly Gln Glu Pro Ala Lys Cys Pro His Trp Lys Asn
        435                 440                 445

Cys Leu Thr Lys Leu Leu Pro Cys Phe Leu Glu His Asn Met Lys Arg
    450                 455                 460

Asp Glu Asp Pro His Lys Ala Ala Lys Glu Met Pro Phe Gln Gly Ser
465                 470                 475                 480

Gly Lys Ser Ala Trp Cys Pro Val Glu Ile Ser Lys Thr Val Leu Trp
                485                 490                 495

Pro Glu Ser Ile Ser Val Val Arg Cys Val Glu Leu Phe Glu Ala Pro
            500                 505                 510

Val Glu Cys Glu Glu Glu Glu Glu Val Glu Glu Glu Lys Gly Ser Phe
        515                 520                 525

Cys Ala Ser Pro Glu Ser Ser Arg Asp Asp Phe Gln Glu Gly Arg Glu
    530                 535                 540

Gly Ile Val Ala Arg Leu Thr Glu Ser Leu Phe Leu Asp Leu Leu Gly
545                 550                 555                 560

Glu Glu Asn Gly Gly Phe Cys Gln Gln Asp Met Gly Glu Ser Cys Leu
                565                 570                 575

Leu Pro Pro Ser Gly Ser Thr Ser Ala His Met Pro Trp Asp Glu Phe
            580                 585                 590

Pro Ser Ala Gly Pro Lys Glu Ala Pro Pro Trp Gly Lys Glu Gln Pro
        595                 600                 605
```

```
Leu His Leu Glu Pro Ser Pro Pro Ala Ser Pro Thr Gln Ser Pro Asp
    610                 615                 620

Asn Leu Thr Cys Thr Glu Thr Pro Leu Val Ile Ala Gly Asn Pro Ala
625                 630                 635                 640

Tyr Arg Ser Phe Ser Asn Ser Leu Ser Gln Ser Pro Cys Pro Arg Glu
                645                 650                 655

Leu Gly Pro Asp Pro Leu Leu Ala Arg His Leu Glu Glu Val Glu Pro
            660                 665                 670

Glu Met Pro Cys Val Pro Gln Leu Ser Glu Pro Thr Thr Val Pro Gln
        675                 680                 685

Pro Glu Pro Glu Thr Trp Glu Gln Ile Leu Arg Arg Asn Val Leu Gln
    690                 695                 700

His Gly Ala Ala Ala Ala Pro Val Ser Ala Pro Thr Ser Gly Tyr Gln
705                 710                 715                 720

Glu Phe Val His Ala Val Glu Gln Gly Gly Thr Gln Ala Ser Ala Val
                725                 730                 735

Val Gly Leu Gly Pro Pro Gly Glu Ala Gly Tyr Lys Ala Phe Ser Ser
            740                 745                 750

Leu Leu Ala Ser Ser Ala Val Ser Pro Glu Lys Cys Gly Phe Gly Ala
        755                 760                 765

Ser Ser Gly Glu Glu Gly Tyr Lys Pro Phe Gln Asp Leu Ile Pro Gly
    770                 775                 780

Cys Pro Gly Asp Pro Ala Pro Val Pro Val Pro Leu Phe Thr Phe Gly
785                 790                 795                 800

Leu Asp Arg Glu Pro Pro Arg Ser Pro Gln Ser Ser His Leu Pro Ser
```

805 810 815

Ser Ser Pro Glu His Leu Gly Leu Glu Pro Gly Glu Lys Val Glu Asp
820 825 830

Met Pro Lys Pro Pro Leu Pro Gln Glu Gln Ala Thr Asp Pro Leu Val
835 840 845

Asp Ser Leu Gly Ser Gly Ile Val Tyr Ser Ala Leu Thr Cys His Leu
850 855 860

Cys Gly His Leu Lys Gln Cys His Gly Gln Glu Asp Gly Gly Gln Thr
865 870 875 880

Pro Val Met Ala Ser Pro Cys Cys Gly Cys Cys Cys Gly Asp Arg Ser
885 890 895

Ser Pro Pro Thr Thr Pro Leu Arg Ala Pro Asp Pro Ser Pro Gly Gly
900 905 910

Val Pro Leu Glu Ala Ser Leu Cys Pro Ala Ser Leu Ala Pro Ser Gly
915 920 925

Ile Ser Glu Lys Ser Lys Ser Ser Ser Ser Phe His Pro Ala Pro Gly
930 935 940

Asn Ala Gln Ser Ser Ser Gln Thr Pro Lys Ile Val Asn Phe Val Ser
945 950 955 960

Val Gly Pro Thr Tyr Met Arg Val Ser
965

<210> 117
<211> 580
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

polypeptide

<400> 117

```
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1               5                  10                  15

His Ala Ala Arg Pro Val Ser Ala Gly Gln Phe Ser Ser Leu His Val
            20                  25                  30

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

His Leu Lys Lys Leu Phe Arg Glu Gly Arg Phe Asn Gly Gly Gly Gly
    50                  55                  60

Ser Leu Thr Cys Leu Gly Gly Phe Ala Ser Pro Gly Pro Val Pro Pro
65                  70                  75                  80

Ser Thr Ala Leu Arg Glu Leu Ile Glu Glu Leu Val Asn Ile Thr Gln
                85                  90                  95

Asn Gln Lys Ala Pro Leu Cys Asn Gly Ser Met Val Trp Ser Ile Asn
            100                 105                 110

Leu Thr Ala Gly Met Tyr Cys Ala Ala Leu Glu Ser Leu Ile Asn Val
        115                 120                 125

Ser Gly Cys Ser Ala Ile Glu Lys Thr Gln Arg Met Leu Ser Gly Phe
    130                 135                 140

Cys Pro His Lys Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
145                 150                 155                 160

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Leu Gln Gly Gly
                165                 170                 175

Gly Gly Ala Ala Pro Thr Glu Thr Gln Pro Pro Val Thr Asn Leu Ser
            180                 185                 190
```

```
Val Ser Val Glu Asn Leu Cys Thr Val Ile Trp Thr Trp Asn Pro Pro
        195                 200                 205

Glu Gly Ala Ser Ser Asn Cys Ser Leu Trp Tyr Phe Ser His Phe Gly
    210                 215                 220

Asp Lys Gln Asp Lys Lys Ile Ala Pro Glu Thr Arg Arg Ser Ile Glu
225                 230                 235                 240

Val Pro Leu Asn Glu Arg Ile Cys Leu Gln Val Gly Ser Gln Cys Ser
                245                 250                 255

Thr Asn Glu Ser Glu Lys Pro Ser Ile Leu Val Glu Lys Cys Ile Ser
            260                 265                 270

Pro Pro Glu Gly Asp Pro Glu Ser Ala Val Thr Glu Leu Gln Cys Ile
        275                 280                 285

Trp His Asn Leu Ser Tyr Met Lys Cys Ser Trp Leu Pro Gly Arg Asn
    290                 295                 300

Thr Ser Pro Asp Thr Asn Tyr Thr Leu Tyr Tyr Trp His Arg Ser Leu
305                 310                 315                 320

Glu Lys Ile His Gln Cys Glu Asn Ile Phe Arg Glu Gly Gln Tyr Phe
                325                 330                 335

Gly Cys Ser Phe Asp Leu Thr Lys Val Lys Asp Ser Ser Phe Glu Gln
            340                 345                 350

His Ser Val Gln Ile Met Val Lys Asp Asn Ala Gly Lys Ile Lys Pro
        355                 360                 365

Ser Phe Asn Ile Val Pro Leu Thr Ser Arg Val Lys Pro Asp Pro Pro
    370                 375                 380

His Ile Lys Asn Leu Ser Phe His Asn Asp Asp Leu Tyr Val Gln Trp
```

```
385                 390                 395                 400

Glu Asn Pro Gln Asn Phe Ile Ser Arg Cys Leu Phe Tyr Glu Val Glu
                405                 410                 415

Val Asn Asn Ser Gln Thr Glu Thr His Asn Val Phe Tyr Val Gln Glu
            420                 425                 430

Ala Lys Cys Glu Asn Pro Glu Phe Glu Arg Asn Val Glu Asn Thr Ser
        435                 440                 445

Cys Phe Met Val Pro Gly Val Leu Pro Asp Thr Leu Asn Thr Val Arg
    450                 455                 460

Ile Arg Val Lys Thr Asn Lys Leu Cys Tyr Glu Asp Asp Lys Leu Trp
465                 470                 475                 480

Ser Asn Trp Ser Gln Glu Met Ser Ile Gly Lys Lys Arg Asn Ser Thr
                485                 490                 495

Leu Tyr Ile Thr Met Leu Leu Ile Val Pro Val Ile Val Ala Gly Ala
            500                 505                 510

Ile Ile Val Leu Leu Leu Tyr Leu Lys Arg Leu Lys Ile Ile Ile Phe
        515                 520                 525

Pro Pro Ile Pro Asp Pro Gly Lys Ile Phe Lys Glu Met Phe Gly Asp
    530                 535                 540

Gln Asn Asp Asp Thr Leu His Trp Lys Lys Tyr Asp Ile Tyr Glu Lys
545                 550                 555                 560

Gln Thr Lys Glu Glu Thr Asp Ser Val Val Leu Ile Glu Asn Leu Lys
                565                 570                 575

Lys Ala Ser Gln
            580
```

<210> 118
<211> 974
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 118
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Val Ser Ala Gly Gln Phe Ser Ser Leu His Val
20 25 30

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

His Leu Lys Lys Leu Phe Arg Glu Gly Arg Phe Asn Gly Gly Gly Gly
50 55 60

Ser Leu Thr Cys Leu Gly Gly Phe Ala Ser Pro Gly Pro Val Pro Pro
65 70 75 80

Ser Thr Ala Leu Arg Glu Leu Ile Glu Glu Leu Val Asn Ile Thr Gln
85 90 95

Asn Gln Lys Ala Pro Leu Cys Asn Gly Ser Met Val Trp Ser Ile Asn
100 105 110

Leu Thr Ala Gly Met Tyr Cys Ala Ala Leu Glu Ser Leu Ile Asn Val
115 120 125

Ser Gly Cys Ser Ala Ile Glu Lys Thr Gln Arg Met Leu Ser Gly Phe
130 135 140

Cys Pro His Lys Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
145 150 155 160

```
Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Leu Gln Met Lys
               165                 170                 175

Val Leu Gln Glu Pro Thr Cys Val Ser Asp Tyr Met Ser Ile Ser Thr
            180                 185                 190

Cys Glu Trp Lys Met Asn Gly Pro Thr Asn Cys Ser Thr Glu Leu Arg
        195                 200                 205

Leu Leu Tyr Gln Leu Val Phe Leu Leu Ser Glu Ala His Thr Cys Ile
    210                 215                 220

Pro Glu Asn Asn Gly Gly Ala Gly Cys Val Cys His Leu Leu Met Asp
225                 230                 235                 240

Asp Val Val Ser Ala Asp Asn Tyr Thr Leu Asp Leu Trp Ala Gly Gln
               245                 250                 255

Gln Leu Leu Trp Lys Gly Ser Phe Lys Pro Ser Glu His Val Lys Pro
            260                 265                 270

Arg Ala Pro Gly Asn Leu Thr Val His Thr Asn Val Ser Asp Thr Leu
        275                 280                 285

Leu Leu Thr Trp Ser Asn Pro Tyr Pro Pro Asp Asn Tyr Leu Tyr Asn
    290                 295                 300

His Leu Thr Tyr Ala Val Asn Ile Trp Ser Glu Asn Asp Pro Ala Asp
305                 310                 315                 320

Phe Arg Ile Tyr Asn Val Thr Tyr Leu Glu Pro Ser Leu Arg Ile Ala
               325                 330                 335

Ala Ser Thr Leu Lys Ser Gly Ile Ser Tyr Arg Ala Arg Val Arg Ala
            340                 345                 350

Trp Ala Gln Cys Tyr Asn Thr Thr Trp Ser Glu Trp Ser Pro Ser Thr
```

```
        355                 360                 365

Lys Trp His Asn Ser Tyr Arg Glu Pro Phe Glu Gln His Leu Leu Leu
    370                 375                 380

Gly Val Ser Val Ser Cys Ile Val Ile Leu Ala Val Cys Leu Leu Cys
385                 390                 395                 400

Tyr Val Ser Ile Thr Lys Ile Lys Lys Glu Trp Trp Asp Gln Ile Pro
                405                 410                 415

Asn Pro Ala Arg Ser Arg Leu Val Ala Ile Ile Ile Gln Asp Ala Gln
            420                 425                 430

Gly Ser Gln Trp Glu Lys Arg Ser Arg Gly Gln Glu Pro Ala Lys Cys
        435                 440                 445

Pro His Trp Lys Asn Cys Leu Thr Lys Leu Leu Pro Cys Phe Leu Glu
    450                 455                 460

His Asn Met Lys Arg Asp Glu Asp Pro His Lys Ala Ala Lys Glu Met
465                 470                 475                 480

Pro Phe Gln Gly Ser Gly Lys Ser Ala Trp Cys Pro Val Glu Ile Ser
                485                 490                 495

Lys Thr Val Leu Trp Pro Glu Ser Ile Ser Val Val Arg Cys Val Glu
            500                 505                 510

Leu Phe Glu Ala Pro Val Glu Cys Glu Glu Glu Glu Glu Val Glu Glu
        515                 520                 525

Glu Lys Gly Ser Phe Cys Ala Ser Pro Glu Ser Ser Arg Asp Asp Phe
    530                 535                 540

Gln Glu Gly Arg Glu Gly Ile Val Ala Arg Leu Thr Glu Ser Leu Phe
545                 550                 555                 560
```

```
Leu Asp Leu Leu Gly Glu Glu Asn Gly Gly Phe Cys Gln Gln Asp Met
                565                 570                 575

Gly Glu Ser Cys Leu Leu Pro Pro Ser Gly Ser Thr Ser Ala His Met
            580                 585                 590

Pro Trp Asp Glu Phe Pro Ser Ala Gly Pro Lys Glu Ala Pro Pro Trp
        595                 600                 605

Gly Lys Glu Gln Pro Leu His Leu Glu Pro Ser Pro Pro Ala Ser Pro
    610                 615                 620

Thr Gln Ser Pro Asp Asn Leu Thr Cys Thr Glu Thr Pro Leu Val Ile
625                 630                 635                 640

Ala Gly Asn Pro Ala Tyr Arg Ser Phe Ser Asn Ser Leu Ser Gln Ser
                645                 650                 655

Pro Cys Pro Arg Glu Leu Gly Pro Asp Pro Leu Leu Ala Arg His Leu
            660                 665                 670

Glu Glu Val Glu Pro Glu Met Pro Cys Val Pro Gln Leu Ser Glu Pro
        675                 680                 685

Thr Thr Val Pro Gln Pro Glu Pro Glu Thr Trp Glu Gln Ile Leu Arg
    690                 695                 700

Arg Asn Val Leu Gln His Gly Ala Ala Ala Ala Pro Val Ser Ala Pro
705                 710                 715                 720

Thr Ser Gly Tyr Gln Glu Phe Val His Ala Val Glu Gln Gly Gly Thr
                725                 730                 735

Gln Ala Ser Ala Val Val Gly Leu Gly Pro Pro Gly Glu Ala Gly Tyr
            740                 745                 750

Lys Ala Phe Ser Ser Leu Leu Ala Ser Ser Ala Val Ser Pro Glu Lys
```

```
        755                 760                 765

Cys Gly Phe Gly Ala Ser Ser Gly Glu Glu Gly Tyr Lys Pro Phe Gln
    770                 775                 780

Asp Leu Ile Pro Gly Cys Pro Gly Asp Pro Ala Pro Val Pro Val Pro
785                 790                 795                 800

Leu Phe Thr Phe Gly Leu Asp Arg Glu Pro Pro Arg Ser Pro Gln Ser
                805                 810                 815

Ser His Leu Pro Ser Ser Ser Pro Glu His Leu Gly Leu Glu Pro Gly
            820                 825                 830

Glu Lys Val Glu Asp Met Pro Lys Pro Pro Leu Pro Gln Glu Gln Ala
        835                 840                 845

Thr Asp Pro Leu Val Asp Ser Leu Gly Ser Gly Ile Val Tyr Ser Ala
    850                 855                 860

Leu Thr Cys His Leu Cys Gly His Leu Lys Gln Cys His Gly Gln Glu
865                 870                 875                 880

Asp Gly Gly Gln Thr Pro Val Met Ala Ser Pro Cys Cys Gly Cys Cys
                885                 890                 895

Cys Gly Asp Arg Ser Ser Pro Pro Thr Thr Pro Leu Arg Ala Pro Asp
            900                 905                 910

Pro Ser Pro Gly Gly Val Pro Leu Glu Ala Ser Leu Cys Pro Ala Ser
        915                 920                 925

Leu Ala Pro Ser Gly Ile Ser Glu Lys Ser Lys Ser Ser Ser Ser Phe
    930                 935                 940

His Pro Ala Pro Gly Asn Ala Gln Ser Ser Ser Gln Thr Pro Lys Ile
945                 950                 955                 960
```

Val Asn Phe Val Ser Val Gly Pro Thr Tyr Met Arg Val Ser
965 970

<210> 119
<211> 727
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 119
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Tyr Phe Gly Lys Leu Glu Ser Lys Leu Ser Val
20 25 30

Ile Arg Asn Leu Asn Asp Gln Val Leu Phe Ile Asp Gln Gly Asn Arg
35 40 45

Pro Leu Phe Glu Asp Met Thr Asp Ser Asp Cys Arg Asp Asn Ala Pro
50 55 60

Arg Thr Ile Phe Ile Ile Ser Met Tyr Lys Asp Ser Gln Pro Arg Gly
65 70 75 80

Met Ala Val Thr Ile Ser Val Lys Cys Glu Lys Ile Ser Thr Leu Ser
85 90 95

Cys Glu Asn Lys Ile Ile Ser Phe Lys Glu Met Asn Pro Pro Asp Asn
100 105 110

Ile Lys Asp Thr Lys Ser Asp Ile Ile Phe Phe Gln Arg Ser Val Pro
115 120 125

Gly His Asp Asn Lys Met Gln Phe Glu Ser Ser Ser Tyr Glu Gly Tyr
130 135 140

```
Phe Leu Ala Cys Glu Lys Glu Arg Asp Leu Phe Lys Leu Ile Leu Lys
145                 150                 155                 160

Lys Glu Asp Glu Leu Gly Asp Arg Ser Ile Met Phe Thr Val Gln Asn
                165                 170                 175

Glu Asp Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
            180                 185                 190

Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Leu Gln Ala Glu Ser Cys
        195                 200                 205

Thr Ser Arg Pro His Ile Thr Val Val Glu Gly Glu Pro Phe Tyr Leu
    210                 215                 220

Lys His Cys Ser Cys Ser Leu Ala His Glu Ile Glu Thr Thr Thr Lys
225                 230                 235                 240

Ser Trp Tyr Lys Ser Ser Gly Ser Gln Glu His Val Glu Leu Asn Pro
                245                 250                 255

Arg Ser Ser Ser Arg Ile Ala Leu His Asp Cys Val Leu Glu Phe Trp
            260                 265                 270

Pro Val Glu Leu Asn Asp Thr Gly Ser Tyr Phe Phe Gln Met Lys Asn
        275                 280                 285

Tyr Thr Gln Lys Trp Lys Leu Asn Val Ile Arg Arg Asn Lys His Ser
    290                 295                 300

Cys Phe Thr Glu Arg Gln Val Thr Ser Lys Ile Val Glu Val Lys Lys
305                 310                 315                 320

Phe Phe Gln Ile Thr Cys Glu Asn Ser Tyr Tyr Gln Thr Leu Val Asn
                325                 330                 335

Ser Thr Ser Leu Tyr Lys Asn Cys Lys Lys Leu Leu Leu Glu Asn Asn
```

```
            340                 345                 350

Lys Asn Pro Thr Ile Lys Lys Asn Ala Glu Phe Glu Asp Gln Gly Tyr
        355                 360                 365

Tyr Ser Cys Val His Phe Leu His His Asn Gly Lys Leu Phe Asn Ile
    370                 375                 380

Thr Lys Thr Phe Asn Ile Thr Ile Val Glu Asp Arg Ser Asn Ile Val
385                 390                 395                 400

Pro Val Leu Leu Gly Pro Lys Leu Asn His Val Ala Val Glu Leu Gly
                405                 410                 415

Lys Asn Val Arg Leu Asn Cys Ser Ala Leu Leu Asn Glu Glu Asp Val
            420                 425                 430

Ile Tyr Trp Met Phe Gly Glu Glu Asn Gly Ser Asp Pro Asn Ile His
        435                 440                 445

Glu Glu Lys Glu Met Arg Ile Met Thr Pro Glu Gly Lys Trp His Ala
    450                 455                 460

Ser Lys Val Leu Arg Ile Glu Asn Ile Gly Glu Ser Asn Leu Asn Val
465                 470                 475                 480

Leu Tyr Asn Cys Thr Val Ala Ser Thr Gly Gly Thr Asp Thr Lys Ser
                485                 490                 495

Phe Ile Leu Val Arg Lys Ala Asp Met Ala Asp Ile Pro Gly His Val
            500                 505                 510

Phe Thr Arg Gly Met Ile Ile Ala Val Leu Ile Leu Val Ala Val Val
        515                 520                 525

Cys Leu Val Thr Val Cys Val Ile Tyr Arg Val Asp Leu Val Leu Phe
    530                 535                 540
```

```
Tyr Arg His Leu Thr Arg Arg Asp Glu Thr Leu Thr Asp Gly Lys Thr
545                 550                 555                 560

Tyr Asp Ala Phe Val Ser Tyr Leu Lys Glu Cys Arg Pro Glu Asn Gly
                565                 570                 575

Glu Glu His Thr Phe Ala Val Glu Ile Leu Pro Arg Val Leu Glu Lys
            580                 585                 590

His Phe Gly Tyr Lys Leu Cys Ile Phe Glu Arg Asp Val Val Pro Gly
        595                 600                 605

Gly Ala Val Val Asp Glu Ile His Ser Leu Ile Glu Lys Ser Arg Arg
    610                 615                 620

Leu Ile Ile Val Leu Ser Lys Ser Tyr Met Ser Asn Glu Val Arg Tyr
625                 630                 635                 640

Glu Leu Glu Ser Gly Leu His Glu Ala Leu Val Glu Arg Lys Ile Lys
                645                 650                 655

Ile Ile Leu Ile Glu Phe Thr Pro Val Thr Asp Phe Thr Phe Leu Pro
            660                 665                 670

Gln Ser Leu Lys Leu Leu Lys Ser His Arg Val Leu Lys Trp Lys Ala
        675                 680                 685

Asp Lys Ser Leu Ser Tyr Asn Ser Arg Phe Trp Lys Asn Leu Leu Tyr
    690                 695                 700

Leu Met Pro Ala Lys Thr Val Lys Pro Gly Arg Asp Glu Pro Glu Val
705                 710                 715                 720

Leu Pro Val Leu Ser Glu Ser
                725
```

<210> 120

<211> 784
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 120
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Tyr Phe Gly Lys Leu Glu Ser Lys Leu Ser Val
20 25 30

Ile Arg Asn Leu Asn Asp Gln Val Leu Phe Ile Asp Gln Gly Asn Arg
35 40 45

Pro Leu Phe Glu Asp Met Thr Asp Ser Asp Cys Arg Asp Asn Ala Pro
50 55 60

Arg Thr Ile Phe Ile Ile Ser Met Tyr Lys Asp Ser Gln Pro Arg Gly
65 70 75 80

Met Ala Val Thr Ile Ser Val Lys Cys Glu Lys Ile Ser Thr Leu Ser
85 90 95

Cys Glu Asn Lys Ile Ile Ser Phe Lys Glu Met Asn Pro Pro Asp Asn
100 105 110

Ile Lys Asp Thr Lys Ser Asp Ile Ile Phe Phe Gln Arg Ser Val Pro
115 120 125

Gly His Asp Asn Lys Met Gln Phe Glu Ser Ser Ser Tyr Glu Gly Tyr
130 135 140

Phe Leu Ala Cys Glu Lys Glu Arg Asp Leu Phe Lys Leu Ile Leu Lys
145 150 155 160

Lys Glu Asp Glu Leu Gly Asp Arg Ser Ile Met Phe Thr Val Gln Asn

```
                165                 170                 175

Glu Asp Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
            180                 185                 190

Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Leu Gln Phe Asn Ile Ser
        195                 200                 205

Gly Cys Ser Thr Lys Lys Leu Leu Trp Thr Tyr Ser Thr Arg Ser Glu
    210                 215                 220

Glu Glu Phe Val Leu Phe Cys Asp Leu Pro Glu Pro Gln Lys Ser His
225                 230                 235                 240

Phe Cys His Arg Asn Arg Leu Ser Pro Lys Gln Val Pro Glu His Leu
                245                 250                 255

Pro Phe Met Gly Ser Asn Asp Leu Ser Asp Val Gln Trp Tyr Gln Gln
            260                 265                 270

Pro Ser Asn Gly Asp Pro Leu Glu Asp Ile Arg Lys Ser Tyr Pro His
        275                 280                 285

Ile Ile Gln Asp Lys Cys Thr Leu His Phe Leu Thr Pro Gly Val Asn
    290                 295                 300

Asn Ser Gly Ser Tyr Ile Cys Arg Pro Lys Met Ile Lys Ser Pro Tyr
305                 310                 315                 320

Asp Val Ala Cys Cys Val Lys Met Ile Leu Glu Val Lys Pro Gln Thr
                325                 330                 335

Asn Ala Ser Cys Glu Tyr Ser Ala Ser His Lys Gln Asp Leu Leu Leu
            340                 345                 350

Gly Ser Thr Gly Ser Ile Ser Cys Pro Ser Leu Ser Cys Gln Ser Asp
        355                 360                 365
```

```
Ala Gln Ser Pro Ala Val Thr Trp Tyr Lys Asn Gly Lys Leu Leu Ser
    370                 375                 380

Val Glu Arg Ser Asn Arg Ile Val Val Asp Glu Val Tyr Asp Tyr His
385                 390                 395                 400

Gln Gly Thr Tyr Val Cys Asp Tyr Thr Gln Ser Asp Thr Val Ser Ser
                405                 410                 415

Trp Thr Val Arg Ala Val Val Gln Val Arg Thr Ile Val Gly Asp Thr
            420                 425                 430

Lys Leu Lys Pro Asp Ile Leu Asp Pro Val Glu Asp Thr Leu Glu Val
        435                 440                 445

Glu Leu Gly Lys Pro Leu Thr Ile Ser Cys Lys Ala Arg Phe Gly Phe
    450                 455                 460

Glu Arg Val Phe Asn Pro Val Ile Lys Trp Tyr Ile Lys Asp Ser Asp
465                 470                 475                 480

Leu Glu Trp Glu Val Ser Val Pro Glu Ala Lys Ser Ile Lys Ser Thr
                485                 490                 495

Leu Lys Asp Glu Ile Ile Glu Arg Asn Ile Ile Leu Glu Lys Val Thr
            500                 505                 510

Gln Arg Asp Leu Arg Arg Lys Phe Val Cys Phe Val Gln Asn Ser Ile
        515                 520                 525

Gly Asn Thr Thr Gln Ser Val Gln Leu Lys Glu Lys Arg Gly Val Val
    530                 535                 540

Leu Leu Tyr Ile Leu Leu Gly Thr Ile Gly Thr Leu Val Ala Val Leu
545                 550                 555                 560

Ala Ala Ser Ala Leu Leu Tyr Arg His Trp Ile Glu Ile Val Leu Leu
```

```
                565                 570                 575

Tyr Arg Thr Tyr Gln Ser Lys Asp Gln Thr Leu Gly Asp Lys Lys Asp
            580                 585                 590

Phe Asp Ala Phe Val Ser Tyr Ala Lys Trp Ser Ser Phe Pro Ser Glu
        595                 600                 605

Ala Thr Ser Ser Leu Ser Glu Glu His Leu Ala Leu Ser Leu Phe Pro
    610                 615                 620

Asp Val Leu Glu Asn Lys Tyr Gly Tyr Ser Leu Cys Leu Leu Glu Arg
625                 630                 635                 640

Asp Val Ala Pro Gly Gly Val Tyr Ala Glu Asp Ile Val Ser Ile Ile
                645                 650                 655

Lys Arg Ser Arg Arg Gly Ile Phe Ile Leu Ser Pro Asn Tyr Val Asn
            660                 665                 670

Gly Pro Ser Ile Phe Glu Leu Gln Ala Ala Val Asn Leu Ala Leu Asp
        675                 680                 685

Asp Gln Thr Leu Lys Leu Ile Leu Ile Lys Phe Cys Tyr Phe Gln Glu
    690                 695                 700

Pro Glu Ser Leu Pro His Leu Val Lys Lys Ala Leu Arg Val Leu Pro
705                 710                 715                 720

Thr Val Thr Trp Arg Gly Leu Lys Ser Val Pro Pro Asn Ser Arg Phe
                725                 730                 735

Trp Ala Lys Met Arg Tyr His Met Pro Val Lys Asn Ser Gln Gly Phe
            740                 745                 750

Thr Trp Asn Gln Leu Arg Ile Thr Ser Arg Ile Phe Gln Trp Lys Gly
        755                 760                 765
```

Leu Ser Arg Thr Glu Thr Thr Gly Arg Ser Ser Gln Pro Lys Glu Trp
770 775 780

<210> 121
<211> 2226
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 121
atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60

ccgtgcgacc ttccacagac ccattccctc ggctctcgaa gaactctgat gttgctggcc 120

cagatgcgga agatttctct tttctcatgt ctgaaagaca ggcacgactt tggttttccc 180

caggaggagt tcggaaacca gttccagaaa gcggaaacca ttcctgtgct gcacgaaatg 240

atccaacaaa ttttcaacct gttttcaact aaagatagct ccgctgcatg ggacgagaca 300

ctcctcgata agttttatac agagctttac cagcagttaa atgatctgga agcttgtgtc 360

atccaagggg tcggcgtaac cgagacgccc ctgatgaagg aggatagcat actggcagtg 420

cggaagtact tccagaggat caccctctat ctaaaggaaa aaaagtacag tccgtgcgcc 480

tgggaagtgg ttagagccga aatcatgcgt agcttttcct tatctacaaa tttgcaggag 540

tcgttgcgca gtaaagagtc tggaggcgga agcgggggtg gcggcagcgg cggtggagga 600

tcaggtggcg gggggtccgg gggcggaagt ctgcagaaga acctgaaatc cccacagaaa 660

gtcgaggtgg acatcatcga tgacaatttc atcttaagat ggaaccgtag cgatgagtcc 720

gtcggaaatg tcacattttc ttttgattat cagaagaccg ggatggacaa ctggattaag 780

ctgtccggtt gccagaacat aaccagtacc aagtgtaact tcagcagcct caaactcaat 840

gtatatgagg aaatcaagct gaggatccgg gccgagaagg aaaacacaag ctcctggtat 900

gaagttgatt catttactcc atttcgaaaa gcgcaaatag gacccccgga agttcacctc 960

gaggctgaag ataaagcaat tgtaatacac atatcgcctg gcaccaagga ctctgtgatg 1020

tgggctttag atgggctgtc attcacgtac agcctggtga tctggaagaa cagttctggg 1080

gtggaggaga gaatagaaaa catttatagt cgccacaaaa tctacaaatt gtcacccgaa 1140

acaacctatt gcctgaaggt caaggcggca ctattgacgt cctggaagat cggcgtgtac 1200

tcaccagtgc attgtataaa gacaacagtg gaaaacgagc ttcccccgcc ggagaatatt 1260

gaggtttccg tgcagaatca gaattatgtg ttgaagtggg actacacata tgccaatatg 1320

accttccagg ttcaatggct tcatgcattt ctgaaaagaa accctggtaa ccacctttac 1380

aaatggaagc agattcctga ctgcgagaat gtcaagacca cacagtgcgt gtttcctcaa 1440

aacgttttcc agaaaggcat ctatctgcta cgggtccagg cttccgatgg caataatacc 1500

tcattttgga gcgaggaaat taaattcgac actgaaatcc aagccttcct actccctccc 1560

gtatttaaca tcaggagtct gtctgatagc ttccatattt acatcggtgc tcccaagcag 1620

tctggaaaca ctcccgtgat ccaggattac cccctcatct acgagatcat tttctgggaa 1680

aacacctcta acgccgaacg gaagattata gagaagaaaa ctgacgtcac tgtgcctaac 1740

ctgaaaccat taactgtcta ttgcgtcaaa gctagggccc acaccatgga tgaaaaactg 1800

aacaagtcta gcgtgttcag cgacgcagtt tgtgagaaaa cgaagccagg aaatacttct 1860

aagatttggc ttatcgtggg catttgtatc gctctgttcg cactgccctt tgtaatctac 1920

gccgccaagg tttttctccg ctgtattaat tatgtgtttt tcccatccct gaagccatca 1980

tcgtcgattg acgagtactt ctctgagcaa cctcttaaaa acctgttgtt gtccaccagt 2040

gaagagcaga ttgagaaatg cttcattatc gaaaatattt caacaatcgc cacagtggag 2100

gagacgaatc agaccgacga ggaccataag aagtacagca gtcagacatc tcaggattcc 2160

gggaattaca gcaatgaaga tgaaagtgaa tccaaaacta gcgaggagct ccaacaggac 2220

tttgtg 2226

<210> 122
<211> 2103
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 122
atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60

ccgtgcgacc ttccacagac ccattccctc ggctctcgaa gaactctgat gttgctggcc 120

cagatgcgga agatttctct tttctcatgt ctgaaagaca ggcacgactt tggttttccc 180

caggaggagt tcggaaacca gttccagaaa gcggaaacca ttcctgtgct gcacgaaatg 240

atccaacaaa ttttcaacct gttttcaact aaagatagct ccgctgcatg ggacgagaca 300

ctcctcgata agttttatac agagctttac cagcagttaa atgatctgga agcttgtgtc 360

atccaagggg tcggcgtaac cgagacgccc ctgatgaagg aggatagcat actggcagtg 420

cggaagtact tccagaggat caccctctat ctaaaggaaa aaaagtacag tccgtgcgcc 480

tgggaagtgg ttagagccga aatcatgcgt agcttttcct tatctacaaa tttgcaggag 540

tcgttgcgca gtaaagagtc tggaggcgga agcgggggtg gcggcagcgg cggtggagga 600

tcaggtggcg gggggtccgg gggcggaagt ctgcagatca gctacgactc ccccgattac 660

accgacgagt cctgtacctt taaaatctcc ctacgtaact tcaggtccat tctctcctgg 720

gaactgaaaa accatagcat tgtgccgact cactatacac tgctgtatac cataatgtct 780

aaacccgagg atctgaaggt ggtgaagaac tgtgcgaaca ccacaagatc cttctgcgac 840

ctgacagatg agtggcgatc tacccatgaa gcctacgtca cggtcctcga gggcttcagc 900

ggtaatacca cacttttcag ctgctcacat aacttttggt tggccatcga tatgtccttt 960

gaaccacccg agttcgagat tgtcggtttc acaaaccaca tcaatgtcat ggtgaaattt 1020

ccttctattg tcgaggaaga actccagttt gatttgagcc tcgtgattga ggagcagtca 1080

gagggaatcg tgaagaagca taagcccgaa ataaagggaa atatgagtgg gaacttcact 1140

tacataatcg acaagctcat ccccaacacg aattattgtg tgtcagtgta tctcgagcac 1200

tcggatgagc aagccgtgat caagtctcca cttaagtgca ctctcctgcc gccaggccag 1260

gagtcagaga gcgctgaatc ggctaagata ggcgggatca ttaccgtctt cctcatcgca 1320

ctggtgttga cttctactat tgttaccctg aagtggatcg gatacatctg cttgcgcaac 1380

tctctgccaa aagttctaaa ctttcacaat tttctggcct ggcccttccc caatcttcct 1440

cctctggagg ccatggacat ggttgaggtt atctatataa atcggaaaaa aaaagtctgg 1500

gactacaatt acgatgacga aagtgactca gacacggagg ccgcaccaag gacctctgga 1560

gggggctata ctatgcacgg ccttaccgtg agacctttag gacaggcatc tgctacaagc 1620

actgaaagcc agctgattga cccagagagc gaggaagagc ctgatctacc agaagtggat 1680

gtagagctgc cgacaatgcc taaggactcc ccccaacagc tcgaactgtt gagcggccct 1740

tgtgaaaggc gcaaaagtcc cttgcaagat ccgttccctg aagaagacta tagcagtacc 1800

gaaggatccg gcggtcggat tacattcaac gtggatttaa atagtgtatt tttacgggtt 1860

ctggacgatg aggacagtga tgatctggag gcgcccctta tgctgtcctc ccatctggag 1920

gagatggtag accccgaaga tccagataac gtgcagtcta atcaccttct ggcttccggg 1980

gaaggtactc agccaacctt tcctagtcct tcttcagagg gcttatggtc agaagacgca 2040

ccaagcgatc agtcagacac aagtgagagc gacgtagacc tcggggacgg gtacattatg 2100

aga 2103

<210> 123
<211> 2229
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 123
atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60

ccgatgagtt ataatttact cggatttcta cagcggtcta gcaacttcca atgtcagaag 120

ctgctgtggc aactcaacgg caggctggag tactgcctca aagatagaat gaactttgat 180

attcccgaag aaatcaagca gcttcagcag ttccagaaag aggacgccgc actaaccata 240

tacgagatgc tgcagaacat tttcgctata ttcagacagg actcgtcctc tactggatgg 300

aatgagacca tcgtcgagaa tttgctggcc aatgtgtatc atcaaattaa ccacctcaag 360

acggtgcttg aagaaaagtt ggaaaaagag gacttcacta gaggcaaact gatgtcatcc 420

cttcacctca aacgctacta tgggaggatc ctgcactact taaaggcgaa ggagtatagc 480

cattgcgctt ggacaatcgt tcgcgtagag attctgcgga atttttactt tatcaatcgt 540

ttgacaggtt acctgcgaaa ctctggaggc ggaagcgggg gtggcggcag cggcggtgga 600

ggatcaggtg gcgggggggtc cgggggcgga agtctgcaga agaacctgaa atccccacag 660

aaagtcgagg tggacatcat cgatgacaat ttcatcttaa gatggaaccg tagcgatgag 720

tccgtcggaa atgtcacatt ttcttttgat tatcagaaga ccgggatgga caactggatt 780

aagctgtccg gttgccagaa cataaccagt accaagtgta acttcagcag cctcaaactc 840

aatgtatatg aggaaatcaa gctgaggatc cgggccgaga aggaaaacac aagctcctgg 900

tatgaagttg attcatttac tccatttcga aaagcgcaaa taggaccccc ggaagttcac 960

ctcgaggctg aagataaagc aattgtaata cacatatcgc ctggcaccaa ggactctgtg 1020

atgtgggctt tagatgggct gtcattcacg tacagcctgg tgatctggaa gaacagttct 1080

ggggtggagg agagaataga aaacatttat agtcgccaca aaatctacaa attgtcaccc 1140

gaaacaacct attgcctgaa ggtcaaggcg gcactattga cgtcctggaa gatcggcgtg 1200

tactcaccag tgcattgtat aaagacaaca gtggaaaacg agcttccccc gccggagaat 1260

attgaggttt ccgtgcagaa tcagaattat gtgttgaagt gggactacac atatgccaat 1320

atgaccttcc aggttcaatg gcttcatgca tttctgaaaa gaaaccctgg taaccacctt 1380

tacaaatgga agcagattcc tgactgcgag aatgtcaaga ccacacagtg cgtgtttcct 1440

caaaacgttt tccagaaagg catctatctg ctacgggtcc aggcttccga tggcaataat 1500

acctcatttt ggagcgagga aattaaattc gacactgaaa tccaagcctt cctactccct 1560

cccgtattta acatcaggag tctgtctgat agcttccata tttacatcgg tgctcccaag 1620

cagtctggaa acactcccgt gatccaggat taccccctca tctacgagat cattttctgg 1680

gaaaacacct ctaacgccga acggaagatt atagagaaga aaactgacgt cactgtgcct 1740

aacctgaaac cattaactgt ctattgcgtc aaagctaggg cccacaccat ggatgaaaaa 1800

ctgaacaagt ctagcgtgtt cagcgacgca gtttgtgaga aaacgaagcc aggaaatact 1860

tctaagattt ggcttatcgt gggcatttgt atcgctctgt tcgcactgcc ctttgtaatc 1920

tacgccgcca aggtttttct ccgctgtatt aattatgtgt ttttcccatc cctgaagcca 1980

tcatcgtcga ttgacgagta cttctctgag caacctctta aaaacctgtt gttgtccacc 2040

agtgaagagc agattgagaa atgcttcatt atcgaaaata tttcaacaat cgccacagtg 2100

gaggagacga atcagaccga cgaggaccat aagaagtaca gcagtcagac atctcaggat 2160

tccgggaatt acagcaatga agatgaaagt gaatccaaaa ctagcgagga gctccaacag 2220

gactttgtg 2229

<210> 124
<211> 2106
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 124
atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60

ccgatgagtt ataatttact cggatttcta cagcggtcta gcaacttcca atgtcagaag 120

ctgctgtggc aactcaacgg caggctggag tactgcctca aagatagaat gaactttgat 180

attcccgaag aaatcaagca gcttcagcag ttccagaaag aggacgccgc actaaccata 240

tacgagatgc tgcagaacat tttcgctata ttcagacagg actcgtcctc tactggatgg 300

aatgagacca tcgtcgagaa tttgctggcc aatgtgtatc atcaaattaa ccacctcaag 360

acggtgcttg aagaaaagtt ggaaaaagag gacttcacta gaggcaaact gatgtcatcc 420

cttcacctca aacgctacta tgggaggatc ctgcactact taaaggcgaa ggagtatagc 480

cattgcgctt ggacaatcgt tcgcgtagag attctgcgga atttttactt tatcaatcgt 540

ttgacaggtt acctgcgaaa ctctggaggc ggaagcgggg gtggcggcag cggcggtgga 600

ggatcaggtg gcgggggtc cgggggcgga agtctgcaga tcagctacga ctcccccgat 660

tacaccgacg agtcctgtac ctttaaaatc tccctacgta acttcaggtc cattctctcc 720

tgggaactga aaaaccatag cattgtgccg actcactata cactgctgta taccataatg 780

tctaaacccg aggatctgaa ggtggtgaag aactgtgcga acaccacaag atccttctgc 840

gacctgacag atgagtggcg atctacccat gaagcctacg tcacggtcct cgagggcttc 900

agcggtaata ccacactttt cagctgctca cataactttt ggttggccat cgatatgtcc 960

tttgaaccac ccgagttcga gattgtcggt ttcacaaacc acatcaatgt catggtgaaa 1020

tttccttcta ttgtcgagga agaactccag tttgatttga gcctcgtgat tgaggagcag 1080

tcagagggaa tcgtgaagaa gcataagccc gaaataaagg gaaatatgag tgggaacttc 1140

acttacataa tcgacaagct catccccaac acgaattatt gtgtgtcagt gtatctcgag 1200

cactcggatg agcaagccgt gatcaagtct ccacttaagt gcactctcct gccgccaggc 1260

caggagtcag agagcgctga atcggctaag ataggcggga tcattaccgt cttcctcatc 1320

gcactggtgt tgacttctac tattgttacc ctgaagtgga tcggatacat ctgcttgcgc 1380

aactctctgc caaaagttct aaactttcac aattttctgg cctggccctt ccccaatctt 1440

cctcctctgg aggccatgga catggttgag gttatctata taaatcggaa aaaaaaagtc 1500

tgggactaca attacgatga cgaaagtgac tcagacacgg aggccgcacc aaggacctct 1560

ggaggggggct atactatgca cggccttacc gtgagacctt taggacaggc atctgctaca 1620

agcactgaaa gccagctgat tgacccagag agcgaggaag agcctgatct accagaagtg 1680

gatgtagagc tgccgacaat gcctaaggac tccccccaac agctcgaact gttgagcggc 1740

ccttgtgaaa ggcgcaaaag tcccttgcaa gatccgttcc ctgaagaaga ctatagcagt 1800

accgaaggat ccggcggtcg gattacattc aacgtggatt taaatagtgt atttttacgg 1860

gttctggacg atgaggacag tgatgatctg gaggcgcccc ttatgctgtc ctcccatctg 1920

gaggagatgg tagaccccga agatccagat aacgtgcagt ctaatcacct tctggcttcc 1980

ggggaaggta ctcagccaac ctttcctagt ccttcttcag agggcttatg gtcagaagac 2040

gcaccaagcg atcagtcaga cacaagtgag agcgacgtag acctcgggga cgggtacatt 2100

atgaga 2106

<210> 125
<211> 1971
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 125
atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60

ccgcaggatc cctacgtgaa ggaagcagaa aatctcaaaa agtatttcaa tgcgggccat 120

agcgatgtgg ccgataacgg caccctgttt ctggggattc ttaagaattg gaaagaggag 180

tctgatagga agattatgca gtcccagatc gtgagcttct atttcaagct gttcaaaaac 240

ttcaaagacg accagtcgat ccaaaaatct gttgagacaa taaaagagga catgaatgtg 300

aagtttttta attcaaacaa aaagaagcgc gacgattttg agaaattaac gaactactcc 360

gtcaccgact tgaacgtaca acgaaaggct attcacgaac taatccaggt catggctgaa 420

ctgagtcctg ccgccaagac tggtaagcgt aaacggagtc agatgctctt tagaggatct 480

ggaggcggaa gcgggggtgg cggcagcggc ggtggaggat caggtggcgg ggggtccggg 540

ggcggaagtc tgcaggaaat ggggactgcc gacttgggac ctagcagtgt ccccactccc 600

accaacgtga ccatcgagtc ttataatatg aatcctattg tttattggga atatcagatc 660

atgcctcagg ttccagtgtt cactgttgaa gtgaaaaatt acggagtgaa gaactcagag 720

tggatagacg cttgcataaa catatctcac cattactgca atatttccga ccacgtgggc 780

gaccccagca acagtttgtg ggtcagagtg aaagctcgcg tgggccagaa ggagagtgct 840

tatgccaaaa gcgaagaatt cgccgtttgt agagatggca agatcgggcc ccccaaatta 900

gacattcgca aagaagaaaa acaaattatg atcgatatct tccatccctc tgtcttcgtc 960

aacggcgacg aacaggaggt agattatgat ccagagacaa cgtgttacat cagggtatac 1020

aacgtttacg tgaggatgaa tgggtcagag atccagtata agatcctcac tcaaaaggag 1080

gacgactgtg acgaaattca gtgtcaactc gccatcccag tgtcttcgct gaatagccag 1140

tactgcgtgt ctgccgaggg tgtgcttcac gtttggggag tcacaactga aaagtccaaa 1200

gaagtttgta ttaccatttt taacagctct atcaagggct ccctgtggat accagtggtg 1260

gcggcactgc tgctgttcct tgtactcagc ctggtcttca tctgcttcta tattaagaag 1320

atcaaccctc tgaaggagaa gagcatcata ctacccaagt cgcttatctc agtcgtgcgg 1380

tccgccaccc tagaaactaa gcccgaatca aaatatgtat ccctgatcac aagctaccag 1440

ccattttcat tagagaaaga agtcgtgtgc gaggagcctc tgtccccagc aactgtgcca 1500

ggtatgcata cggaggacaa tccgggtaaa gtagagcaca ccgaggagct gtccagcatt 1560

acagaggtcg tcaccacaga ggagaacata cccgatgtgg tgcctggaag tcatctcaca 1620

cctattgagc gtgaatctag cagtcccttg tcttctaatc agagtgaacc ggggagtatt 1680

gcattaaact cctaccactc ccggaattgc agcgaaagcg accactcgag aaatgggttt 1740

gataccgata gttcttgtct ggaatcccac tcatcactga gcgattctga gtttccgcca 1800

aacaacaagg gcgaaattaa aacggaggga caagagctca tcaccgtcat caaggctcca 1860

accagttttg gttacgacaa gcctcatgtt ttggtggatc tgcttgtgga tgactcaggc 1920

aaggagtccc tcattggata ccgacctaca gaggattcca aagagtttag c 1971

<210> 126
<211> 1503
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 126
atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60

ccgcaggatc cctacgtgaa ggaagcagaa aatctcaaaa agtatttcaa tgcgggccat 120

agcgatgtgg ccgataacgg caccctgttt ctggggattc ttaagaattg gaaagaggag 180

tctgatagga agattatgca gtcccagatc gtgagcttct atttcaagct gttcaaaaac 240

ttcaaagacg accagtcgat ccaaaaatct gttgagacaa taaaagagga catgaatgtg 300

aagtttttta attcaaacaa aaagaagcgc gacgattttg agaaattaac gaactactcc 360

gtcaccgact tgaacgtaca acgaaaggct attcacgaac taatccaggt catggctgaa 420

ctgagtcctg ccgccaagac tggtaagcgt aaacggagtc agatgctctt tagaggatct 480

ggaggcggaa gcgggggtgg cggcagcggc ggtggaggat caggtggcgg ggggtccggg 540

ggcggaagtc tgcaggcccc ccctgatcct ctctcacagc tacccgcccc acagcatccc 600

aagataagac tgtacaatgc cgagcaggtg cttagctggg agcccgtggc actatcaaac 660

agtacgagac ccgtggtgta ccaggtacag ttcaagtaca cagacagcaa gtggtttacc 720

gctgacatta tgagcattgg agtcaattgc actcagatca ccgcaaccga gtgtgacttt 780

acagcagctt caccctccgc cggattccct atggacttca acgtcactct gcggcttcgt 840

gcagaactgg gcgctcttca ttccgcctgg gtgacaatgc cttggttcca gcactatcgg 900

aacgtcaccg tagggccccc tgaaaatatc gaagtaaccc ctggagaagg ttcgctgata 960

ataaggttca gctctccgtt tgacattgct gatacatcca ctgcgttctt ctgctactat 1020

gtgcactact gggagaaggg cgggattcaa caagtgaaag ggccattcag gagcaacagt 1080

atcagtctcg acaacctgaa accttctcgc gtctattgcc tccaagtgca ggctcaactg 1140

ctgtggaaca aaagtaatat tttccgagtt ggccacctgt ctaatatctc ctgttatgag 1200

accatggccg acgcatctac ggagttgcag caggtcatcc tcatttctgt gggcacattt 1260

tccctgctgt cggttctggc cggtgcctgt ttttttctcg ttttgaaata ccgcggcttg 1320

atcaaatact ggtttcatac cccaccatca ataccattac agatcgaaga gtatcttaaa 1380

gatccaactc agccaatttt agaggcgctc gataaggact ctagcccgaa ggacgatgtg 1440

tgggattccg tgtccatcat cagctttccc gaaaaggagc aggaagatgt tctgcaaact 1500

ttg 1503

<210> 127
<211> 2343
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 127
atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60

ccgcaggatc cctacgtgaa agaagccgag aacttaaaga aatatttcaa cgcaggccat 120

tcagacgtcg ctgataatgg aacacttttt ttgggcattc tgaaaaattg gaaggaagaa 180

tcggaccgaa aaattatgca gagccagata gtatcctttt atttcaagtt atttaaaaac 240

ttcaaagacg atcagtctat ccaaaaaagt gtggagacta tcaaggagga catgaatgtg 300

aagttcttca acagcaataa aaagaaacgg gatgactttg aaaagctcac caattactca 360

gtcactgatc tgaacgtgca gagaaaggcg attcatgagc taatccaagt gatggctgag 420

ctcggagcca acgtgagcgg agagtttgtg aaggaagccg agaatctgaa gaagtatttc 480

aacgctggtc actctgacgt ggcagataac ggcacgctgt tcctggggat cctgaagaat 540

tggaaagaag agtccgacag gaagattatg caatcccaga tcgtcagttt ctactttaag 600

cttttcaaga atttcaaaga cgatcagagt atccagaagt ctgtcgagac cataaaagaa 660

gacatgaatg taaagttttt taattcaaac aaaaagaagc gtgacgattt cgaaaaactc 720

accaactact ccgttacaga tctgaacgtt cagagaaaag ccattcacga gttgatccaa 780

gttatggccg agctctctcc tgcagctaag acaggtaaga ggaaacggag ccagatgctg 840

tttcgcgggt ctggaggcgg aagcgggggt ggcggcagcg gcggtggagg atcaggtggc 900

ggggggtccg ggggcggaag tctgcaggaa atggggactg ccgacttggg acctagcagt 960

gtccccactc ccaccaacgt gaccatcgag tcttataata tgaatcctat tgtttattgg 1020

gaatatcaga tcatgcctca ggttccagtg ttcactgttg aagtgaaaaa ttacggagtg 1080

aagaactcag agtggataga cgcttgcata aacatatctc accattactg caatatttcc 1140

gaccacgtgg gcgaccccag caacagtttg tgggtcagag tgaaagctcg cgtgggccag 1200

aaggagagtg cttatgccaa aagcgaagaa ttcgccgttt gtagagatgg caagatcggg 1260

ccccccaaat tagacattcg caaagaagaa aaacaaatta tgatcgatat cttccatccc 1320

tctgtcttcg tcaacggcga cgaacaggag gtagattatg atccagagac aacgtgttac 1380

atcagggtat acaacgttta cgtgaggatg aatgggtcag agatccagta taagatcctc 1440

actcaaaagg aggacgactg tgacgaaatt cagtgtcaac tcgccatccc agtgtcttcg 1500

ctgaatagcc agtactgcgt gtctgccgag ggtgtgcttc acgtttgggg agtcacaact 1560

gaaaagtcca aagaagtttg tattaccatt tttaacagct ctatcaaggg ctccctgtgg 1620

ataccagtgg tggcggcact gctgctgttc cttgtactca gcctggtctt catctgcttc 1680

tatattaaga agatcaaccc tctgaaggag aagagcatca tactacccaa gtcgcttatc 1740

tcagtcgtgc ggtccgccac cctagaaact aagcccgaat caaaatatgt atccctgatc 1800

acaagctacc agccattttc attagagaaa gaagtcgtgt gcgaggagcc tctgtcccca 1860

gcaactgtgc caggtatgca tacggaggac aatccgggta aagtagagca caccgaggag 1920

ctgtccagca ttacagaggt cgtcaccaca gaggagaaca tacccgatgt ggtgcctgga 1980

agtcatctca cacctattga gcgtgaatct agcagtccct tgtcttctaa tcagagtgaa 2040

ccggggagta ttgcattaaa ctcctaccac tcccggaatt gcagcgaaag cgaccactcg 2100

agaaatgggt ttgataccga tagttcttgt ctggaatccc actcatcact gagcgattct 2160

gagtttccgc caaacaacaa gggcgaaatt aaaacggagg gacaagagct catcaccgtc 2220

atcaaggctc caaccagttt tggttacgac aagcctcatg ttttggtgga tctgcttgtg 2280

gatgactcag gcaaggagtc cctcattgga taccgaccta cagaggattc caaagagttt 2340

agc 2343

<210> 128
<211> 1875
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 128
atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60

ccgcaggatc cctacgtgaa agaagccgag aacttaaaga aatatttcaa cgcaggccat 120

tcagacgtcg ctgataatgg aacacttttt ttgggcattc tgaaaaattg gaaggaagaa 180

tcggaccgaa aaattatgca gagccagata gtatcctttt atttcaagtt atttaaaaac 240

ttcaaagacg atcagtctat ccaaaaaagt gtggagacta tcaaggagga catgaatgtg 300

aagttcttca acagcaataa aaagaaacgg gatgactttg aaaagctcac caattactca 360

gtcactgatc tgaacgtgca gagaaaggcg attcatgagc taatccaagt gatggctgag 420

ctcggagcca acgtgagcgg agagtttgtg aaggaagccg agaatctgaa gaagtatttc 480

aacgctggtc actctgacgt ggcagataac ggcacgctgt tcctggggat cctgaagaat 540

tggaaagaag agtccgacag gaagattatg caatcccaga tcgtcagttt ctactttaag 600

cttttcaaga atttcaaaga cgatcagagt atccagaagt ctgtcgagac cataaaagaa 660

gacatgaatg taaagttttt taattcaaac aaaaagaagc gtgacgattt cgaaaaactc 720

accaactact ccgttacaga tctgaacgtt cagagaaaag ccattcacga gttgatccaa 780

gttatggccg agctctctcc tgcagctaag acaggtaaga ggaaacggag ccagatgctg 840

tttcgcgggt ctggaggcgg aagcgggggt ggcggcagcg gcggtggagg atcaggtggc 900

ggggggtccg ggggcggaag tctgcaggcc ccccctgatc ctctctcaca gctacccgcc 960

ccacagcatc ccaagataag actgtacaat gccgagcagg tgcttagctg ggagcccgtg 1020

gcactatcaa acagtacgag acccgtggtg taccaggtac agttcaagta cacagacagc 1080

aagtggttta ccgctgacat tatgagcatt ggagtcaatt gcactcagat caccgcaacc 1140

gagtgtgact ttacagcagc ttcaccctcc gccggattcc ctatggactt caacgtcact 1200

ctgcggcttc gtgcagaact gggcgctctt cattccgcct gggtgacaat gccttggttc 1260

cagcactatc ggaacgtcac cgtagggccc cctgaaaata tcgaagtaac ccctggagaa 1320

ggttcgctga taataaggtt cagctctccg tttgacattg ctgatacatc cactgcgttc 1380

ttctgctact atgtgcacta ctgggagaag ggcgggattc aacaagtgaa agggccattc 1440

aggagcaaca gtatcagtct cgacaacctg aaaccttctc gcgtctattg cctccaagtg 1500

caggctcaac tgctgtggaa caaaagtaat attttccgag ttggccacct gtctaatatc 1560

tcctgttatg agaccatggc cgacgcatct acggagttgc agcaggtcat cctcatttct 1620

gtgggcacat tttccctgct gtcggttctg gccggtgcct gttttttttct cgttttgaaa 1680

taccgcggct tgatcaaata ctggtttcat accccaccat caataccatt acagatcgaa 1740

gagtatctta aagatccaac tcagccaatt ttagaggcgc tcgataagga ctctagcccg 1800

aaggacgatg tgtgggattc cgtgtccatc atcagctttc ccgaaaagga gcaggaagat 1860

gttctgcaaa ctttg 1875

<210> 129
<211> 1890
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 129
atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60

ccggtgcgat cttcaagccg gacaccctca gacaagccag tggcacacgt ggtagcgaac 120

ccacaagctg aggggcagct ccagtggctc aatcggcgtg ccaacgccct gttagccaat 180

ggggtcgagc ttagggacaa ccaacttgtg gtaccctcgg aaggattata cttgatttac 240

agtcaggtgc tgttcaaagg acagggctgc ccttccacac atgttctgct cactcacacg 300

atctcccgca ttgcagtgtc ttatcagacc aaggtcaact tgctaagcgc tatcaaaagt 360

ccatgtcaga gagagacccc ggagggtgct gaggctaagc cttggtacga acctatttat 420

ctgggcggag tctttcaact ggaaaaaggt gatagactga gcgcagagat caataggccc 480

gattacctgg acttcgccga atccggccag gtttattttg ggataatcgc cctctctgga 540

ggcggaagcg ggggtggcgg cagcggcggt ggaggatcag gtggcggggg gtccgggggc 600

ggaagtctgc agttggtacc ccatcttggc gaccgagaga aacgggatag tgtctgtccc 660

caagggaaat atatacaccc acagaataac tctatctgct gcactaagtg ccataaagga 720

acgtaccttt ataacgactg cccaggcccc ggccaagata ctgactgcag agagtgcgag 780

tctgggagct tcaccgcctc cgagaatcac ttgagacatt gcctgagttg tagcaagtgc 840

aggaaggaga tggggcaggt tgagatctca tcatgtaccg ttgatcggga caccgtctgt 900

ggatgccgca aaaatcagta tcggcattat tggtccgaaa acctatttca gtgttttaac 960

tgttctttgt gcctgaacgg aacagtccac ctgagttgcc aggaaaaaca gaatacagtt 1020

tgcacttgcc acgctggctt ttttctccgc gagaacgaat gtgtgtcctg ttccaattgt 1080

aagaagtctc tagaatgtac aaagctgtgt ctgccccaaa tcgagaacgt gaaaggaact 1140

gaggacagtg gtacaaccgt gttgctgcct ctggtgatct tcttcgggct ctgcctcctc 1200

agtctgcttt tcattgggct aatgtaccgg taccagcgtt ggaaatctaa gttatactca 1260

attgtctgtg ggaagtccac ccctgagaag gaaggagaac tggaaggtac taccaccaaa 1320

ccactggctc caaacccctc cttctctcct acacccggct ttactcctac cctgggcttc 1380

tcaccggtgc ccagctcaac gttcaccagc tcgagcacat acacccctgg cgattgtccc 1440

aacttcgcag caccaaggcg tgaagtggcc ccaccctacc agggtgctga tccaatactt 1500

gccaccgcat tagccagcga tccgattcct aatcctttac agaagtggga ggattcggcc 1560

cacaaacccc agagcctgga cactgacgac cccgccacgc tgtatgctgt ggtcgagaat 1620

gtaccgcctc tcagatggaa ggaatttgtg aggcgactgg gcctgtccga tcacgagatc 1680

gacagactgg agttgcaaaa tggtcgatgc ctccgggagg cccagtacag catgctggct 1740

acatggagga ggcgcacacc tcgcagggag gcgactcttg aattgctggg acgcgtgctc 1800

agagatatgg acttactcgg atgtcttgaa gacattgaag aggcgctctg cggcccagca 1860

gccctgcctc cggcaccatc cctgctcaga 1890

<210> 130
<211> 1929
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 130
atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60

ccggtgcgat cttcaagccg gacaccctca gacaagccag tggcacacgt ggtagcgaac 120

ccacaagctg aggggcagct ccagtggctc aatcggcgtg ccaacgccct gttagccaat 180

ggggtcgagc ttagggacaa ccaacttgtg gtaccctcgg aaggattata cttgatttac 240

agtcaggtgc tgttcaaagg acagggctgc ccttccacac atgttctgct cactcacacg 300

atctcccgca ttgcagtgtc ttatcagacc aaggtcaact tgctaagcgc tatcaaaagt 360

ccatgtcaga gagagacccc ggagggtgct gaggctaagc cttggtacga acctatttat 420

ctgggcggag tctttcaact ggaaaaaggt gatagactga gcgcagagat caataggccc 480

gattacctgg acttcgccga atccggccag gtttattttg ggataatcgc cctctctgga 540

ggcggaagcg ggggtggcgg cagcggcggt ggaggatcag gtggcggggg gtccgggggc 600

ggaagtctgc agctgcctgc ccaggtcgct tttacaccat atgcacctga gcctggttcc 660

acgtgtaggc ttagggagta ctacgatcaa accgctcaga tgtgttgctc caagtgtagt 720

ccaggccagc acgcaaaagt cttttgtaca aagacgtcag ataccgtgtg cgacagctgc 780

gaagatagca cctataccca gctgtggaat tgggttcccg aatgtttgtc ttgtggctcc 840

cgctgctcta gtgaccaggt ggaaacacag gcctgcactc gggaacagaa ccgtatttgt 900

acctgcaggc ccggttggta ctgcgcactg tccaaacaag aggggtgtag actgtgtgcc 960

cctttgcgca agtgtcgtcc aggcttcggt gtggcaagac ctggaacaga gacttcagac 1020

gtcgtttgta agccctgcgc ccctggcaca ttctccaata ccacctcatc taccgacata 1080

tgcagacccc accaaatatg caacgtggtg gctatccctg ggaacgcctc catggacgct 1140

gtttgcactt ccacttctcc cactcggtct atggctcccg gtgccgtgca tttaccccaa 1200

cccgtgagca ctcggagcca acacacacag ccaacacccg agccaagtac cgccccgagt 1260

accagcttcc tactccccat gggcccatct ccaccggctg agggatctac cggggatttt 1320

gctctgcctg tcgggctaat cgtcggggtg acggcgctcg gattgctcat tatcggagtg 1380

gtaaactgcg tgattatgac tcaggtgaaa aagaagcctt tatgcctcca gagagaagcg 1440

aaagttcccc acctgcctgc agacaaggcc aggggtacac agggcccgga acagcaacat 1500

ctgctgatca ccgccccctc ttcaagctcc agcagcctgg aatccagtgc cagtgcactt 1560

gatcggcgcg caccaacgcg aaaccagccc caggcccctg gggtagaggc atcaggcgct 1620

ggagaagcgc gcgctagcac aggcagttcc gattccagcc ctggagggca tggaacacag 1680

gtaaatgtca cctgcatcgt taatgtgtgc tcgtcctcgg accacagctc tcaatgttca 1740

agccaggcct caagcactat gggcgacact gatagctctc cctccgagtc accgaaggac 1800

gagcaggtcc catttagtaa agaggagtgt gccttccgaa gtcagctgga gacaccagaa 1860

accctgcttg ggtctactga agagaaacca ctccctcttg gcgtgccaga tgcgggaatg 1920

aagccgtcg 1929

<210> 131
<211> 2256
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 131
atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60

ccggcgcctg tcagaagcct caactgcacg ctgagggact cacagcaaaa gagcctggtc 120

atgagtggcc cctacgagct gaaagcactc caccttcagg ggcaggacat ggaacaacag 180

gtggttttct ccatgtcttt cgtacaggga gaggagtcta acgataagat ccccgtggct 240

ttgggcttaa aagagaaaaa cctgtatctg agctgtgtgc taaaggacga taagcccaca 300

cttcagctcg agtccgttga tccaaaaaat tatccaaaga agaaaatgga aaagcggttt 360

gtgtttaaca agattgagat taataacaaa ttggaattcg aatcagccca gttccctaat 420

tggtacatca gtacctctca agccgaaaat atgccggtgt ttctgggagg gaccaagggt 480

ggccaggata taacagactt cactatgcag tttgtctcgt cctctggagg cggaagcggg 540

ggtggcggca gcggcggtgg aggatcaggt ggcggggggt ccgggggcgg aagtctgcag 600

ctcgaggccg ataagtgcaa agaaagagag gaaaaaatca ttctggtttc tagcgccaac 660

gaaatcgatg tccgcccctg tccactgaat cctaacgagc ataaggggac tataacatgg 720

tataaggacg acagcaagac ccctgtgtct acagaacaag caagcaggat acaccagcac 780

aaagaaaagc tttggtttgt accagcaaag gtcgaggaca gcgggcatta ttattgcgtg 840

gtacgaaaca gttcttactg cctcagaatc aagatttccg ctaagtttgt cgagaacgaa 900

cctaacttat gttacaacgc acaggctatt tttaaacaga agctcccagt tgctggggat 960

ggcggcctgg tgtgtcccta catggagttt tttaaaaatg agaataatga gctacctaaa 1020

ctgcaatggt acaaggactg caaacccctt ttgctcgaca atattcactt cagcggagtg 1080

aaagatcggc tgattgtgat gaacgtggct gagaaacacc gcgggaacta tacatgccac 1140

gcctcttata cgtacctggg caagcagtac ccgatcacta gagtgattga atttataaca 1200

ctggaagaga acaagccaac tcgtcctgtc atagtatccc ccgcaaacga aaccatggag 1260

gtggacttgg gttctcagat ccagctgatt tgcaatgtta ccgggcaatt gagtgatatc 1320

gcctattgga agtggaatgg ttctgtcatt gacgaagacg atccagtgtt aggagaggac 1380

tattatagcg tagaaaatcc tgcgaacaag aggcggtcga ctctgataac tgtcctgaac 1440

atcagtgaga tcgagagccg attttataaa catccattca catgtttcgc caaaaataca 1500

cacgggatcg acgccgccta cattcagctg atctaccccg taaccaattt ccagaagcac 1560

atgatcggga tatgcgtgac gctaaccgtg atcattgttt gctcagtgtt catttacaag 1620

atcttcaaga tcgacatcgt cctttggtat agggatagct gttacgactt tctgcccatt 1680

aaggcatcgg atggcaaaac ctacgacgct tacatcttgt acccaaagac cgtgggagaa 1740

ggctcaacct ccgactgtga cattttcgtc tttaaggtgc tccctgaggt cctcgagaaa 1800

cagtgtggct ataaactgtt catctatggc cgggatgact acgtgggcga ggatatagtt 1860

gaagtcataa atgaaaatgt taagaaatca cggaggctga tcatcattct agtgcgggag 1920

acctcaggtt tttcctggct cggcggctcc tcagaggagc agattgcgat gtacaacgct 1980

ctggtgcaag atggaatcaa ggtggttctg ttggagctcg aaaagatcca ggattacgag 2040

aaaatgcccg agagcattaa gttcatcaaa caaaaacacg gagccattag atggagtggt 2100

gatttcacgc aaggaccgca gtccgccaag acacgtttct ggaaaaacgt gcgctatcat 2160

atgcccgtgc agaggagatc cccctccagt aaacatcagc tgttatctcc ggcgactaag 2220

gaaaagcttc agcgcgaagc ccatgttcct cttgga 2256

<210> 132
<211> 2250
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 132

atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60

ccggcgcctg tcagaagcct caactgcacg ctgagggact cacagcaaaa gagcctggtc 120

atgagtggcc cctacgagct gaaagcactc caccttcagg ggcaggacat ggaacaacag 180

gtggttttct ccatgtcttt cgtacaggga gaggagtcta acgataagat ccccgtggct 240

ttgggcttaa aagagaaaaa cctgtatctg agctgtgtgc taaaggacga taagcccaca 300

cttcagctcg agtccgttga tccaaaaaat tatccaaaga agaaaatgga aaagcggttt 360

gtgtttaaca agattgagat taataacaaa ttggaattcg aatcagccca gttccctaat 420

tggtacatca gtacctctca agccgaaaat atgccggtgt ttctgggagg gaccaagggt 480

ggccaggata taacagactt cactatgcag tttgtctcgt cctctggagg cggaagcggg 540

ggtggcggca gcggcggtgg aggatcaggt ggcggggggt ccgggggcgg aagtctgcag 600

tccgagcggt gcgatgattg gggcttagat accatgcggc agattcaggt gttcgaagac 660

gagcctgctc gcattaaatg cccgctcttt gagcacttcc tgaagtttaa ttacagcact 720

gctcactccg caggactcac actgatctgg tattggacac gccaagacag agatctggag 780

gagcccatta attttaggct ccccgagaac aggatctcta aggagaagga cgtgctgtgg 840

tttcggccga cactactgaa cgatactggg aattacacat gtatgcttcg aaatactacc 900

tattgctcca aggtggcttt tccacttgag gtggtgcaga aagacagctg ttttaatagc 960

ccaatgaaac tgcccgtgca caagctgtac atcgaatatg gcatacagag aatcacatgc 1020

cctaacgtcg acggctactt ccctagctca gttaagccga ccataacttg gtatatgggc 1080

tgctataaaa tacagaactt caataatgta atccccgagg gtatgaactt gagtttcctg 1140

atcgcactga tatctaacaa cgggaactac acctgtgtgg tgacttatcc cgagaacgga 1200

cgcacattcc atttgacaag gacgttaact gtcaaggtag tgggtagtcc taagaatgca 1260

gttcctcccg tgattcacag ccctaatgat cacgtggtgt atgaaaaaga accaggtgaa 1320

gaactcctga tcccctgcac ggtgtacttc tctttttttaa tggactcccg taatgaagtt 1380

tggtggacca tcgacggcaa aaaacctgat gatattacca tcgacgtgac aatcaacgag 1440

agcatttcac atagtcggac cgaagatgag acaagaaccc agattcttag cataaaaaaa 1500

gtgacttctg aagacctgaa gcgcagttac gtatgtcacg cgcgatccgc aaaaggggaa 1560

gttgccaagg ctgccaaggt gaagcagaaa gtccctgccc cacggtacac cgtagagctg 1620

gcctgtggct tcggagctac ggttttgctg gttgttatcc ttatcgtcgt ctatcatgtg 1680

tactggttgg agatggtgct tttttatcgg gcccatttcg ggaccgatga gacgattcta 1740

gacggaaagg agtacgatat ttacgtctcg tacgccagaa atgcggagga agaggaattc 1800

gtgctcttaa ccctgagggg agtactggaa aacgagtttg gctacaagtt gtgtattttt 1860

gacagagatt cactgccagg aggaattgtc actgacgaga cactctcatt catccagaaa 1920

tctaggaggt tgctcgttgt cctgagtcca aattatgtgc tccaaggcac ccaggccttg 1980

ctagaactga aggcggggct tgaaaacatg gcctctcgcg ggaacatcaa cgtaattctg 2040

gtgcagtaca aagcagtgaa ggagaccaaa gttaaagagc tgaaacgagc caagacagtc 2100

ctcactgtca tcaagtggaa aggtgaaaaa tcaaagtatc cacaagggag attctggaag 2160

cagcttcaag tcgctatgcc cgtgaagaag tccccccgtc gttcctcctc ggacgagcag 2220

ggcctgagct acagctctct caagaatgtc 2250

<210> 133
<211> 2301
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 133
atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60

ccgaactacc ccaaaaaaaa gatggagaag cggtttgttt ttaacaagat tgagatcaac 120

aataagctgg aattcgagtc tgcgcagttc ccaaactggt atattagcac atcgcaagca 180

gaaaatatgc ccgtgttcct cggcggaacc aaaggcgggc aggatatcac agactttacg 240

atgcagttcg tgtcatctgg tggtggtgga agcggcgggg gaggcagtgg gggaggcggg 300

tccgccccag tgaggtccct gaactgtacc ttaagagact cacagcaaaa gtccctggtc 360

atgtctggcc cctacgaact gaaagccctt cacctgcagg ggcaagatat ggagcagcag 420

gtggttttca gcatgagttt tgtacagggc gaagagagta atgacaagat acctgtggct 480

ctaggactca aggaaaagaa tttgtatctc agctgcgtcc tgaaggacga taaacctact 540

cttcagttgg agtccgtcga tccgaaatct ggaggcggaa gcgggggtgg cggcagcggc 600

ggtggaggat caggtggcgg ggggtccggg ggcggaagtc tgcagctcga ggccgataag 660

tgcaaagaaa gagaggaaaa aatcattctg gtttctagcg ccaacgaaat cgatgtccgc 720

ccctgtccac tgaatcctaa cgagcataag gggactataa catggtataa ggacgacagc 780

aagacccctg tgtctacaga acaagcaagc aggatacacc agcacaaaga aaagctttgg 840

tttgtaccag caaaggtcga ggacagcggg cattattatt gcgtggtacg aaacagttct 900

tactgcctca gaatcaagat ttccgctaag tttgtcgaga acgaacctaa cttatgttac 960

aacgcacagg ctatttttaa acagaagctc ccagttgctg gggatggcgg cctggtgtgt 1020

ccctacatgg agtttttaa aaatgagaat aatgagctac ctaaactgca atggtacaag 1080

gactgcaaac ccctttgct cgacaatatt cacttcagcg gagtgaaaga tcggctgatt 1140

gtgatgaacg tggctgagaa acaccgcggg aactatacat gccacgcctc ttatacgtac 1200

ctgggcaagc agtacccgat cactagagtg attgaattta taacactgga agagaacaag 1260

ccaactcgtc ctgtcatagt atcccccgca aacgaaacca tggaggtgga cttgggttct 1320

cagatccagc tgatttgcaa tgttaccggg caattgagtg atatcgccta ttggaagtgg 1380

aatggttctg tcattgacga agacgatcca gtgttaggag aggactatta tagcgtagaa 1440

aatcctgcga acaagaggcg gtcgactctg ataactgtcc tgaacatcag tgagatcgag 1500

agccgatttt ataaacatcc attcacatgt ttcgccaaaa atacacacgg gatcgacgcc 1560

gcctacattc agctgatcta ccccgtaacc aatttccaga agcacatgat cgggatatgc 1620

gtgacgctaa ccgtgatcat tgtttgctca gtgttcattt acaagatctt caagatcgac 1680

atcgtccttt ggtataggga tagctgttac gactttctgc ccattaaggc atcggatggc 1740

aaaacctacg acgcttacat cttgtaccca aagaccgtgg gagaaggctc aacctccgac 1800

tgtgacattt tcgtctttaa ggtgctccct gaggtcctcg agaaacagtg tggctataaa 1860

ctgttcatct atggccggga tgactacgtg ggcgaggata tagttgaagt cataaatgaa 1920

aatgttaaga aatcacggag gctgatcatc attctagtgc gggagacctc aggtttttcc 1980

tggctcggcg gctcctcaga ggagcagatt gcgatgtaca acgctctggt gcaagatgga 2040

atcaaggtgg ttctgttgga gctcgaaaag atccaggatt acgagaaaat gcccgagagc 2100

attaagttca tcaaacaaaa acacggagcc attagatgga gtggtgattt cacgcaagga 2160

ccgcagtccg ccaagacacg tttctggaaa aacgtgcgct atcatatgcc cgtgcagagg 2220

agatccccct ccagtaaaca tcagctgtta tctccggcga ctaaggaaaa gcttcagcgc 2280

gaagcccatg ttcctcttgg a 2301

<210> 134
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 134
atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60

ccgaactacc ccaaaaaaaa gatggagaag cggtttgttt ttaacaagat tgagatcaac 120

aataagctgg aattcgagtc tgcgcagttc ccaaactggt atattagcac atcgcaagca 180

gaaaatatgc ccgtgttcct cggcggaacc aaaggcgggc aggatatcac agactttacg 240

atgcagttcg tgtcatctgg tggtggtgga agcggcgggg gaggcagtgg gggaggcggg 300

tccgccccag tgaggtccct gaactgtacc ttaagagact cacagcaaaa gtccctggtc 360

atgtctggcc cctacgaact gaaagccctt cacctgcagg ggcaagatat ggagcagcag 420

gtggttttca gcatgagttt tgtacagggc gaagagagta atgacaagat acctgtggct 480

ctaggactca aggaaaagaa tttgtatctc agctgcgtcc tgaaggacga taaacctact 540

cttcagttgg agtccgtcga tccgaaatct ggaggcggaa gcgggggtgg cggcagcggc 600

ggtggaggat caggtggcgg ggggtccggg ggcggaagtc tgcagtccga gcggtgcgat 660

gattggggct tagataccat gcggcagatt caggtgttcg aagacgagcc tgctcgcatt 720

aaatgcccgc tctttgagca cttcctgaag tttaattaca gcactgctca ctccgcagga 780

ctcacactga tctggtattg gacacgccaa gacagagatc tggaggagcc cattaatttt 840

aggctccccg agaacaggat ctctaaggag aaggacgtgc tgtggtttcg gccgacacta 900

ctgaacgata ctgggaatta cacatgtatg cttcgaaata ctacctattg ctccaaggtg 960

gcttttccac ttgaggtggt gcagaaagac agctgtttta atagcccaat gaaactgccc 1020

gtgcacaagc tgtacatcga atatggcata cagagaatca catgccctaa cgtcgacggc 1080

tacttcccta gctcagttaa gccgaccata acttggtata tgggctgcta taaaatacag 1140

aacttcaata atgtaatccc cgagggtatg aacttgagtt tcctgatcgc actgatatct 1200

aacaacggga actacacctg tgtggtgact tatcccgaga acggacgcac attccatttg 1260

acaaggacgt taactgtcaa ggtagtgggt agtcctaaga atgcagttcc tcccgtgatt 1320

cacagcccta atgatcacgt ggtgtatgaa aaagaaccag gtgaagaact cctgatcccc 1380

tgcacggtgt acttctcttt tttaatggac tcccgtaatg aagtttggtg gaccatcgac 1440

ggcaaaaaac ctgatgatat taccatcgac gtgacaatca acgagagcat ttcacatagt 1500

cggaccgaag atgagacaag aacccagatt cttagcataa aaaaagtgac ttctgaagac 1560

ctgaagcgca gttacgtatg tcacgcgcga tccgcaaaag gggaagttgc caaggctgcc 1620

aaggtgaagc agaaagtccc tgccccacgg tacaccgtag agctggcctg tggcttcgga 1680

gctacggttt tgctggttgt tatccttatc gtcgtctatc atgtgtactg gttggagatg 1740

gtgctttttt atcgggccca tttcgggacc gatgagacga ttctagacgg aaaggagtac 1800

gatatttacg tctcgtacgc cagaaatgcg gaggaagagg aattcgtgct cttaaccctg 1860

aggggagtac tggaaaacga gtttggctac aagttgtgta tttttgacag agattcactg 1920

ccaggaggaa ttgtcactga cgagacactc tcattcatcc agaaatctag gaggttgctc 1980

gttgtcctga gtccaaatta tgtgctccaa ggcacccagg ccttgctaga actgaaggcg 2040

gggcttgaaa acatggcctc tcgcgggaac atcaacgtaa ttctggtgca gtacaaagca 2100

gtgaaggaga ccaaagttaa agagctgaaa cgagccaaga cagtcctcac tgtcatcaag 2160

tggaaaggtg aaaaatcaaa gtatccacaa gggagattct ggaagcagct tcaagtcgct 2220

atgcccgtga agaagtcccc ccgtcgttcc tcctcggacg agcagggcct gagctacagc 2280

tctctcaaga atgtc 2295

<210> 135
<211> 2037
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 135
atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60

ccggtgccgc ccggggaaga tagcaaggat gtggctgctc ctcacaggca gccactgaca 120

agcagcgaga gaatcgacaa gcaaataagg tatattcttg atggaatcag cgcgctgcga 180

aaggagacat gtaacaagtc gaatatgtgc gagtcttcca aagaagcact tgctgaaaat 240

aatctgaacc tcccaaaaat ggccgagaaa gacggctgct ttcagtccgg ttttaacgag 300

gagacttgtt tagtaaagat tataacgggc ttgttggaat tcgaagtcta cctagaatac 360

ctccaaaata gattcgagag tagtgaggaa caggcccgcg ctgttcagat gtcaacaaaa 420

gtgttgatcc aattcctgca gaaaaaagcc aagaacttag atgcaatcac cacacctgac 480

cccactacca atgcctctct gctcaccaag ctgcaagccc agaaccagtg gctgcaggac 540

atgactaccc atctaattct gcggtctttt aaggagttcc tccagtcatc cctgcgtgca 600

cttcggcaga tgtctggagg cggaagcggg ggtggcggca gcggcggtgg aggatcaggt 660

ggcgggggt ccgggggcgg aagtctgcag cttgcaccaa gacgctgtcc ggctcaggag 720

gtcgctaggg gagtgctgac ctcgctgccg ggcgactccg tgaccctgac atgtcctgga 780

gtggagcctg aggacaacgc aacagttcac tgggtgctac ggaagcccgc cgctggctcc 840

catccttcca ggtgggccgg gatggggcgc agactgcttc tcagatcagt gcagttacat 900

gatagcggta attacagctg ctaccgcgct ggaaggccgg caggcactgt gcacctccta 960

gtggatgttc cacctgagga gccacagttg agctgctttc gaaaaagtcc cttgtctaac 1020

gtcgtatgcg agtggggccc tagatcaact ccctccctca ccaccaaagc ggttctcctc 1080

gtacgtaagt tccaaaactc tcctgccgaa gattttcaag agccatgtca gtatagccag 1140

gagagtcaga agttctcatg ccagcttgca gtcccggagg gtgactcatc cttctatatt 1200

gttagtatgt gcgtcgcctc gtctgtgggg tctaagttta gcaagactca aacttttcag 1260

ggctgcggca tcctccaacc agacccccct gccaacatta cagtgaccgc agttgccaga 1320

aaccctaggt ggttgagcgt gacgtggcag gatccccatt cctggaattc atcattctac 1380

agactgcggt tcgagctccg atacagggcg gaacgtagca agacattcac cacgtggatg 1440

gtcaaagacc tgcagcacca ctgtgtaatc catgacgctt ggagcggtct gcgccacgtg 1500

gtccagctgc gggcacaaga ggaattcgga cagggtgaat ggagtgaatg gtctcctgag 1560

gctatgggca ctccgtggac cgaatctcgg tctccaccag ccgaaaacga agtgtccacc 1620

cctatgcagg ctctgactac taataaggat gacgataata tcttgtttag ggactccgca 1680

aatgctacat cactgcctgt acaggattcc agtagtgttc ccctaccaac ctttttagtc 1740

gccggagggt ctctggcgtt cgggacgttg ctctgtatag ccattgtgct gcgtttcaaa 1800

aagacctgga aactgcgcgc cttaaaggag ggaaaaacaa gcatgcaccc cccatattct 1860

cttgggcagc tggtgcccga acggcccaga ccaacaccag tcctggtgcc tcttatatcc 1920

ccccccgtga gcccctctag cctgggcagt gacaatacca gtagccataa taggcccgac 1980

gcccgagacc ctcgctcccc atacgatatc tcaaacacag attatttttt tccccgg 2037

<210> 136
<211> 3378
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 136
atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60

ccggtgccgc ccggggaaga tagcaaggat gtggctgctc ctcacaggca gccactgaca 120

agcagcgaga gaatcgacaa gcaaataagg tatattcttg atggaatcag cgcgctgcga 180

aaggagacat gtaacaagtc gaatatgtgc gagtcttcca aagaagcact tgctgaaaat 240

aatctgaacc tcccaaaaat ggccgagaaa gacggctgct ttcagtccgg ttttaacgag 300

gagacttgtt tagtaaagat tataacgggc ttgttggaat tcgaagtcta cctagaatac 360

ctccaaaata gattcgagag tagtgaggaa caggcccgcg ctgttcagat gtcaacaaaa 420

gtgttgatcc aattcctgca gaaaaaagcc aagaacttag atgcaatcac cacacctgac 480

cccactacca atgcctctct gctcaccaag ctgcaagccc agaaccagtg gctgcaggac 540

atgactaccc atctaattct gcggtctttt aaggagttcc tccagtcatc cctgcgtgca 600

cttcggcaga tgtctggagg cggaagcggg ggtggcggca gcggcggtgg aggatcaggt 660

ggcgggggggt ccgggggcgg aagtctgcag gaactcctgg acccctgcgg gtatattagc 720

cccgagtctc ccgtggtgca actgcattct aacttcaccg cagtttgtgt gctcaaagaa 780

aagtgtatgg attacttcca tgttaacgcc aactacattg tgtggaaaac taatcatttt 840

acgataccaa aggagcagta cacaattatc aacagaaccg catcatccgt cacatttacc 900

gatatcgcct ccttgaacat tcagctgaca tgtaatatct taacattcgg tcaactggaa 960

caaaacgtgt atggcatcac catcatctct ggacttcctc cagaaaaacc caaaaatttg 1020

tcgtgtatcg tgaatgaggg aaaaaaaatg cgctgtgaat gggacggggg ccgggagact 1080

cacctcgaga cgaacttcac ccttaagtca gagtgggcga cacataaatt tgccgactgc 1140

aaagcaaaga gagatacccc cacttcctgc accgtcgact attcaactgt gtacttcgtc 1200

aacattgagg tgtgggtgga ggcggagaat gcccttggca aggttacttc cgaccacatc 1260

aactttgatc ccgtctacaa ggtgaaaccg aacccacccc acaacctgtc cgtcattaat 1320

tcagaggagc taagttctat actcaagtta acttggacga atccctccat aaagagtgta 1380

attattctca agtataacat ccaatatagg actaaagatg cttcaacctg gtcacagatc 1440

ccaccggagg acaccgcctc tacaaggtca tcgttcaccg tgcaggatct taagcctttc 1500

accgagtatg tgttcagaat ccgatgcatg aaagaggacg gcaaggggta ttggagcgat 1560

tggagcgaag aagcttccgg cattacctac gaggacaggc cttcgaaagc accttctttc 1620

tggtacaaaa tcgatccttc tcacactcag ggctaccgga ccgtgcagct tgtgtggaag 1680

actttgccac cattcgaggc aaatggaaag atactggatt atgaggtcac actgacccgc 1740

tggaaaagtc acttgcagaa ctatacagta aacgccacca aactgacagt caatctcact 1800

aacgatagat atttagcaac cctgactgta cgaaacctgg tgggaaaatc tgacgccgcg 1860

gtactgacta tccctgcttg tgactttcag gctacccacc ctgttatgga tctgaaggcc 1920

ttccctaagg ataacatgct atgggtcgag tggaccacac caagggaaag cgtcaaaaag 1980

tatattctcg agtggtgcgt tctgagcgac aaggccccat gtattacaga ctggcaacag 2040

gaggacggga cagttcatcg gacatatctg cgcggcaatc tagctgaaag taaatgctac 2100

cttatcaccg tcacgccagt ctacgccgac ggcccgggct ctccagagtc aatcaaggct 2160

tacctaaagc aggcccctcc ctctaagggg ccaactgtga gaacaaaaaa ggtaggtaag 2220

aatgaagccg tcctggagtg ggatcaactg ccagtggacg tacagaacgg tttcattcgc 2280

aactacacca tcttttacag gacgatcatt gggaatgaga cagcagtgaa cgtggattct 2340

tcccataccg aatacacgct cagcagtctg acgtcggaca cattgtacat ggtcaggatg 2400

gctgcatata cagacgaagg agggaaggat gggcctgagt tcacctttac cacccctaag 2460

ttcgctcagg gcgagattga agcaattgtg gtgcccgtat gcctggcctt tctccttacg 2520

acactgctgg gtgttctctt ttgctttaat aagcgggacc tcatcaagaa acacatttgg 2580

cctaatgtgc ccgaccccag caaaagtcac atagcccagt ggagccctca tactcccccc 2640

cgtcataatt ttaatagcaa ggatcagatg tacagcgacg gcaattttac agacgtgtcc 2700

gtcgtcgaaa tagaagctaa tgataagaag ccctttcctg aagacctgaa atccttggac 2760

ttattcaaaa aggagaagat caataccgaa gggcactcct cagggatagg gggcagcagt 2820

tgcatgtcct catcccgtcc ctctatcagc tccagcgatg agaacgagag cagccagaat 2880

actagttcca ctgttcagta cagcactgta gttcacagtg gctatagaca tcaggtcccg 2940

agtgttcagg tgttctccag gagtgaatct acccagccgt tgttagactc agaagaacgc 3000

ccagaagacc tgcagctggt ggaccacgtg gatggaggtg atggcattct gccgcgccag 3060

caatacttta agcagaactg ttctcagcat gaatccagcc ctgacatctc tcactttgag 3120

cgaagcaaac aggtgtcaag cgtgaacgaa gaggatttcg ttcggcttaa gcaacagata 3180

tctgaccaca tctcacaatc ctgcggaagt ggacaaatga agatgtttca ggaggttagt 3240

gcggccgatg ctttcggccc tggcactgag ggtcaggtgg aaagattcga gacagtgggt 3300

atggaagccg ctacagatga gggaatgccc aaaagctacc tcccacaaac cgtgcggcag 3360

ggaggatata tgccacag 3378

<210> 137
<211> 3621
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 137
atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60

ccgatctggg agctcaaaaa ggatgtttat gtggtcgaac ttgactggta cccggacgca 120

ccaggggaga tggtggtgtt gacctgcgac acccccgaag aggacgggat tacatggact 180

ttggaccagt ccagtgaagt cctgggctcg ggaaagaccc tgactatcca ggtgaaggag 240

ttcggagatg ctggacaata tacatgccac aagggcgggg aagttttgag ccattccctc 300

ctgctgctgc ataaaaaaga ggatggtatt tggagcactg atattctgaa agaccagaag 360

gaacccaaga acaaaacttt tctgcggtgt gaggccaaga attacagtgg aagattcacc 420

tgttggtggt taaccacaat ctctaccgat cttacctttt ccgtcaaatc aagtcgcggc 480

agcagcgatc cacagggcgt gacgtgcggc gctgccacac taagcgcgga gagagtgcgg 540

ggtgacaaca aggaatacga gtactccgtt gagtgtcaag aagactctgc atgccctgcc 600

gcagaggaat cattaccgat cgaagtaatg gtggatgctg ttcacaaact gaagtatgaa 660

aactacactt cttcattttt cataagggac attatcaagc ctgatcctcc aaagaacctc 720

caacttaaac cactcaagaa tagccgtcag gtagaggtgt cctgggagta ccccgatacc 780

tggtcaacgc cccactcata tttctccctg acgttctgtg tgcaggtgca ggggaaatcc 840

aagagggaga agaaagacag ggtctttaca gataagacat ctgccactgt catctgcaga 900

aaaaatgcct ctatatccgt gcgagcccag gaccgctact attctagtag ctggagcgag 960

tgggctagtg taccttgttc gggctcaacc agcggatccg ggaaacccgg ttctggcgag 1020

gggagtacaa agggacgaaa tctgccagtg gctacccccg acccgggcat gtttccctgc 1080

ctccatcata gccagaatct gctcagagcg gtcagcaaca tgctacagaa ggcccgccag 1140

accttagagt tttacccttg cacctctgag gaaatcgatc acgaagacat caccaaagat 1200

aagactagca ccgttgaagc ctgtctccca ttggaactta caaaaaatga atcttgtctg 1260

aattccagag agacatcttt tatcactaat ggaagttgcc tcgccagtcg gaaaacttcc 1320

ttcatgatgg ccctgtgtct gagttcaatc tacgaggatc ttaagatgta tcaagtggaa 1380

ttcaaaacga tgaacgcaaa actgttgatg gatcctaaga ggcagatatt tttggatcag 1440

aacatgttag ctgtgatcga cgagctgatg caagcactca acttcaactc agagacagtc 1500

ccccagaagt cctccctgga ggagcctgac ttctacaaga cgaaaattaa gctatgcatt 1560

ctgcttcacg cattcaggat acgggccgta acaattgacc gtgtgatgag ctatctgaac 1620

gcttcgtctg gaggcggaag cgggggtggc ggcagcggcg gtggaggatc aggtggcggg 1680

gggtccgggg gcggaagtct gcagtgcaga actagcgaat gttgtttcca ggacccccg 1740

tatcccgacg ccgattccgg aagcgcatcc ggaccacgtg acctgcggtg ctatcggatt 1800

tctagcgata ggtacgaatg ctcatggcag tacgaggggc ccactgctgg ggtgagtcac 1860

ttcttaagat gctgtttaag ttccgggagg tgctgctatt tcgccgcagg gtcagctact 1920

cgactacagt tttctgacca ggctggagta agcgtgcttt atacagtgac actgtgggtc 1980

gaatcctggg ccaggaacca aacggagaag tcacccgagg tgaccctgca actgtataac 2040

tcagtcaaat acgagcctcc tctgggtgac attaaagtgt cgaaactcgc cggacagctt 2100

agaatggagt gggagacccc cgataaccag gttggcgcag aggtgcagtt ccggcaccga 2160

acaccctcat ctccttggaa actgggcgat tgtggtccgc aggacgacga taccgagagt 2220

tgcttgtgtc ccctagagat gaatgtcgca caggagtttc agctgaggag gcgtcagctc 2280

ggcagccaag gcagttcttg gtcaaaatgg tcctcccccg tctgcgttcc ccctgaaaat 2340

cctccacagc cgcaggttcg attcagcgtg gaacaactcg ggcaggacgg gagacgccgc 2400

ttgactctta aggagcaacc aacgcagctc gaactcccag aaggttgcca gggcctggca 2460

cctggcaccg aggtgaccta ccgtttgcag ttacatatgc ttagttgccc ttgtaaggcc 2520

aaggctacac ggacccttca cctaggcaaa atgccatacc taagcggtgc tgcatacaac 2580

gtggcggtca tttcttccaa ccagttcgga cccggtctga atcagacctg gcacatcccc 2640

gcagataccc ataccgaacc tgtggcgctg aatatcagcg tgggcacaaa tggcactacg 2700

atgtattggc cggcccgcgc tcaatctatg acttactgca tcgaatggca gcctgttggg 2760

caagatggag gactcgcgac atgcagcctt actgccccgc aggaccctga tccagcaggt 2820

atggccactt attcttggag ccgcgagtcc ggggccatgg gacaggagaa gtgttactac 2880

atcaccatat ttgcgtcagc tcatccagaa aagctgaccc tgtggtcaac cgttctgagc 2940

acataccact tcgggggcaa tgcgtccgct gcaggcaccc cacaccacgt gtcggtgaaa 3000

aaccactctc tggacagtgt gagtgttgac tgggccccaa gcctgttgtc cacatgtccc 3060

ggggtgctca aggaatatgt tgtccgctgt cgagacgagg actccaaaca agtgtcggaa 3120

catcccgtac agccaacgga gacccaagtc actctgtctg gactgagagc cggcgtggcc 3180

tacacagtcc aagtgcgggc agatacagct tggttacggg gcgtatggag ccagccacaa 3240

aggttcagca ttgaggtaca ggtctctgat tggttgattt tttttgccag tctgggcagt 3300

tttctctcta tcctgttggt cggagtgttg ggctatctgg gactgaatcg cgccgccaga 3360

catctgtgcc ccccactccc aaccccatgt gcctcctccg ccatagaatt tcctgggggt 3420

aaagagacat ggcagtggat caaccctgta gacttccagg aggaggctag cctccaggaa 3480

gccctggttg tggaaatgtc atgggataag ggcgagagaa cggaacctct cgagaagact 3540

gaacttcccg agggagctcc tgagctcgca cttgacacag aactgtcttt agaggatggg 3600

gataggtgta aggctaagat g 3621

<210> 138
<211> 4221
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 138
atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60

ccgatctggg agctcaaaaa ggatgtttat gtggtcgaac ttgactggta cccggacgca 120

ccaggggaga tggtggtgtt gacctgcgac acccccgaag aggacgggat tacatggact 180

ttggaccagt ccagtgaagt cctgggctcg ggaaagaccc tgactatcca ggtgaaggag 240

ttcggagatg ctggacaata tacatgccac aagggcgggg aagttttgag ccattccctc 300

ctgctgctgc ataaaaaaga ggatggtatt tggagcactg atattctgaa agaccagaag 360

gaacccaaga acaaaacttt tctgcggtgt gaggccaaga attacagtgg aagattcacc 420

tgttggtggt taaccacaat ctctaccgat cttacctttt ccgtcaaatc aagtcgcggc 480

agcagcgatc cacagggcgt gacgtgcggc gctgccacac taagcgcgga gagagtgcgg 540

ggtgacaaca aggaatacga gtactccgtt gagtgtcaag aagactctgc atgccctgcc 600

gcagaggaat cattaccgat cgaagtaatg gtggatgctg ttcacaaact gaagtatgaa 660

aactacactt cttcattttt cataagggac attatcaagc ctgatcctcc aaagaacctc 720

caacttaaac cactcaagaa tagccgtcag gtagaggtgt cctgggagta ccccgatacc 780

tggtcaacgc cccactcata tttctccctg acgttctgtg tgcaggtgca ggggaaatcc 840

aagagggaga agaaagacag ggtctttaca gataagacat ctgccactgt catctgcaga 900

aaaaatgcct ctatatccgt gcgagcccag gaccgctact attctagtag ctggagcgag 960

tgggctagtg taccttgttc gggctcaacc agcggatccg ggaaacccgg ttctggcgag 1020

gggagtacaa agggacgaaa tctgccagtg gctacccccg acccgggcat gtttccctgc 1080

ctccatcata gccagaatct gctcagagcg gtcagcaaca tgctacagaa ggcccgccag 1140

accttagagt tttacccttg cacctctgag gaaatcgatc acgaagacat caccaaagat 1200

aagactagca ccgttgaagc ctgtctccca ttggaactta caaaaaatga atcttgtctg 1260

aattccagag agacatcttt tatcactaat ggaagttgcc tcgccagtcg gaaaacttcc 1320

ttcatgatgg ccctgtgtct gagttcaatc tacgaggatc ttaagatgta tcaagtggaa 1380

ttcaaaacga tgaacgcaaa actgttgatg gatcctaaga ggcagatatt tttggatcag 1440

aacatgttag ctgtgatcga cgagctgatg caagcactca acttcaactc agagacagtc 1500

ccccagaagt cctccctgga ggagcctgac ttctacaaga cgaaaattaa gctatgcatt 1560

ctgcttcacg cattcaggat acgggccgta acaattgacc gtgtgatgag ctatctgaac 1620

gcttcgtctg gaggcggaag cgggggtggc ggcagcggcg gtggaggatc aggtggcggg 1680

gggtccgggg gcggaagtct gcagaagatt gacgcctgta agcgaggaga tgtcacagtg 1740

aagcccagtc acgtgattct cctcggaagc acagttaata tcacttgctc cctaaagcca 1800

aggcagggct gctttcacta ctcccggaga aataagctca tcctgtacaa gtttgaccgc 1860

agaatcaact tccatcacgg tcactctctg aattcgcagg tgacagggct gccgctgggt 1920

acgacgttat ttgtgtgcaa actggcctgc atcaactctg acgagattca gatctgtgga 1980

gctgaaattt tcgttggcgt ggctccagag cagccacaga acctctcttg tattcagaaa 2040

ggggagcagg gcacagttgc ctgtacctgg gagcgcggtc gagacactca cctgtacact 2100

gaatatacgc tgcagctgtc tgggccaaaa aacctcacct ggcagaagca atgcaaagat 2160

atctattgcg actacctgga cttcggcata aacctcaccc cagagtcccc agaaagcaat 2220

ttcacagcaa aggtgaccgc ggtgaactct cttggcagct cctcatctct ccctagcacc 2280

tttacgtttc tggacatcgt tcgaccctta ccccccctggg acatacggat caagtttcag 2340

aaagccagtg tgtcacgttg cacccтttac tggcgagacg agggtttggt cttgttgaac 2400

cgccttcggt atcgcccatc taacagccgc ctgtggaata tggtcaacgt taccaaagcg 2460

aaaggcagac acgatctgtt ggatctgaaa cctttcacag agtatgagtt ccagattagt 2520

agcaagctac acctgtataa aggatcatgg tccgactggt cagagtcact gagggcccag 2580

acacctgagg aagagcccac cggcatgttg gacgtctggt acatgaagag gcacattgac 2640

tacagccggc agcaaattag cctgttctgg aagaatttga gtgtcagcga agctagaggg 2700

aagatcctac actaccaggt aaccctccaa gagctaacag gggggaaagc tatgactcaa 2760

aatatcactg gacatacctc ctggaccact gtgatccctc gtacgggcaa ttgggcagtg 2820

gcggttagcg cagcaaattc caagggaagt agtttaccca caagaatcaa cattatgaac 2880

ctgtgtgaag ctgggctgtt agctccccgg caggtcagcg cgaactccga aggtatggat 2940

aatatccttg tgacctggca acccccccgt aaggatccct ccgccgtcca ggagtatgtg 3000

gtggagtgga gggaacttca tcctggaggc gatacacagg taccgctgaa ctggcttcgg 3060

agtcggccct acaacgtgag cgccctgatc tctgagaata tcaagagcta tatttgttat 3120

gagattcgcg tgtatgcatt atcgggtgat caggggggtt gctcaagcat attgggcaat 3180

tcaaaacata aggccccact cagtggccca catattaatg ctatcaccga ggaaaagggc 3240

tcaattctca tcagctggaa ctcaatccca gtacaggaac aaatgggctg cctacttcat 3300

tataggatct actggaagga gagggattct aattcccagc cgcaactttg tgaaatcccc 3360

tacagagtgt cccagaacag tcatccaatc aattccttac agcccagagt gacatatgtg 3420

ctctggatga ctgctctgac cgcagccgga gaatccagcc acgggaacga gagggagttt 3480

tgtcttcagg gaaaggcaaa ctggatggcc ttcgtggccc cttccatttg catcgcaata 3540

attatggtcg gcatctttag tactcactac tttcagcaaa aagttttcgt actgctcgcc 3600

gccctgcgcc ctcagtggtg tagcagagaa attccagacc ctgcgaattc cacatgcgcc 3660

aaaaaatacc ccatagctga ggagaagacc cagctgcctc tagataggct gctgattgac 3720

tggccaactc ccgaagatcc tgaaccactt gtaattagtg aggtattaca tcaggtgaca 3780

ccagtcttca ggcatcctcc ttgttcaaac tggccgcagc gagaaaaagg catacaaggg 3840

catcaagcta gcgaaaaaga tatgatgcat agtgcctcgt ctcctcctcc tccgcgggca 3900

ctgcaggcag agtcacggca gctggtcgat ctgtacaaag tgttggaatc tcgcggatcg 3960

gacccgaagc ccgagaatcc cgcctgcccg tggaccgtcc tccctgctgg cgacttgcct 4020

actcacgatg ggtacctccc ctctaacata gacgacctgc ctagccacga agccccctc 4080

gctgactctc tggaggaact ggagccccag cacatatccc tgtccgtttt cccatctagc 4140

tcattgcacc cactcacctt ttcttgtgga gataaattga ctctcgatca actgaagatg 4200

agatgcgatt ccctgatgct t 4221

<210> 139
<211> 2928
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 139
atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60

ccgcacaagt gtgatattac actccaagaa ataatcaaga ccctgaacag cctaaccgag 120

cagaaaactc tctgtacgga attgaccgtt accgatatct tcgcagctag taagaataca 180

actgaaaaag agacgttttg tcgtgccgcc acagtcctga ggcagtttta ttcacatcac 240

gagaaagaca cccggtgcct tggggcaact gcccaacagt ttcatcgcca caaacagctg 300

atcagattct tgaagcggct ggacaggaat ctctggggat tagctggcct gaattcttgc 360

cccgtgaagg aggcgaacca gagcactctg gagaacttcc tggaacgact taagacaatt 420

atgagagaga agtactccaa atgctcctct tctggaggcg gaagcggggg tggcggcagc 480

ggcggtggag gatcaggtgg cgggggtcc gggggcggaa gtctgcagat gaaagtgctg 540

caggaaccga cctgcgtgag cgattatatg agcattagca cctgcgaatg gaaaatgaac 600

ggcccgacca actgcagcac cgaactgcgc ctgctgtatc agctggtgtt tctgctgagc 660

gaagcgcata cctgcattcc ggaaaacaac ggcggcgcgg gctgcgtgtg ccatctgctg 720

atggatgatg tggtgagcgc ggataactat accctggatc tgtgggcggg ccagcagctg 780

ctgtggaaag gcagctttaa accgagcgaa catgtgaaac cgcgcgcgcc gggcaacctg 840

accgtgcata ccaacgtgag cgataccctg ctgctgacct ggagcaaccc gtatccgccg 900

gataactatc tgtataacca tctgacctat gcggtgaaca tttggagcga aaacgatccg 960

gcggattttc gcatttataa cgtgacctat ctggaaccga gcctgcgcat tgcggcgagc 1020

accctgaaaa gcggcattag ctatcgcgcg cgcgtgcgcg cgtgggcgca gtgctataac 1080

accacctgga gcgaatggag cccgagcacc aaatggcata acagctatcg cgaaccgttt 1140

gaacagcatc tgctgctggg cgtgagcgtg agctgcattg tgattctggc ggtgtgcctg 1200

ctgtgctatg tgagcattac caaaattaaa aaagaatggt gggatcagat tccgaacccg 1260

gcgcgcagcc gcctggtggc gattattatt caggatgcgc agggcagcca gtgggaaaaa 1320

cgcagccgcg gccaggaacc ggcgaaatgc ccgcattgga aaaactgcct gaccaaactg 1380

ctgccgtgct ttctggaaca taacatgaaa cgcgatgaag atccgcataa agcggcgaaa 1440

gaaatgccgt ttcagggcag cggcaaaagc gcgtggtgcc cggtggaaat tagcaaaacc 1500

gtgctgtggc cggaaagcat tagcgtggtg cgctgcgtgg aactgtttga agcgccggtg 1560

gaatgcgaag aagaagaaga agtggaagaa gaaaaaggca gcttttgcgc gagcccggaa 1620

agcagccgcg atgattttca ggaaggccgc gaaggcattg tggcgcgcct gaccgaaagc 1680

ctgtttctgg atctgctggg cgaagaaaac ggcggctttt gccagcagga tatgggcgaa 1740

agctgcctgc tgccgccgag cggcagcacc agcgcgcata tgccgtggga tgaatttccg 1800

agcgcgggcc cgaaagaagc gccgccgtgg ggcaaagaac agccgctgca tctggaaccg 1860

agcccgccgg cgagcccgac ccagagcccg gataacctga cctgcaccga aaccccgctg 1920

gtgattgcgg gcaacccggc gtatcgcagc tttagcaaca gcctgagcca gagcccgtgc 1980

ccgcgcgaac tgggcccgga tccgctgctg gcgcgccatc tggaagaagt ggaaccggaa 2040

atgccgtgcg tgccgcagct gagcgaaccg accaccgtgc cgcagccgga accggaaacc 2100

tgggaacaga ttctgcgccg caacgtgctg cagcatggcg cggcggcggc gccggtgagc 2160

gcgccgacca gcggctatca ggaatttgtg catgcggtgg aacagggcgg cacccaggcg 2220

agcgcggtgg tgggcctggg cccgccgggc gaagcgggct ataaagcgtt tagcagcctg 2280

ctggcgagca gcgcggtgag cccggaaaaa tgcggctttg gcgcgagcag cggcgaagaa 2340

ggctataaac cgtttcagga tctgattccg ggctgcccgg gcgatccggc gccggtgccg 2400

gtgccgctgt ttacctttgg cctggatcgc gaaccgccgc gcagcccgca gagcagccat 2460

ctgccgagca gcagcccgga acatctgggc ctggaaccgg gcgaaaaagt ggaagatatg 2520

ccgaaaccgc cgctgccgca ggaacaggcg accgatccgc tggtggatag cctgggcagc 2580

ggcattgtgt atagcgcgct gacctgccat ctgtgcggcc atctgaaaca gtgccatggc 2640

caggaagatg gcggccagac cccggtgatg gcgagcccgt gctgcggctg ctgctgcggc 2700

gatcgcagca gcccgccgac caccccgctg cgcgcgccgg atccgagccc gggcggcgtg 2760

ccgctggaag cgagcctgtg cccggcgagc ctggcgccga gcggcattag cgaaaaaagc 2820

aaaagcagca gcagctttca tccggcgccg ggcaacgcgc agagcagcag ccagaccccg 2880

aaaattgtga actttgtgag cgtgggcccg acctatatgc gcgtgagc 2928

<210> 140
<211> 1569
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 140
atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60

ccgcacaagt gtgatattac actccaagaa ataatcaaga ccctgaacag cctaaccgag 120

cagaaaactc tctgtacgga attgaccgtt accgatatct tcgcagctag taagaataca 180

actgaaaaag agacgttttg tcgtgccgcc acagtcctga ggcagtttta ttcacatcac 240

gagaaagaca cccggtgcct tggggcaact gcccaacagt ttcatcgcca caaacagctg 300

atcagattct tgaagcggct ggacaggaat ctctggggat tagctggcct gaattcttgc 360

cccgtgaagg aggcgaacca gagcactctg gagaacttcc tggaacgact taagacaatt 420

atgagagaga agtactccaa atgctcctct tctggaggcg gaagcggggg tggcggcagc 480

ggcggtggag gatcaggtgg cgggggtcc gggggcggaa gtctgcagct gaacacaaca 540

attctcaccc ctaacggcaa cgaagacact accgcagatt ttttcctcac tactatgccc 600

actgattccc tttccgtgtc gaccttgccg ctgccagaag tgcagtgctt cgtctttaat 660

gttgagtata tgaattgtac atggaattct agcagcgaac cgcagccaac caatttgaca 720

ttgcactact ggtataaaaa ctcagataac gacaaagtgc agaagtgttc ccactactta 780

tttagcgagg aaataacctc tgggtgccag ctgcagaaga aggagatcca tctgtaccag 840

accttcgtcg tgcagctcca ggatccacgg gaaccacgcc ggcaagctac ccaaatgcta 900

aagctgcaaa atctcgttat cccatgggca cctgagaatt tgacacttca taagctgtcg 960

gaatcccagc tggagctcaa ttggaacaac cgtttcctca accattgtct ggagcacctg 1020

gtgcagtaca gaaccgactg ggaccatagt tggacggagc agagtgtcga ttatagacac 1080

aaattctcac taccctcagt ggacgggcag aagaggtaca catttagagt aaggagtcgg 1140

ttcaatcccc tgtgcgggtc cgcccaacac tggagtgagt ggtctcatcc tattcactgg 1200

ggcagcaaca cgtccaagga gaacccttтc ttgtttgctc tggaagctgt tgtgatttca 1260

gtaggctcta tgggattaat catcagcctc ctgtgtgtct atttttggct ggagcgaaca 1320

atgcccagga tccccactct caaaaatctg gaagaccttg tgacggagta tcacggcaac 1380

ttcagcgcgt ggtctggcgt ctctaaaggt cttgccgaga gcctgcagcc tgattacagt 1440

gagcgcttat gcctggtgag cgagatacca cctaaaggag gagcccttgg tgaaggaccg 1500

ggggcatccc cctgtaatca acactcacca tactgggccc ccccctgcta taccctaaag 1560

cctgaaact 1569

<210> 141
<211> 1746
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 141
atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60

ccgcacaagt gtgatattac actccaagaa ataatcaaga ccctgaacag cctaaccgag 120

cagaaaactc tctgtacgga attgaccgtt accgatatct tcgcagctag taagaataca 180

actgaaaaag agacgttttg tcgtgccgcc acagtcctga ggcagtttta ttcacatcac 240

gagaaagaca cccggtgcct tggggcaact gcccaacagt ttcatcgcca caaacagctg 300

atcagattct tgaagcggct ggacaggaat ctctggggat tagctggcct gaattcttgc 360

cccgtgaagg aggcgaacca gagcactctg gagaacttcc tggaacgact taagacaatt 420

atgagagaga agtactccaa atgctcctct tctggaggcg gaagcggggg tggcggcagc 480

ggcggtggag gatcaggtgg cgggggtcc gggggcggaa gtctgcaggg cggcggcggc 540

gcggcgccga ccgaaaccca gccgccggtg accaacctga gcgtgagcgt ggaaaacctg 600

tgcaccgtga tttggacctg gaacccgccg gaaggcgcga gcagcaactg cagcctgtgg 660

tattttagcc attttggcga taaacaggat aaaaaaattg cgccggaaac ccgccgcagc 720

attgaagtgc cgctgaacga acgcatttgc ctgcaggtgg gcagccagtg cagcaccaac 780

gaaagcgaaa aaccgagcat tctggtggaa aaatgcatta gcccgccgga aggcgatccg 840

gaaagcgcgg tgaccgaact gcagtgcatt tggcataacc tgagctatat gaaatgcagc 900

tggctgccgg gccgcaacac cagcccggat accaactata ccctgtatta ttggcatcgc 960

agcctggaaa aaattcatca gtgcgaaaac atttttcgcg aaggccagta ttttggctgc 1020

agctttgatc tgaccaaagt gaaagatagc agctttgaac agcatagcgt gcagattatg 1080

gtgaaagata acgcgggcaa aattaaaccg agctttaaca ttgtgccgct gaccagccgc 1140

gtgaaaccgg atccgccgca tattaaaaac ctgagctttc ataacgatga tctgtatgtg 1200

cagtgggaaa acccgcagaa ctttattagc cgctgcctgt tttatgaagt ggaagtgaac 1260

aacagccaga ccgaaaccca taacgtgttt tatgtgcagg aagcgaaatg cgaaaacccg 1320

gaatttgaac gcaacgtgga aaacaccagc tgctttatgg tgccgggcgt gctgccggat 1380

accctgaaca ccgtgcgcat tcgcgtgaaa accaacaaac tgtgctatga agatgataaa 1440

ctgtggagca actggagcca ggaaatgagc attggcaaaa aacgcaacag caccctgtat 1500

attaccatgc tgctgattgt gccggtgatt gtggcgggcg cgattattgt gctgctgctg 1560

tatctgaaac gcctgaaaat tattattttt ccgccgattc cggatccggg caaaattttt 1620

aaagaaatgt ttggcgatca gaacgatgat accctgcatt ggaaaaaata tgatatttat 1680

gaaaaacaga ccaaagaaga aaccgatagc gtggtgctga ttgaaaacct gaaaaaagcg 1740

agccag 1746

<210> 142
<211> 2943
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 142

atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60

ccgaatacga ctgagaaaga gacctttttgt agggctgcca cagtcctgcg gcagttctat 120

agtcaccatg agaaagacac cagatgtctg ggggcaaccg ctcagcaatt ccatagacac 180

aagcagttaa tccgatttct gaagcggctt gatcgtaact tgtggggact agccggcctg 240

aactcatgcc ccgtgaaaga agcgaatcag tccactcttg agaacttcct cgaaaggctc 300

aagacaatta tgcgcgaaaa gtacagcaag tgcagctctg gcggaaacgg tgggcacaag 360

tgtgatatta cgctccaaga aatcatcaag actctgaact ccctgaccga gcagaaaaca 420

ctttgcactg agttgacagt gaccgacata ttcgccgcta gcaaatctgg aggcggaagc 480

gggggtggcg gcagcggcgg tggaggatca ggtggcgggg ggtccggggg cggaagtctg 540

cagatgaaag tgctgcagga accgacctgc gtgagcgatt atatgagcat tagcacctgc 600

gaatggaaaa tgaacggccc gaccaactgc agcaccgaac tgcgcctgct gtatcagctg 660

gtgtttctgc tgagcgaagc gcatacctgc attccggaaa acaacggcgg cgcgggctgc 720

gtgtgccatc tgctgatgga tgatgtggtg agcgcggata actataccct ggatctgtgg 780

gcgggccagc agctgctgtg gaaaggcagc tttaaaccga gcgaacatgt gaaaccgcgc 840

gcgccgggca acctgaccgt gcataccaac gtgagcgata ccctgctgct gacctggagc 900

aacccgtatc cgccggataa ctatctgtat aaccatctga cctatgcggt gaacatttgg 960

agcgaaaacg atccggcgga ttttcgcatt tataacgtga cctatctgga accgagcctg 1020

cgcattgcgg cgagcaccct gaaaagcggc attagctatc gcgcgcgcgt gcgcgcgtgg 1080

gcgcagtgct ataacaccac ctggagcgaa tggagcccga gcaccaaatg gcataacagc 1140

tatcgcgaac cgtttgaaca gcatctgctg ctgggcgtga gcgtgagctg cattgtgatt 1200

ctggcggtgt gcctgctgtg ctatgtgagc attaccaaaa ttaaaaaaga atggtgggat 1260

cagattccga acccggcgcg cagccgcctg gtggcgatta ttattcagga tgcgcagggc 1320

agccagtggg aaaaacgcag ccgcggccag gaaccggcga aatgcccgca ttggaaaaac 1380

tgcctgacca aactgctgcc gtgctttctg gaacataaca tgaaacgcga tgaagatccg 1440

cataaagcgg cgaaagaaat gccgtttcag ggcagcggca aaagcgcgtg gtgcccggtg 1500

gaaattagca aaaccgtgct gtggccggaa agcattagcg tggtgcgctg cgtggaactg 1560

tttgaagcgc cggtggaatg cgaagaagaa gaagaagtgg aagaagaaaa aggcagcttt 1620

tgcgcgagcc cggaaagcag ccgcgatgat tttcaggaag gccgcgaagg cattgtggcg 1680

cgcctgaccg aaagcctgtt tctggatctg ctgggcgaag aaaacggcgg cttttgccag 1740

caggatatgg gcgaaagctg cctgctgccg ccgagcggca gcaccagcgc gcatatgccg 1800

tgggatgaat ttccgagcgc gggcccgaaa gaagcgccgc cgtggggcaa agaacagccg 1860

ctgcatctgg aaccgagccc gccggcgagc ccgacccaga gcccggataa cctgacctgc 1920

accgaaaccc cgctggtgat tgcgggcaac ccggcgtatc gcagctttag caacagcctg 1980

agccagagcc cgtgcccgcg cgaactgggc ccggatccgc tgctggcgcg ccatctggaa 2040

gaagtggaac cggaaatgcc gtgcgtgccg cagctgagcg aaccgaccac cgtgccgcag 2100

ccggaaccgg aaacctggga acagattctg cgccgcaacg tgctgcagca tggcgcggcg 2160

gcggcgccgg tgagcgcgcc gaccagcggc tatcaggaat ttgtgcatgc ggtggaacag 2220

ggcggcaccc aggcgagcgc ggtggtgggc ctgggcccgc cgggcgaagc gggctataaa 2280

gcgtttagca gcctgctggc gagcagcgcg gtgagcccgg aaaaatgcgg ctttggcgcg 2340

agcagcggcg aagaaggcta taaaccgttt caggatctga ttccgggctg cccgggcgat 2400

ccggcgccgg tgccggtgcc gctgtttacc tttggcctgg atcgcgaacc gccgcgcagc 2460

ccgcagagca gccatctgcc gagcagcagc ccggaacatc tgggcctgga accgggcgaa 2520

aaagtggaag atatgccgaa accgccgctg ccgcaggaac aggcgaccga tccgctggtg 2580

gatagcctgg gcagcggcat tgtgtatagc gcgctgacct gccatctgtg cggccatctg 2640

aaacagtgcc atggccagga agatggcggc cagaccccgg tgatggcgag cccgtgctgc 2700

ggctgctgct gcggcgatcg cagcagcccg ccgaccaccc cgctgcgcgc gccggatccg 2760

agcccgggcg gcgtgccgct ggaagcgagc ctgtgcccgg cgagcctggc gccgagcggc 2820

attagcgaaa aaagcaaaag cagcagcagc tttcatccgg cgccgggcaa cgcgcagagc 2880

agcagccaga ccccgaaaat tgtgaacttt gtgagcgtgg gcccgaccta tatgcgcgtg 2940

agc 2943

<210> 143
<211> 1584
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 143
atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60

ccgaatacga ctgagaaaga gacctttttgt agggctgcca cagtcctgcg gcagttctat 120

agtcaccatg agaaagacac cagatgtctg ggggcaaccg ctcagcaatt ccatagacac 180

aagcagttaa tccgatttct gaagcggctt gatcgtaact tgtggggact agccggcctg 240

aactcatgcc ccgtgaaaga agcgaatcag tccactcttg agaacttcct cgaaaggctc 300

aagacaatta tgcgcgaaaa gtacagcaag tgcagctctg gcggaaacgg tgggcacaag 360

tgtgatatta cgctccaaga aatcatcaag actctgaact ccctgaccga gcagaaaaca 420

ctttgcactg agttgacagt gaccgacata ttcgccgcta gcaaatctgg aggcggaagc 480

gggggtggcg gcagcggcgg tggaggatca ggtggcgggg ggtccggggg cggaagtctg 540

cagctgaaca caacaattct cacccctaac ggcaacgaag acactaccgc agatttttc 600

ctcactacta tgcccactga ttccctttcc gtgtcgacct tgccgctgcc agaagtgcag 660

tgcttcgtct ttaatgttga gtatatgaat tgtacatgga attctagcag cgaaccgcag 720

ccaaccaatt tgacattgca ctactggtat aaaaactcag ataacgacaa agtgcagaag 780

tgttcccact acttatttag cgaggaaata acctctgggt gccagctgca gaagaaggag 840

atccatctgt accagacctt cgtcgtgcag ctccaggatc cacgggaacc acgccggcaa 900

gctacccaaa tgctaaagct gcaaaatctc gttatcccat gggcacctga gaatttgaca 960

cttcataagc tgtcggaatc ccagctggag ctcaattgga acaaccgttt cctcaaccat 1020

tgtctggagc acctggtgca gtacagaacc gactgggacc atagttggac ggagcagagt 1080

gtcgattata gacacaaatt ctcactaccc tcagtggacg ggcagaagag gtacacattt 1140

agagtaagga gtcggttcaa tcccctgtgc gggtccgccc aacactggag tgagtggtct 1200

catcctattc actggggcag caacacgtcc aaggagaacc ctttcttgtt tgctctggaa 1260

gctgttgtga tttcagtagg ctctatggga ttaatcatca gcctcctgtg tgtctatttt 1320

tggctggagc gaacaatgcc caggatcccc actctcaaaa atctggaaga ccttgtgacg 1380

gagtatcacg gcaacttcag cgcgtggtct ggcgtctcta aaggtcttgc cgagagcctg 1440

cagcctgatt acagtgagcg cttatgcctg gtgagcgaga taccacctaa aggaggagcc 1500

cttggtgaag gaccgggggc atccccctgt aatcaacact caccatactg ggccccccc 1560

tgctataccc taaagcctga aact 1584

<210> 144
<211> 1761
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 144
atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60

ccgaatacga ctgagaaaga gacctttgt agggctgcca cagtcctgcg gcagttctat 120

agtcaccatg agaaagacac cagatgtctg ggggcaaccg ctcagcaatt ccatagacac 180

aagcagttaa tccgatttct gaagcggctt gatcgtaact tgtggggact agccggcctg 240

aactcatgcc ccgtgaaaga agcgaatcag tccactcttg agaacttcct cgaaaggctc 300

aagacaatta tgcgcgaaaa gtacagcaag tgcagctctg gcggaaacgg tgggcacaag 360

tgtgatatta cgctccaaga aatcatcaag actctgaact ccctgaccga gcagaaaaca 420

ctttgcactg agttgacagt gaccgacata ttcgccgcta gcaaatctgg aggcggaagc 480

gggggtggcg gcagcggcgg tggaggatca ggtggcgggg ggtccggggg cggaagtctg 540

cagggcggcg gcggcgcggc gccgaccgaa acccagccgc cggtgaccaa cctgagcgtg 600

agcgtggaaa acctgtgcac cgtgatttgg acctggaacc cgccggaagg cgcgagcagc 660

aactgcagcc tgtggtattt tagccatttt ggcgataaac aggataaaaa aattgcgccg 720

gaaacccgcc gcagcattga agtgccgctg aacgaacgca tttgcctgca ggtgggcagc 780

cagtgcagca ccaacgaaag cgaaaaaccg agcattctgg tggaaaaatg cattagcccg 840

ccggaaggcg atccggaaag cgcggtgacc gaactgcagt gcatttggca taacctgagc 900

tatatgaaat gcagctggct gccgggccgc aacaccagcc cggataccaa ctataccctg 960

tattattggc atcgcagcct ggaaaaaatt catcagtgcg aaaacatttt tcgcgaaggc 1020

cagtattttg gctgcagctt tgatctgacc aaagtgaaag atagcagctt tgaacagcat 1080

agcgtgcaga ttatggtgaa agataacgcg ggcaaaatta aaccgagctt taacattgtg 1140

ccgctgacca gccgcgtgaa accggatccg ccgcatatta aaaacctgag ctttcataac 1200

gatgatctgt atgtgcagtg ggaaaacccg cagaacttta ttagccgctg cctgttttat 1260

gaagtggaag tgaacaacag ccagaccgaa acccataacg tgttttatgt gcaggaagcg 1320

aaatgcgaaa acccggaatt tgaacgcaac gtggaaaaca ccagctgctt tatggtgccg 1380

ggcgtgctgc cggataccct gaacaccgtg cgcattcgcg tgaaaaccaa caaactgtgc 1440

tatgaagatg ataaactgtg gagcaactgg agccaggaaa tgagcattgg caaaaaacgc 1500

aacagcaccc tgtatattac catgctgctg attgtgccgg tgattgtggc gggcgcgatt 1560

attgtgctgc tgctgtatct gaaacgcctg aaaattatta tttttccgcc gattccggat 1620

ccgggcaaaa tttttaaaga aatgtttggc gatcagaacg atgataccct gcattggaaa 1680

aaatatgata tttatgaaaa acagaccaaa gaagaaaccg atagcgtggt gctgattgaa 1740

aacctgaaaa aagcgagcca g 1761

<210> 145
<211> 2292
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 145
atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60

ccgtcacccg gacagggtac tcaatctgaa aatagttgca cccattttcc aggaaatctg 120

cctaacatgc tgagggactt acgcgatgca ttttcgcgtg taaaaacatt ctttcagatg 180

aaagatcaac tggataacct gttgctaaaa gagagcctgc ttgaggattt caagggctat 240

ctgggctgtc aggcgctctc cgaaatgatt caattctacc tcgaagaggt gatgccccag 300

gccgagaacc aggacccaga catcaaggcc cacgtgaatt ctctgggggа gaatctgaaa 360

acgctcagat tgcgactcag acggtgccac aggtttttac cttgtgaaaa caagagcaaa 420

gccgttgagc aggtcaagaa cgcttttaat aagcttcagg aaaaagggat ctataaggca 480

atgtccgagt tcgacatatt cattaattac attgaggctt acatgaccat gaagatccgg 540

aactctggag gcggaagcgg gggtggcggc agcggcggtg gaggatcagg tggcgggggg 600

tccgggggcg gaagtctgca gcatgggacc gagctcccca gtcctccttc tgtttggttc 660

gaagccgaat tctttcacca tattctgcac tggactccta tcccaaatca atcagaatca 720

acatgttacg aggtggcact gctgaggtac ggaatcgagt cttggaatag catttcaaac 780

tgtagccaaa ccctgtctta cgatcttacc gctgtgacgc tggacctgta tcatagcaac 840

ggctaccgtg ccagggttag ggcagttgat ggcagcagac actccaattg gacagttacg 900

aatacccgat tcagtgtcga cgaggtgact ttaactgtcg ggagtgttaa ccttgaaatt 960

cacaacgggt tcatattggg aaagatccag ctcccccggc caaaaatggc cccagccaac 1020

gacacatacg agagtatatt ttctcatttt agagagtatg agatcgcaat ccgcaaggtg 1080

cctgggaatt tcacatttac tcataagaag gtaaaacacg agaacttctc cttgctcacc 1140

tccggcgaag tgggggagtt ctgcgtgcag gtgaagccct cggtggcttc acgctccaat 1200

aaaggcatgt ggagcaaaga agaatgtatt tctctgactc ggcagtactt taccgtgact 1260

aacgtaatca tatttttgc cttcgtgctc ctgctgtctg gtgccctggc ctattgcctg 1320

gcgcttcaac tttatgtgcg gaggaggaag aagctgccgt ccgtgctgtt gtttaagaaa 1380

ccgtctccct tcatttttat cagccagcgc ccctcacccg aaacacagga tactattcac 1440

ccccttgacg aagaagcctt ccttaaagtg tcccccgagc taaaaaacct cgacctgcac 1500

gggtccaccg atagcgggtt tggtagcacc aaaccatcct tgcaaaccga ggagccccag 1560

ttcttgctcc ctgatccaca cccacaggct gacagaacgt tgggaaacag agagccccca 1620

gtcctggggg attcctgttc gtcagggtct agtaatagta ccgatagcgg gatttgcctg 1680

caggagccga gcctgtcacc ctcaaccggt ccgacctggg agcagcaagt aggatctaac 1740

tcccgcgggc aggatgactc cggcatagac ctcgtacaga attcggaagg ccgggcgggt 1800

gacacacagg gcggctccgc tctgggccac cattccccac cagagcccga ggtccctggc 1860

gaggaggacc ctgcagccgt cgcttttcaa ggctatctgc gtcagacacg atgtgctgaa 1920

gagaaagcta ctaagacggg atgtcttgaa gaggaatctc cgcttacaga cggattggga 1980

ccaaagttcg gcagatgcct agtggatgag gcgggactac atcctcccgc attagcaaag 2040

ggctacctga agcaggatcc actagaaatg acactggcct catctggcgc ccctacagga 2100

cagtggaacc agccaaccga agagtggtcc ttgctcgctt taagctcttg cagtgacctg 2160

ggtatctcag attggagttt tgcacacgac ctcgcccctc tgggttgcgt cgccgctcct 2220

ggtggactct taggaagttt caatagcgat ctcgtcactc tgcctctcat cagtagctta 2280

cagagcagcg aa 2292

<210> 146
<211> 1539
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 146
atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60

ccgtcacccg gacagggtac tcaatctgaa aatagttgca cccattttcc aggaaatctg 120

cctaacatgc tgagggactt acgcgatgca ttttcgcgtg taaaaacatt ctttcagatg 180

aaagatcaac tggataacct gttgctaaaa gagagcctgc ttgaggattt caagggctat 240

ctgggctgtc aggcgctctc cgaaatgatt caattctacc tcgaagaggt gatgccccag 300

gccgagaacc aggacccaga catcaaggcc cacgtgaatt ctctggggga gaatctgaaa 360

acgctcagat tgcgactcag acggtgccac aggtttttac cttgtgaaaa caagagcaaa 420

gccgttgagc aggtcaagaa cgcttttaat aagcttcagg aaaaagggat ctataaggca 480

atgtccgagt tcgacatatt cattaattac attgaggctt acatgaccat gaagatccgg 540

aactctggag gcggaagcgg gggtggcggc agcggcggtg gaggatcagg tggcgggggg 600

tccgggggcg gaagtctgca gatggtacca ccacctgaaa atgtgaggat gaactctgtg 660

aattttaaga acattctcca gtgggaaagt cccgcttttg ctaaggggaa cctgaccttc 720

acagcccaat acttatccta ccgaatcttc caagacaagt gcatgaatac cactttaact 780

gaatgcgact tctcaagcct gtctaagtat ggcgatcata cactgcgggt tcgtgccgag 840

tttgccgacg agcactctga ctgggtgaat ataaccttct gccccgtcga tgatactata 900

attgggccac caggtatgca agttgaagtg ttggcagatt cgctgcacat gaggtttctc 960

gcccccaaaa tcgagaacga gtacgagacc tggacgatga agaatgtcta caactcttgg 1020

acatataatg ttcagtattg gaaaaacgga accgacgaga agtttcagat cactccgcag 1080

tatgatttcg aagtcctgag aaacctcgag ccttggacaa cttactgtgt ccaagtgcgc 1140

ggctttctcc ctgaccggaa caaggcagga gagtggtcag aaccggtgtg tgagcagacc 1200

acccacgacg agacagtacc cagctggatg gtagctgtga tccttatggc ctccgtgttc 1260

atggtttgtc tagctttgtt gggctgtttt gcccttctat ggtgcgtcta taaaaagacc 1320

aaatacgcgt tttcacctag aaacagcctt ccacagcacc tcaaggagtt cctggggcat 1380

cctcatcaca atacactgct gttcttctcc ttccccctga gtgacgaaaa cgatgtgttt 1440

gataaactgt ccgtgattgc agaagacagt gagtccggca aacagaatcc aggagatagt 1500

tgcagcctgg gtacgcctcc cggacagggc ccccagagc 1539

<210> 147
<211> 2310
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 147
atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60

ccgtcgcctg gccagggaac gcagagtgaa aatagctgta cccactttcc cggcaaccta 120

ccaaatatgc tcagagatct gcgggatgca ttctcccggg tgaagacatt tttccaaatg 180

aaggatcagt tggacaacct tctgttgaag gagtcactct tagaggactt caagggatac 240

ctggggtgcc aagccctgtc tgagatgatt cagttctacc tcgaagaggt aatgccacag 300

gccgaaaacc aggaccctga tataaaagct catgtcaata gtttaggcga gaatctgaaa 360

actctcaggc tgcgtctgcg aagatgccac cgctttctgc cctgtgagaa cgggggaggg 420

tctggtggca aaagcaaagc tgtggagcaa gttaaaaatg cattcaacaa acttcaggag 480

aagggtattt ataaggcgat gtccgaattt gacatcttta ttaattacat cgaagcctat 540

atgaccatga agatcaggaa ctctggaggc ggaagcgggg gtggcggcag cggcggtgga 600

ggatcaggtg gcgggggtc cgggggcgga agtctgcagc atgggaccga gctccccagt 660

cctccttctg tttggttcga agccgaattc tttcaccata ttctgcactg gactcctatc 720

ccaaatcaat cagaatcaac atgttacgag gtggcactgc tgaggtacgg aatcgagtct 780

tggaatagca tttcaaactg tagccaaacc ctgtcttacg atcttaccgc tgtgacgctg 840

gacctgtatc atagcaacgg ctaccgtgcc agggttaggg cagttgatgg cagcagacac 900

tccaattgga cagttacgaa tacccgattc agtgtcgacg aggtgacttt aactgtcggg 960

agtgttaacc ttgaaattca caacgggttc atattgggaa agatccagct cccccggcca 1020

aaaatggccc cagccaacga cacatacgag agtatatttt ctcattttag agagtatgag 1080

atcgcaatcc gcaaggtgcc tgggaatttc acatttactc ataagaaggt aaaacacgag 1140

aacttctcct tgctcacctc cggcgaagtg ggggagttct gcgtgcaggt gaagccctcg 1200

gtggcttcac gctccaataa aggcatgtgg agcaaagaag aatgtatttc tctgactcgg 1260

cagtacttta ccgtgactaa cgtaatcata ttttttgcct tcgtgctcct gctgtctggt 1320

gccctggcct attgcctggc gcttcaactt tatgtgcgga ggaggaagaa gctgccgtcc 1380

gtgctgttgt ttaagaaacc gtctcccttc atttttatca gccagcgccc ctcacccgaa 1440

acacaggata ctattcaccc ccttgacgaa gaagccttcc ttaaagtgtc ccccgagcta 1500

aaaaacctcg acctgcacgg gtccaccgat agcgggtttg gtagcaccaa accatccttg 1560

caaaccgagg agccccagtt cttgctccct gatccacacc cacaggctga cagaacgttg 1620

ggaaacagag agcccccagt cctgggggat tcctgttcgt cagggtctag taatagtacc 1680

gatagcggga tttgcctgca ggagccgagc ctgtcaccct caaccggtcc gacctgggag 1740

cagcaagtag gatctaactc ccgcgggcag gatgactccg gcatagacct cgtacagaat 1800

tcggaaggcc gggcgggtga cacacagggc ggctccgctc tgggccacca ttccccacca 1860

gagcccgagg tccctggcga ggaggaccct gcagccgtcg cttttcaagg ctatctgcgt 1920

cagacacgat gtgctgaaga gaaagctact aagacgggat gtcttgaaga ggaatctccg 1980

cttacagacg gattgggacc aaagttcggc agatgcctag tggatgaggc gggactacat 2040

cctcccgcat tagcaaaggg ctacctgaag caggatccac tagaaatgac actggcctca 2100

tctggcgccc ctacaggaca gtggaaccag ccaaccgaag agtggtcctt gctcgcttta 2160

agctcttgca gtgacctggg tatctcagat tggagttttg cacacgacct cgcccctctg 2220

ggttgcgtcg ccgctcctgg tggactctta ggaagtttca atagcgatct cgtcactctg 2280

cctctcatca gtagcttaca gagcagcgaa 2310

<210> 148
<211> 1557
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 148
atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60

ccgtcgcctg gccagggaac gcagagtgaa aatagctgta cccactttcc cggcaaccta 120

ccaaatatgc tcagagatct gcgggatgca ttctcccggg tgaagacatt tttccaaatg 180

aaggatcagt tggacaacct tctgttgaag gagtcactct tagaggactt caagggatac 240

ctggggtgcc aagccctgtc tgagatgatt cagttctacc tcgaagaggt aatgccacag 300

gccgaaaacc aggaccctga tataaaagct catgtcaata gtttaggcga gaatctgaaa 360

actctcaggc tgcgtctgcg aagatgccac cgctttctgc cctgtgagaa cgggggaggg 420

tctggtggca aaagcaaagc tgtggagcaa gttaaaaatg cattcaacaa acttcaggag 480

aagggtattt ataaggcgat gtccgaattt gacatcttta ttaattacat cgaagcctat 540

atgaccatga agatcaggaa ctctggaggc ggaagcgggg gtggcggcag cggcggtgga 600

ggatcaggtg gcgggggtc cgggggcgga agtctgcaga tggtaccacc acctgaaaat 660

gtgaggatga actctgtgaa ttttaagaac attctccagt gggaaagtcc cgcttttgct 720

aaggggaacc tgaccttcac agcccaatac ttatcctacc gaatcttcca agacaagtgc 780

atgaatacca ctttaactga atgcgacttc tcaagcctgt ctaagtatgg cgatcataca 840

ctgcgggttc gtgccgagtt tgccgacgag cactctgact gggtgaatat aaccttctgc 900

cccgtcgatg atactataat tgggccacca ggtatgcaag ttgaagtgtt ggcagattcg 960

ctgcacatga ggtttctcgc ccccaaaatc gagaacgagt acgagacctg gacgatgaag 1020

aatgtctaca actcttggac atataatgtt cagtattgga aaaacggaac cgacgagaag 1080

tttcagatca ctccgcagta tgatttcgaa gtcctgagaa acctcgagcc ttggacaact 1140

tactgtgtcc aagtgcgcgg ctttctccct gaccggaaca aggcaggaga gtggtcagaa 1200

ccggtgtgtg agcagaccac ccacgacgag acagtaccca gctggatggt agctgtgatc 1260

cttatggcct ccgtgttcat ggtttgtcta gctttgttgg gctgttttgc ccttctatgg 1320

tgcgtctata aaaagaccaa atacgcgttt tcacctagaa acagccttcc acagcacctc 1380

aaggagttcc tggggcatcc tcatcacaat acactgctgt tcttctcctt ccccctgagt 1440

gacgaaaacg atgtgtttga taaactgtcc gtgattgcag aagacagtga gtccggcaaa 1500

cagaatccag gagatagttg cagcctgggt acgcctcccg gacagggccc ccagagc 1557

<210> 149
<211> 2337
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 149
atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60

ccgggttact tgggctgtca ggctctgagt gaaatgattc agttctatct tgaagaggtt 120

atgcctcagg cggagaacca agacccagac atcaaggccc atgtgaactc tctcggggag 180

aatctgaaaa cactgcgact gcggttaaga cgttgccaca ggttcctacc ctgcgaaaat 240

aaaagcaagg ccgtcgagca agtgaaaaac gcattcaata aactccagga aaagggaatt 300

tacaaggcca tgtccgagtt tgatatcttt ataaactata ttgaggctta catgaccatg 360

aagatccgca atggtggtgg tggaagcggc gggggaggca gtgggggagg cgggtcctcc 420

cctggccagg gaactcagtc agaaaatagc tgcacacact ttccagggaa tctccccaac 480

atgttgagag atctgaggga cgccttctct cgggtgaaaa ccttttcca aatgaaagac 540

cagctggaca acctccttct gaaggagagt ttactagagg atttcaagtc tggaggcgga 600

agcgggggtg gcggcagcgg cggtggagga tcaggtggcg gggggtccgg gggcggaagt 660

ctgcagcatg ggaccgagct ccccagtcct ccttctgttt ggttcgaagc cgaattcttt 720

caccatattc tgcactggac tcctatccca aatcaatcag aatcaacatg ttacgaggtg 780

gcactgctga ggtacggaat cgagtcttgg aatagcattt caaactgtag ccaaaccctg 840

tcttacgatc ttaccgctgt gacgctggac ctgtatcata gcaacggcta ccgtgccagg 900

gttagggcag ttgatggcag cagacactcc aattggacag ttacgaatac ccgattcagt 960

gtcgacgagg tgactttaac tgtcgggagt gttaaccttg aaattcacaa cgggttcata 1020

ttgggaaaga tccagctccc ccggccaaaa atggccccag ccaacgacac atacgagagt 1080

atattttctc attttagaga gtatgagatc gcaatccgca aggtgcctgg gaatttcaca 1140

tttactcata agaaggtaaa acacgagaac ttctccttgc tcacctccgg cgaagtgggg 1200

gagttctgcg tgcaggtgaa gccctcggtg gcttcacgct ccaataaagg catgtggagc 1260

aaagaagaat gtatttctct gactcggcag tactttaccg tgactaacgt aatcatattt 1320

tttgccttcg tgctcctgct gtctggtgcc ctggcctatt gcctggcgct tcaactttat 1380

gtgcggagga ggaagaagct gccgtccgtg ctgttgttta agaaaccgtc tcccttcatt 1440

tttatcagcc agcgcccctc acccgaaaca caggatacta ttcaccccct tgacgaagaa 1500

gccttcctta aagtgtcccc cgagctaaaa aacctcgacc tgcacgggtc caccgatagc 1560

gggtttggta gcaccaaacc atccttgcaa accgaggagc cccagttctt gctccctgat 1620

ccacacccac aggctgacag aacgttggga aacagagagc ccccagtcct gggggattcc 1680

tgttcgtcag ggtctagtaa tagtaccgat agcgggattt gcctgcagga gccgagcctg 1740

tcaccctcaa ccggtccgac ctgggagcag caagtaggat ctaactcccg cgggcaggat 1800

gactccggca tagacctcgt acagaattcg gaaggccggg cgggtgacac acagggcggc 1860

tccgctctgg gccaccattc cccaccagag cccgaggtcc ctggcgagga ggaccctgca 1920

gccgtcgctt ttcaaggcta tctgcgtcag acacgatgtg ctgaagagaa agctactaag 1980

acgggatgtc ttgaagagga atctccgctt acagacggat tgggaccaaa gttcggcaga 2040

tgcctagtgg atgaggcggg actacatcct cccgcattag caaagggcta cctgaagcag 2100

gatccactag aaatgacact ggcctcatct ggcgccccta caggacagtg gaaccagcca 2160

accgaagagt ggtccttgct cgctttaagc tcttgcagtg acctgggtat ctcagattgg 2220

agttttgcac acgacctcgc ccctctgggt tgcgtcgccg ctcctggtgg actcttagga 2280

agtttcaata gcgatctcgt cactctgcct ctcatcagta gcttacagag cagcgaa 2337

<210> 150
<211> 1584
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 150
atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60

ccgggttact tgggctgtca ggctctgagt gaaatgattc agttctatct tgaagaggtt 120

atgcctcagg cggagaacca agacccagac atcaaggccc atgtgaactc tctcggggag 180

aatctgaaaa cactgcgact gcggttaaga cgttgccaca ggttcctacc ctgcgaaaat 240

aaaagcaagg ccgtcgagca agtgaaaaac gcattcaata aactccagga aaagggaatt 300

tacaaggcca tgtccgagtt tgatatcttt ataaactata ttgaggctta catgaccatg 360

aagatccgca atggtggtgg tggaagcggc gggggaggca gtgggggagg cgggtcctcc 420

cctggccagg gaactcagtc agaaaatagc tgcacacact ttccagggaa tctccccaac 480

atgttgagag atctgaggga cgccttctct cgggtgaaaa ccttttcca aatgaaagac 540

cagctggaca acctccttct gaaggagagt ttactagagg atttcaagtc tggaggcgga 600

agcgggggtg gcggcagcgg cggtggagga tcaggtggcg gggggtccgg gggcggaagt 660

ctgcagatgg taccaccacc tgaaaatgtg aggatgaact ctgtgaattt taagaacatt 720

ctccagtggg aaagtcccgc ttttgctaag gggaacctga ccttcacagc ccaatactta 780

tcctaccgaa tcttccaaga caagtgcatg aataccactt taactgaatg cgacttctca 840

agcctgtcta agtatggcga tcatacactg cgggttcgtg ccgagtttgc cgacgagcac 900

tctgactggg tgaatataac cttctgcccc gtcgatgata ctataattgg gccaccaggt 960

atgcaagttg aagtgttggc agattcgctg cacatgaggt ttctcgcccc caaaatcgag 1020

aacgagtacg agacctggac gatgaagaat gtctacaact cttggacata taatgttcag 1080

tattggaaaa acggaaccga cgagaagttt cagatcactc cgcagtatga tttcgaagtc 1140

ctgagaaacc tcgagccttg gacaacttac tgtgtccaag tgcgcggctt tctccctgac 1200

cggaacaagg caggagagtg gtcagaaccg gtgtgtgagc agaccaccca cgacgagaca 1260

gtacccagct ggatggtagc tgtgatcctt atggcctccg tgttcatggt ttgtctagct 1320

ttgttgggct gttttgccct tctatggtgc gtctataaaa agaccaaata cgcgttttca 1380

cctagaaaca gccttccaca gcacctcaag gagttcctgg ggcatcctca tcacaataca 1440

ctgctgttct tctccttccc cctgagtgac gaaaacgatg tgtttgataa actgtccgtg 1500

attgcagaag acagtgagtc cggcaaacag aatccaggag atagttgcag cctgggtacg 1560

cctcccggac agggccccca gagc 1584

<210> 151
<211> 2817
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 151
atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60

ccgtctccgg gacagggaac ccagagcgaa aactcctgca ctcattttcc tggcaacctc 120

cccaatatgc tgcgagactt gcgcgacgca ttctcaaggg tgaagacgtt cttccagatg 180

aaggatcaac tggacaactt attgctgaaa gaatctctgc tcgaggattt caaaggatac 240

ctgggatgtc aggcactgag cgagatgatc caattttacc tggaggaggt catgcctcag 300

gctgagaatc aggatcctga catcaaggcc cacgtgaaca gtcttggaga gaatcttaag 360

acccttaggc tgagacttag acggtgtcac cgctttctgc cctgcgaaaa taaatcaaaa 420

gcggtggaac aggttaagaa cgcttttaat aagctgcagg aaaagggcat ttataaagct 480

atgagtgaat ttgacatttt cattaactat atcgaggcct atatgacaat gaaaattagg 540

aacgggggag gcgggagcgg gggcggcggc tcaggcggtg gggggtcctc tccaggtcaa 600

ggaacacaat ctgagaactc ctgcacacac ttccccggca atctaccaaa catgctcaga 660

gatctcaggg acgcgttcag tcgagtgaaa actttcttcc agatgaagga tcagctggac 720

aatctactgc tgaaagaaag cttgcttgag gattttaaag gctatctggg ttgtcaggcc 780

ttatcggaga tgatccagtt ttacttggag gaagttatgc ctcaggcaga aaaccaagac 840

cccgatatca aggctcatgt gaattccctc ggtgaaaacc taaagacctt acgcctgcgt 900

ctcagacggt gtcatcggtt tttgccatgc gagaataagt ccaaagccgt agagcaggtc 960

aagaatgcct tcaataagct ccaggagaag gggatataca aagcaatgag cgaatttgac 1020

attttcatca actacataga ggcctacatg accatgaaga tccggaactc tggaggcgga 1080

agcgggggtg gcggcagcgg cggtggagga tcaggtggcg gggggtccgg gggcggaagt 1140

ctgcagcatg ggaccgagct ccccagtcct ccttctgttt ggttcgaagc cgaattcttt 1200

caccatattc tgcactggac tcctatccca aatcaatcag aatcaacatg ttacgaggtg 1260

gcactgctga ggtacggaat cgagtcttgg aatagcattt caaactgtag ccaaaccctg 1320

tcttacgatc ttaccgctgt gacgctggac ctgtatcata gcaacggcta ccgtgccagg 1380

gttagggcag ttgatggcag cagacactcc aattggacag ttacgaatac ccgattcagt 1440

gtcgacgagg tgactttaac tgtcgggagt gttaaccttg aaattcacaa cgggttcata 1500

ttgggaaaga tccagctccc ccggccaaaa atggccccag ccaacgacac atacgagagt 1560

atattttctc attttagaga gtatgagatc gcaatccgca aggtgcctgg gaatttcaca 1620

tttactcata agaaggtaaa acacgagaac ttctccttgc tcacctccgg cgaagtgggg 1680

gagttctgcg tgcaggtgaa gccctcggtg gcttcacgct ccaataaagg catgtggagc 1740

aaagaagaat gtatttctct gactcggcag tactttaccg tgactaacgt aatcatattt 1800

tttgccttcg tgctcctgct gtctggtgcc ctggcctatt gcctggcgct tcaactttat 1860

gtgcggagga ggaagaagct gccgtccgtg ctgttgttta agaaaccgtc tcccttcatt 1920

tttatcagcc agcgcccctc acccgaaaca caggatacta ttcaccccct tgacgaagaa 1980

gccttcctta aagtgtcccc cgagctaaaa aacctcgacc tgcacgggtc caccgatagc 2040

gggtttggta gcaccaaacc atccttgcaa accgaggagc cccagttctt gctccctgat 2100

ccacacccac aggctgacag aacgttggga aacagagagc ccccagtcct gggggattcc 2160

tgttcgtcag ggtctagtaa tagtaccgat agcgggattt gcctgcagga gccgagcctg 2220

tcaccctcaa ccggtccgac ctgggagcag caagtaggat ctaactcccg cgggcaggat 2280

gactccggca tagacctcgt acagaattcg gaaggccggg cgggtgacac acagggcggc 2340

tccgctctgg gccaccattc cccaccagag cccgaggtcc ctggcgagga ggaccctgca 2400

gccgtcgctt ttcaaggcta tctgcgtcag acacgatgtg ctgaagagaa agctactaag 2460

acgggatgtc ttgaagagga atctccgctt acagacggat tgggaccaaa gttcggcaga 2520

tgcctagtgg atgaggcggg actacatcct cccgcattag caaagggcta cctgaagcag 2580

gatccactag aaatgacact ggcctcatct ggcgccccta caggacagtg gaaccagcca 2640

accgaagagt ggtccttgct cgctttaagc tcttgcagtg acctgggtat ctcagattgg 2700

agttttgcac acgacctcgc ccctctgggt tgcgtcgccg ctcctggtgg actcttagga 2760

agtttcaata gcgatctcgt cactctgcct ctcatcagta gcttacagag cagcgaa 2817

<210> 152
<211> 2064
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 152
atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60

ccgtctccgg gacagggaac ccagagcgaa aactcctgca ctcattttcc tggcaacctc 120

cccaatatgc tgcgagactt gcgcgacgca ttctcaaggg tgaagacgtt cttccagatg 180

aaggatcaac tggacaactt attgctgaaa gaatctctgc tcgaggattt caaaggatac 240

ctgggatgtc aggcactgag cgagatgatc caattttacc tggaggaggt catgcctcag 300

gctgagaatc aggatcctga catcaaggcc cacgtgaaca gtcttggaga gaatcttaag 360

acccttaggc tgagacttag acggtgtcac cgctttctgc cctgcgaaaa taaatcaaaa 420

gcggtggaac aggttaagaa cgcttttaat aagctgcagg aaaagggcat ttataaagct 480

atgagtgaat ttgacatttt cattaactat atcgaggcct atatgacaat gaaaattagg 540

aacgggggag gcgggagcgg gggcggcggc tcaggcggtg gggggtcctc tccaggtcaa 600

ggaacacaat ctgagaactc ctgcacacac ttccccggca atctaccaaa catgctcaga 660

gatctcaggg acgcgttcag tcgagtgaaa actttcttcc agatgaagga tcagctggac 720

aatctactgc tgaaagaaag cttgcttgag gattttaaag gctatctggg ttgtcaggcc 780

ttatcggaga tgatccagtt ttacttggag gaagttatgc ctcaggcaga aaaccaagac 840

cccgatatca aggctcatgt gaattccctc ggtgaaaacc taaagacctt acgcctgcgt 900

ctcagacggt gtcatcggtt tttgccatgc gagaataagt ccaaagccgt agagcaggtc 960

aagaatgcct tcaataagct ccaggagaag gggatataca aagcaatgag cgaatttgac 1020

attttcatca actacataga ggcctacatg accatgaaga tccggaactc tggaggcgga 1080

agcgggggtg gcggcagcgg cggtggagga tcaggtggcg gggggtccgg gggcggaagt 1140

ctgcagatgg taccaccacc tgaaaatgtg aggatgaact ctgtgaattt taagaacatt 1200

ctccagtggg aaagtcccgc ttttgctaag gggaacctga ccttcacagc ccaatactta 1260

tcctaccgaa tcttccaaga caagtgcatg aataccactt taactgaatg cgacttctca 1320

agcctgtcta agtatggcga tcatacactg cgggttcgtg ccgagtttgc cgacgagcac 1380

tctgactggg tgaatataac cttctgcccc gtcgatgata ctataattgg gccaccaggt 1440

atgcaagttg aagtgttggc agattcgctg cacatgaggt ttctcgcccc caaaatcgag 1500

aacgagtacg agacctggac gatgaagaat gtctacaact cttggacata taatgttcag 1560

tattggaaaa acggaaccga cgagaagttt cagatcactc cgcagtatga tttcgaagtc 1620

ctgagaaacc tcgagccttg gacaacttac tgtgtccaag tgcgcggctt tctccctgac 1680

cggaacaagg caggagagtg gtcagaaccg gtgtgtgagc agaccaccca cgacgagaca 1740

gtacccagct ggatggtagc tgtgatcctt atggcctccg tgttcatggt ttgtctagct 1800

ttgttgggct gttttgccct tctatggtgc gtctataaaa agaccaaata cgcgttttca 1860

cctagaaaca gccttccaca gcacctcaag gagttcctgg ggcatcctca tcacaataca 1920

ctgctgttct tctccttccc cctgagtgac gaaaacgatg tgtttgataa actgtccgtg 1980

attgcagaag acagtgagtc cggcaaacag aatccaggag atagttgcag cctgggtacg 2040

cctcccggac agggccccca gagc 2064

<210> 153
<211> 1725
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 153
atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60

ccgttaacat gtctgggcgg gttcgcctca cctggaccag ttccccttc aaccgctctc 120

agagaactga ttgaggagct cgtcaatatc acccagaacc aaaaagcccc actctgcaat 180

ggaagtatgg tgtggtctat taacttgact gccggcatgt actgtgccgc actggagtct 240

ttgatcaacg tgtccgggtg cagtgcaatc gaaaagacgc agcggatgct gagcggcttt 300

tgcccccaca aggtgagcgc tggtcagttt tccagccttc acgtgcgaga tacaaagata 360

gaagtagcgc agttcgtcaa ggacctgctg ctgcatctta aaaaactatt tcgcgagggt 420

aggttcaatt ctggaggcgg aagcgggggt ggcggcagcg gcggtggagg atcaggtggc 480

ggggggtccg ggggcggaag tctgcagggc ggcggcggcg cggcgccgac cgaaacccag 540

ccgccggtga ccaacctgag cgtgagcgtg gaaaacctgt gcaccgtgat ttggacctgg 600

aacccgccgg aaggcgcgag cagcaactgc agcctgtggt attttagcca ttttggcgat 660

aaacaggata aaaaaattgc gccggaaacc cgccgcagca ttgaagtgcc gctgaacgaa 720

cgcatttgcc tgcaggtggg cagccagtgc agcaccaacg aaagcgaaaa accgagcatt 780

ctggtggaaa aatgcattag cccgccggaa ggcgatccgg aaagcgcggt gaccgaactg 840

cagtgcattt ggcataacct gagctatatg aaatgcagct ggctgccggg ccgcaacacc 900

agcccggata ccaactatac cctgtattat tggcatcgca gcctggaaaa aattcatcag 960

tgcgaaaaca tttttcgcga aggccagtat tttggctgca gctttgatct gaccaaagtg 1020

aaagatagca gctttgaaca gcatagcgtg cagattatgg tgaaagataa cgcgggcaaa 1080

attaaaccga gctttaacat tgtgccgctg accagccgcg tgaaaccgga tccgccgcat 1140

attaaaaacc tgagctttca taacgatgat ctgtatgtgc agtgggaaaa cccgcagaac 1200

tttattagcc gctgcctgtt ttatgaagtg gaagtgaaca acagccagac cgaaacccat 1260

aacgtgtttt atgtgcagga agcgaaatgc gaaaacccgg aatttgaacg caacgtggaa 1320

aacaccagct gctttatggt gccgggcgtg ctgccggata ccctgaacac cgtgcgcatt 1380

cgcgtgaaaa ccaacaaact gtgctatgaa gatgataaac tgtggagcaa ctggagccag 1440

gaaatgagca ttggcaaaaa acgcaacagc accctgtata ttaccatgct gctgattgtg 1500

ccggtgattg tggcgggcgc gattattgtg ctgctgctgt atctgaaacg cctgaaaatt 1560

attatttttc cgccgattcc ggatccgggc aaaattttta aagaaatgtt tggcgatcag 1620

aacgatgata ccctgcattg gaaaaaatat gatatttatg aaaaacagac caaagaagaa 1680

accgatagcg tggtgctgat tgaaaacctg aaaaaagcga gccag 1725

<210> 154
<211> 2907
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 154
atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60

ccgttaacat gtctgggcgg gttcgcctca cctggaccag ttccccccttc aaccgctctc 120

agagaactga ttgaggagct cgtcaatatc acccagaacc aaaaagcccc actctgcaat 180

ggaagtatgg tgtggtctat taacttgact gccggcatgt actgtgccgc actggagtct 240

ttgatcaacg tgtccgggtg cagtgcaatc gaaaagacgc agcggatgct gagcggcttt 300

tgcccccaca aggtgagcgc tggtcagttt tccagccttc acgtgcgaga tacaaagata 360

gaagtagcgc agttcgtcaa ggacctgctg ctgcatctta aaaaactatt tcgcgagggt 420

aggttcaatt ctggaggcgg aagcgggggt ggcggcagcg gcggtggagg atcaggtggc 480

ggggggtccg ggggcggaag tctgcagatg aaagtgctgc aggaaccgac ctgcgtgagc 540

gattatatga gcattagcac ctgcgaatgg aaaatgaacg gcccgaccaa ctgcagcacc 600

gaactgcgcc tgctgtatca gctggtgttt ctgctgagcg aagcgcatac ctgcattccg 660

gaaaacaacg gcggcgcggg ctgcgtgtgc catctgctga tggatgatgt ggtgagcgcg 720

gataactata ccctggatct gtgggcgggc cagcagctgc tgtggaaagg cagctttaaa 780

ccgagcgaac atgtgaaacc gcgcgcgccg ggcaacctga ccgtgcatac caacgtgagc 840

gataccctgc tgctgacctg gagcaacccg tatccgccgg ataactatct gtataaccat 900

ctgacctatg cggtgaacat ttggagcgaa aacgatccgg cggattttcg catttataac 960

gtgacctatc tggaaccgag cctgcgcatt gcggcgagca ccctgaaaag cggcattagc 1020

tatcgcgcgc gcgtgcgcgc gtgggcgcag tgctataaca ccacctggag cgaatggagc 1080

ccgagcacca aatggcataa cagctatcgc gaaccgtttg aacagcatct gctgctgggc 1140

gtgagcgtga gctgcattgt gattctggcg gtgtgcctgc tgtgctatgt gagcattacc 1200

aaaattaaaa aagaatggtg ggatcagatt ccgaacccgg cgcgcagccg cctggtggcg 1260

attattattc aggatgcgca gggcagccag tgggaaaaac gcagccgcgg ccaggaaccg 1320

gcgaaatgcc cgcattggaa aaactgcctg accaaactgc tgccgtgctt tctggaacat 1380

aacatgaaac gcgatgaaga tccgcataaa gcggcgaaag aaatgccgtt tcagggcagc 1440

ggcaaaagcg cgtggtgccc ggtggaaatt agcaaaaccg tgctgtggcc ggaaagcatt 1500

agcgtggtgc gctgcgtgga actgtttgaa gcgccggtgg aatgcgaaga agaagaagaa 1560

gtggaagaag aaaaaggcag cttttgcgcg agcccggaaa gcagccgcga tgattttcag 1620

gaaggccgcg aaggcattgt ggcgcgcctg accgaaagcc tgtttctgga tctgctgggc 1680

gaagaaaacg gcggcttttg ccagcaggat atgggcgaaa gctgcctgct gccgccgagc 1740

ggcagcacca gcgcgcatat gccgtgggat gaatttccga gcgcgggccc gaaagaagcg 1800

ccgccgtggg gcaaagaaca gccgctgcat ctggaaccga gcccgccggc gagcccgacc 1860

cagagcccgg ataacctgac ctgcaccgaa accccgctgg tgattgcggg caacccggcg 1920

tatcgcagct ttagcaacag cctgagccag agcccgtgcc cgcgcgaact gggcccggat 1980

ccgctgctgg cgcgccatct ggaagaagtg gaaccggaaa tgccgtgcgt gccgcagctg 2040

agcgaaccga ccaccgtgcc gcagccggaa ccggaaacct gggaacagat tctgcgccgc 2100

aacgtgctgc agcatggcgc ggcggcggcg ccggtgagcg cgccgaccag cggctatcag 2160

gaatttgtgc atgcggtgga acagggcggc acccaggcga gcgcggtggt gggcctgggc 2220

ccgccgggcg aagcgggcta taaagcgttt agcagcctgc tggcgagcag cgcggtgagc 2280

ccggaaaaat gcggctttgg cgcgagcagc ggcgaagaag gctataaacc gtttcaggat 2340

ctgattccgg gctgcccggg cgatccggcg ccggtgccgg tgccgctgtt tacctttggc 2400

ctggatcgcg aaccgccgcg cagcccgcag agcagccatc tgccgagcag cagcccggaa 2460

catctgggcc tggaaccggg cgaaaaagtg gaagatatgc cgaaaccgcc gctgccgcag 2520

gaacaggcga ccgatccgct ggtggatagc ctgggcagcg gcattgtgta tagcgcgctg 2580

acctgccatc tgtgcggcca tctgaaacag tgccatggcc aggaagatgg cggccagacc 2640

ccggtgatgg cgagcccgtg ctgcggctgc tgctgcggcg atcgcagcag cccgccgacc 2700

accccgctgc gcgcgccgga tccgagcccg ggcggcgtgc cgctggaagc gagcctgtgc 2760

ccggcgagcc tggcgccgag cggcattagc gaaaaaagca aaagcagcag cagctttcat 2820

ccggcgccgg gcaacgcgca gagcagcagc cagaccccga aaattgtgaa ctttgtgagc 2880

gtgggcccga cctatatgcg cgtgagc 2907

<210> 155
<211> 1740
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 155
atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60

ccggtgagcg cgggccagtt tagcagcctg catgtgcgcg ataccaaaat tgaagtggcg 120

cagtttgtga aagatctgct gctgcatctg aaaaaactgt ttcgcgaagg ccgctttaac 180

ggaggaggtg gatctctgac ctgcctgggc ggctttgcga gcccgggccc ggtgccgccg 240

agcaccgcgc tgcgcgaact gattgaagaa ctggtgaaca ttacccagaa ccagaaagcg 300

ccgctgtgca acggcagcat ggtgtggagc attaacctga ccgcgggcat gtattgcgcg 360

gcgctggaaa gcctgattaa cgtgagcggc tgcagcgcga ttgaaaaaac ccagcgcatg 420

ctgagcggct tttgcccgca taaatctgga ggcggaagcg ggggtggcgg cagcggcggt 480

ggaggatcag gtggcggggg gtccgggggc ggaagtctgc agggcggcgg cggcgcggcg 540

ccgaccgaaa cccagccgcc ggtgaccaac ctgagcgtga gcgtggaaaa cctgtgcacc 600

gtgatttgga cctggaaccc gccggaaggc gcgagcagca actgcagcct gtggtatttt 660

agccattttg gcgataaaca ggataaaaaa attgcgccgg aaacccgccg cagcattgaa 720

gtgccgctga acgaacgcat ttgcctgcag gtgggcagcc agtgcagcac caacgaaagc 780

gaaaaaccga gcattctggt ggaaaaatgc attagcccgc cggaaggcga tccggaaagc 840

gcggtgaccg aactgcagtg catttggcat aacctgagct atatgaaatg cagctggctg 900

ccgggccgca acaccagccc ggataccaac tataccctgt attattggca tcgcagcctg 960

gaaaaaattc atcagtgcga aaacattttt cgcgaaggcc agtattttgg ctgcagcttt 1020

gatctgacca aagtgaaaga tagcagcttt gaacagcata gcgtgcagat tatggtgaaa 1080

gataacgcgg gcaaaattaa accgagcttt aacattgtgc cgctgaccag ccgcgtgaaa 1140

ccggatccgc cgcatattaa aaacctgagc tttcataacg atgatctgta tgtgcagtgg 1200

gaaaacccgc agaactttat tagccgctgc ctgttttatg aagtggaagt gaacaacagc 1260

cagaccgaaa cccataacgt gttttatgtg caggaagcga aatgcgaaaa cccggaattt 1320

gaacgcaacg tggaaaacac cagctgcttt atggtgccgg gcgtgctgcc ggataccctg 1380

aacaccgtgc gcattcgcgt gaaaaccaac aaactgtgct atgaagatga taaactgtgg 1440

agcaactgga gccaggaaat gagcattggc aaaaaacgca acagcaccct gtatattacc 1500

atgctgctga ttgtgccggt gattgtggcg ggcgcgatta ttgtgctgct gctgtatctg 1560

aaacgcctga aaattattat ttttccgccg attccggatc cgggcaaaat ttttaaagaa 1620

atgtttggcg atcagaacga tgataccctg cattggaaaa aatatgatat ttatgaaaaa 1680

cagaccaaag aagaaaccga tagcgtggtg ctgattgaaa acctgaaaaa agcgagccag 1740

<210> 156
<211> 2922
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 156
atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60

ccggtgagcg cgggccagtt tagcagcctg catgtgcgcg ataccaaaat tgaagtggcg 120

cagtttgtga aagatctgct gctgcatctg aaaaaactgt ttcgcgaagg ccgctttaac 180

ggaggaggtg gatctctgac ctgcctgggc ggctttgcga gcccgggccc ggtgccgccg 240

agcaccgcgc tgcgcgaact gattgaagaa ctggtgaaca ttacccagaa ccagaaagcg 300

ccgctgtgca acggcagcat ggtgtggagc attaacctga ccgcgggcat gtattgcgcg 360

gcgctggaaa gcctgattaa cgtgagcggc tgcagcgcga ttgaaaaaac ccagcgcatg 420

ctgagcggct tttgcccgca taaatctgga ggcggaagcg ggggtggcgg cagcggcggt 480

ggaggatcag gtggcggggg gtccgggggc ggaagtctgc agatgaaagt gctgcaggaa 540

ccgacctgcg tgagcgatta tatgagcatt agcacctgcg aatggaaaat gaacggcccg 600

accaactgca gcaccgaact gcgcctgctg tatcagctgg tgtttctgct gagcgaagcg 660

catacctgca ttccggaaaa caacggcggc gcgggctgcg tgtgccatct gctgatggat 720

gatgtggtga gcgcggataa ctataccctg gatctgtggg cgggccagca gctgctgtgg 780

aaaggcagct ttaaaccgag cgaacatgtg aaaccgcgcg cgccgggcaa cctgaccgtg 840

cataccaacg tgagcgatac cctgctgctg acctggagca acccgtatcc gccggataac 900

tatctgtata accatctgac ctatgcggtg aacatttgga gcgaaaacga tccggcggat 960

tttcgcattt ataacgtgac ctatctggaa ccgagcctgc gcattgcggc gagcaccctg 1020

aaaagcggca ttagctatcg cgcgcgcgtg cgcgcgtggg cgcagtgcta taacaccacc 1080

tggagcgaat ggagcccgag caccaaatgg cataacagct atcgcgaacc gtttgaacag 1140

catctgctgc tgggcgtgag cgtgagctgc attgtgattc tggcggtgtg cctgctgtgc 1200

tatgtgagca ttaccaaaat taaaaaagaa tggtgggatc agattccgaa cccggcgcgc 1260

agccgcctgg tggcgattat tattcaggat gcgcagggca gccagtggga aaaacgcagc 1320

cgcggccagg aaccggcgaa atgcccgcat tggaaaaact gcctgaccaa actgctgccg 1380

tgctttctgg aacataacat gaaacgcgat gaagatccgc ataaagcggc gaaagaaatg 1440

ccgtttcagg gcagcggcaa aagcgcgtgg tgcccggtgg aaattagcaa aaccgtgctg 1500

tggccggaaa gcattagcgt ggtgcgctgc gtggaactgt ttgaagcgcc ggtggaatgc 1560

gaagaagaag aagaagtgga agaagaaaaa ggcagctttt gcgcgagccc ggaaagcagc 1620

cgcgatgatt ttcaggaagg ccgcgaaggc attgtggcgc gcctgaccga aagcctgttt 1680

ctggatctgc tgggcgaaga aaacggcggc ttttgccagc aggatatggg cgaaagctgc 1740

ctgctgccgc cgagcggcag caccagcgcg catatgccgt gggatgaatt tccgagcgcg 1800

ggcccgaaag aagcgccgcc gtggggcaaa gaacagccgc tgcatctgga accgagcccg 1860

ccggcgagcc cgacccagag cccggataac ctgacctgca ccgaaacccc gctggtgatt 1920

gcgggcaacc cggcgtatcg cagctttagc aacagcctga gccagagccc gtgcccgcgc 1980

gaactgggcc cggatccgct gctggcgcgc catctggaag aagtggaacc ggaaatgccg 2040

tgcgtgccgc agctgagcga accgaccacc gtgccgcagc cggaaccgga aacctgggaa 2100

cagattctgc gccgcaacgt gctgcagcat ggcgcggcgg cggcgccggt gagcgcgccg 2160

accagcggct atcaggaatt tgtgcatgcg gtggaacagg gcggcaccca ggcgagcgcg 2220

gtggtgggcc tgggcccgcc gggcgaagcg ggctataaag cgtttagcag cctgctggcg 2280

agcagcgcgg tgagcccgga aaaatgcggc tttggcgcga gcagcggcga agaaggctat 2340

aaaccgtttc aggatctgat tccgggctgc ccgggcgatc cggcgccggt gccggtgccg 2400

ctgtttacct ttggcctgga tcgcgaaccg ccgcgcagcc cgcagagcag ccatctgccg 2460

agcagcagcc cggaacatct gggcctggaa ccgggcgaaa aagtggaaga tatgccgaaa 2520

ccgccgctgc cgcaggaaca ggcgaccgat ccgctggtgg atagcctggg cagcggcatt 2580

gtgtatagcg cgctgacctg ccatctgtgc ggccatctga aacagtgcca tggccaggaa 2640

gatggcggcc agaccccggt gatggcgagc ccgtgctgcg gctgctgctg cggcgatcgc 2700

agcagcccgc cgaccacccc gctgcgcgcg ccggatccga gcccgggcgg cgtgccgctg 2760

gaagcgagcc tgtgcccggc gagcctggcg ccgagcggca ttagcgaaaa aagcaaaagc 2820

agcagcagct ttcatccggc gccgggcaac gcgcagagca gcagccagac cccgaaaatt 2880

gtgaactttg tgagcgtggg cccgacctat atgcgcgtga gc 2922

<210> 157
<211> 2181
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 157
atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60

ccgtattttg gcaaactcga aagtaagctg agcgtgattc ggaatcttaa cgatcaggtg 120

ttattcatcg atcaaggcaa cagaccactc tttgaagata tgacagattc agactgtagg 180

gataatgccc ctaggaccat ctttattata agcatgtata aggactctca gccccgcggt 240

atggcagtaa cgattagcgt taagtgcgag aagatttcta cactttcatg cgaaaacaaa 300

atcatctcct tcaaagagat gaaccctccc gataatatca aagataccaa gtcggacata 360

attttctttc agagatccgt cccaggacac gacaataaga tgcaattcga atccagcagt 420

tacgagggat actttctggc ttgtgagaag gaacgtgact tgttcaaact gatcctgaag 480

aaagaggacg agctagggga ccgatctatc atgttcactg tgcagaacga ggactctgga 540

ggcggaagcg ggggtggcgg cagcggcggt ggaggatcag gtggcggggg gtccgggggc 600

ggaagtctgc aggccgagag ctgcactagc cggccccata taactgtggt cgaaggggag 660

ccattctatc tgaaacattg ttcctgctcc cttgcccatg aaattgaaac cacaaccaag 720

agctggtaca aatctagtgg gtctcaagag cacgtcgagt tgaacccaag atcatctagt 780

aggatcgccc tgcatgactg cgttctagag ttttggccgg tggaattaaa tgacaccgga 840

tcttacttct tccagatgaa gaattacacc cagaaatgga agctgaacgt gatacgacgc 900

aacaagcact catgcttcac agaacgtcag gtgacctcga aaatcgtgga agtgaaaaag 960

ttctttcaga ttacatgcga gaacagttac tatcaaacgc tagtgaatag cacgagcctg 1020

tacaaaaact gtaagaaact tctgctggag aacaataaaa accctactat caaaaaaaat 1080

gcagaattcg aggatcaggg ctattacagt tgtgtgcatt ttctccacca caatggtaag 1140

ctattcaata tcaccaagac gttcaacatc accattgtgg aggatcgctc caacatagta 1200

cctgtgttat tgggtcctaa acttaaccac gtggcagtgg agctggggaa aaacgtgaga 1260

ctcaattgct cagccttgct gaacgaagag gatgttattt attggatgtt tggggaagaa 1320

aatggaagtg acccgaacat tcacgaagag aaggagatgc gaatcatgac accagagggg 1380

aaatggcacg cgagtaaggt cctcagaatt gaaaatattg gcgaatcaaa tctcaacgtc 1440

ctctataact gtaccgtagc atccacaggc ggcactgata ctaagtcctt tatccttgtg 1500

cgtaaggccg atatggctga catccccggc cacgtattca cacggggaat gatcattgct 1560

gttctgatcc tggtggcagt agtgtgtttg gttactgtat gtgttatcta ccgcgtggac 1620

ttagttctgt tttataggca cctgacccga agagacgaaa cccttacaga tggcaagact 1680

tatgacgcgt tcgtgtcgta tcttaaagaa tgccggcccg agaatggaga ggagcacacg 1740

tttgctgtcg aaattctccc cagagtcctg gagaagcatt ttggttacaa gctgtgcatc 1800

ttcgaaagag acgtcgtgcc cggtggcgcc gtggtcgacg agatacattc cctgatcgag 1860

aagtcccgca ggttgatcat agtcctctca aagtcttaca tgagcaatga ggtgcggtac 1920

gaactcgaga gcggactgca tgaggcttta gtcgagagga agattaagat tattttgatc 1980

gagtttacac ctgtgactga ctttaccttc ctccctcagt cactgaaact ccttaagtct 2040

cacagggtac tgaagtggaa agctgataaa tccctctctt ataatagccg gttttggaag 2100

aacctattgt acctgatgcc agccaaaaca gtcaagcctg gacgcgatga gcccgaagtt 2160

ctgccagttc tgagcgagtc c 2181

<210> 158
<211> 2352
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 158
atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60

ccgtattttg gcaaactcga aagtaagctg agcgtgattc ggaatcttaa cgatcaggtg 120

ttattcatcg atcaaggcaa cagaccactc tttgaagata tgacagattc agactgtagg 180

gataatgccc ctaggaccat ctttattata agcatgtata aggactctca gccccgcggt 240

atggcagtaa cgattagcgt taagtgcgag aagatttcta cactttcatg cgaaaacaaa 300

atcatctcct tcaaagagat gaaccctccc gataatatca aagataccaa gtcggacata 360

attttctttc agagatccgt cccaggacac gacaataaga tgcaattcga atccagcagt 420

tacgagggat actttctggc ttgtgagaag gaacgtgact tgttcaaact gatcctgaag 480

aaagaggacg agctagggga ccgatctatc atgttcactg tgcagaacga ggactctgga 540

ggcggaagcg ggggtggcgg cagcggcggt ggaggatcag gtggcggggg gtccgggggc 600

ggaagtctgc agtttaatat ctctggatgc agtacgaaga aattgctctg gacatactct 660

actaggagcg aggaagagtt cgtgcttttc tgcgatttac cagaaccaca gaaatcccat 720

ttttgtcaca gaaatcgtct ttctcctaag caggttcccg aacacctgcc cttcatgggc 780

tccaacgacc ttagtgacgt tcaatggtac cagcaaccaa gcaatggcga ccctctggaa 840

gacatacgca agagttaccc ccatattatc caggataaat gcacgctaca tttcctgacc 900

ccaggcgtca acaacagtgg atcttatata tgtaggccta agatgatcaa atccccctac 960

gacgtggctt gttgcgtcaa gatgattctc gaggtgaagc cccagaccaa tgcctcatgt 1020

gagtactccg cctctcacaa acaggacctt ctgctggggt cgaccggcag tataagctgc 1080

ccatcgctct cttgtcagag tgatgcgcag agccctgctg tgacatggta caaaaacgga 1140

aagctactgt cagtggagcg ctcaaaccgt attgtagtag acgaagtcta cgactatcac 1200

caaggcacct acgtgtgcga ttatacacag tctgatacgg tctccagttg gactgtgcgg 1260

gccgtggtgc aggtacggac catcgtgggg gacacaaaac tgaagcccga catccttgat 1320

ccagttgagg acaccctgga ggtggagctc gggaagcccc tgactatctc ctgtaaagca 1380

agatttggct tcgagcgagt atttaaccct gttatcaagt ggtatattaa agatagcgat 1440

ctcgagtggg aggtatcagt gcctgaagcc aaatccatca aatcaactct gaaggatgaa 1500

atcattgagc gaaatattat tcttgagaag gttacccagc gcgatctccg ccgcaaattt 1560

gtctgcttcg tgcaaaacag cataggcaat actactcaga gcgtgcagct gaaagagaag 1620

cgtggtgtcg tcttgttgta catcctgctc ggaacaattg gtacactcgt agccgtgttg 1680

gccgcctcag ccctgctcta caggcattgg attgaaatcg tgttgcttta caggacatat 1740

cagagcaagg accagactct gggcgacaaa aaggatttcg atgcattcgt tagctatgct 1800

aaatggtctt catttcctag cgaagctaca tcctccctga gcgaggaaca cttagcctta 1860

tcactgtttc cagatgtgtt agaaaataaa tatggctata gcctgtgttt gctggagcgc 1920

gacgttgcac cagggggggt gtatgctgaa gacatcgtca gcatcatcaa gcggtccagg 1980

aggggaatat ttatattaag ccctaactac gtcaacggtc catcgatttt cgaactgcag 2040

gctgcagtga acttggcgct cgatgaccag acgctcaagc tgattctcat caagttctgc 2100

tactttcaag agcccgagtc tcttcctcac ctagtcaaga aggcgctgag agtcctgccg 2160

accgtgacat ggcgaggact aaagtctgtg ccgccgaatt ccagattctg ggcaaagatg 2220

cggtatcata tgcccgttaa aaattcccaa ggttttactt ggaaccagct gcggattacc 2280

agtcggatct tccagtggaa ggggctgtct agaaccgaga ccaccggaag atccagtcaa 2340

cccaaagaat gg 2352

<210> 159
<211> 246
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 159
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Val Asn Thr Ala
20 25 30

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

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

Ser Arg Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro Pro
85 90 95

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

Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Glu Val Gln Leu
115 120 125

Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu
130 135 140

Ser Cys Ala Ala Ser Gly Phe Asn Ile Lys Asp Thr Tyr Ile His Trp
145 150 155 160

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Tyr
165 170 175

Pro Thr Asn Gly Tyr Thr Arg Tyr Ala Asp Ser Val Lys Gly Arg Phe
180 185 190

Thr Ile Ser Ala Asp Thr Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn
195 200 205

Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ser Arg Trp Gly
210 215 220

Gly Asp Gly Phe Tyr Ala Met Asp Val Trp Gly Gln Gly Thr Leu Val
225 230 235 240

Thr Val Ser Ser Ser Gly
245

<210> 160
<211> 45
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 160
Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala
1 5 10 15

Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly
20 25 30

Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp
35 40 45

<210> 161
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 161
Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu
1 5 10 15

Ser Leu Val Ile Thr Leu Tyr Cys
20

<210> 162
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 162
Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly
1 5 10 15

Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr
20 25 30

Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys
35 40 45

Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys

50 55 60

Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg
65 70 75 80

Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala
85 90 95

Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
100 105 110

<210> 163
<211> 448
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 163
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu
20 25 30

Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln
35 40 45

Asp Val Asn Thr Ala Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala
50 55 60

Pro Lys Leu Leu Ile Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro
65 70 75 80

Ser Arg Phe Ser Gly Ser Arg Ser Gly Thr Asp Phe Thr Leu Thr Ile
85 90 95

Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His

```
            100                 105                 110

Tyr Thr Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
        115                 120                 125

Arg Thr Gly Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly
    130                 135                 140

Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
145                 150                 155                 160

Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Asn Ile Lys Asp
                165                 170                 175

Thr Tyr Ile His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
            180                 185                 190

Val Ala Arg Ile Tyr Pro Thr Asn Gly Tyr Thr Arg Tyr Ala Asp Ser
        195                 200                 205

Val Lys Gly Arg Phe Thr Ile Ser Ala Asp Thr Ser Lys Asn Thr Ala
    210                 215                 220

Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr
225                 230                 235                 240

Cys Ser Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Val Trp Gly
                245                 250                 255

Gln Gly Thr Leu Val Thr Val Ser Ser Ser Gly Thr Thr Thr Pro Ala
            260                 265                 270

Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser
        275                 280                 285

Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr
    290                 295                 300
```

```
Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala
305                 310                 315                 320


Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys
                325                 330                 335


Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly
            340                 345                 350


Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr
        355                 360                 365


Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys
    370                 375                 380


Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys
385                 390                 395                 400


Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg
                405                 410                 415


Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala
            420                 425                 430


Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
        435                 440                 445


<210> 164
<211> 63
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide

<400> 164
atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg       60

ccg                                                                     63
```

<210> 165
<211> 738
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 165
gacattcaaa tgacacagag tccctcatcc ctcagtgcca gcgtgggcga tcgggtgact 60

ataacctgca gagcttctca ggacgtgaat accgctgtgg cgtggtacca gcagaagcca 120

ggcaaagcgc ctaagcttct catttatagt gccagcttcc tgtactcagg tgttccgtct 180

cgcttttctg gaagtagaag tgggaccgat ttcacattga cgatcagcag cttgcagccc 240

gaagatttcg ccacctacta ctgtcagcag cactacacta ccccaccgac atttggtcaa 300

ggcacaaaag tagagattaa acgcactggt tccaccagcg ggagcgggaa acccggctct 360

ggggagggga gcgaggtcca gctggtggaa tccgggggtg gtcttgtgca gccaggagga 420

tccttgaggt tgtcctgcgc cgcaagcggc tttaacatca aagatacata catccattgg 480

gtccgacagg cccctggaaa gggcctggag tgggtcgccc ggatctaccc aactaacggg 540

tacactcgct acgctgatag cgtcaagggt cggtttacta tttctgccga cacctcaaaa 600

aacacagcct acctccagat gaactctctc agagctgagg atacagccgt gtactattgc 660

agccggtggg gaggcgacgg gttctacgct atggatgtgt gggggcaggg cacactggtc 720

accgtgagct catccgga 738

<210> 166
<211> 135
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 166
accacgacgc cagcgccgcg accaccaaca ccggcgccca ccatcgcgtc gcagcccctg 60

tccctgcgcc cagaggcgtg ccggccagcg gcgggggcg cagtgcacac gagggggctg 120

gacttcgcct gtgat 135

<210> 167
<211> 72
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 167
atctacatct gggcgccctt ggccgggact tgtggggtcc ttctcctgtc actggttatc 60

acccttact gc 72

<210> 168
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 168
agagtgaagt tcagcaggag cgcagacgcc cccgcgtacc agcagggcca gaaccagctc 60

tataacgagc tcaatctagg acgaagagag gagtacgatg ttttggacaa gagacgtggc 120

cgggaccctg agatgggggg aaagccgaga aggaagaacc ctcaggaagg cctgtacaat 180

gaactgcaga aagataagat ggcggaggcc tacagtgaga ttgggatgaa aggcgagcgc 240

cggaggggca aggggcacga tggcctttac cagggtctca gtacagccac caaggacacc 300

tacgacgccc ttcacatgca ggccctgccc cctcgc 336

<210> 169
<211> 1344
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 169
atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60

ccggacattc aaatgacaca gagtccctca tccctcagtg ccagcgtggg cgatcgggtg 120

actataacct gcagagcttc tcaggacgtg aataccgctg tggcgtggta ccagcagaag 180

ccaggcaaag cgcctaagct tctcatttat agtgccagct tcctgtactc aggtgttccg 240

tctcgctttt ctggaagtag aagtgggacc gatttcacat tgacgatcag cagcttgcag 300

cccgaagatt tcgccaccta ctactgtcag cagcactaca ctaccccacc gacatttggt 360

caaggcacaa aagtagagat taaacgcact ggttccacca gcgggagcgg gaaacccggc 420

tctggggagg ggagcgaggt ccagctggtg gaatccgggg gtggtcttgt gcagccagga 480

ggatccttga ggttgtcctg cgccgcaagc ggctttaaca tcaaagatac atacatccat 540

tgggtccgac aggcccctgg aaagggcctg gagtgggtcg cccggatcta cccaactaac 600

gggtacactc gctacgctga tagcgtcaag ggtcggttta ctatttctgc cgacacctca 660

aaaaacacag cctacctcca gatgaactct ctcagagctg aggatacagc cgtgtactat 720

tgcagccggt ggggaggcga cgggttctac gctatggatg tgtgggggca gggcacactg 780

gtcaccgtga gctcatccgg aaccacgacg ccagcgccgc gaccaccaac accggcgccc 840

accatcgcgt cgcagcccct gtccctgcgc ccagaggcgt gccggccagc ggcgggggggc 900

gcagtgcaca cgagggggct ggacttcgcc tgtgatatct acatctgggc gcccttggcc 960

gggacttgtg gggtccttct cctgtcactg gttatcaccc tttactgcag agtgaagttc 1020

agcaggagcg cagacgcccc cgcgtaccag cagggccaga accagctcta taacgagctc 1080

aatctaggac gaagagagga gtacgatgtt ttggacaaga gacgtggccg ggaccctgag 1140

atgggggggaa agccgagaag gaagaaccct caggaaggcc tgtacaatga actgcagaaa 1200

gataagatgg cggaggccta cagtgagatt gggatgaaag gcgagcgccg gaggggcaag 1260

gggcacgatg gcctttacca gggtctcagt acagccacca aggacaccta cgacgccctt 1320

cacatgcagg ccctgccccc tcgc 1344

<210> 170
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<220>
<221> SITE
<222> (1)..(25)
<223> This sequence may encompass 1-5 "Gly Gly Gly Gly Ser"
repeating units

<400> 170
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
1 5 10 15

Gly Gly Gly Ser Gly Gly Gly Gly Ser
20 25

<210> 171
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 171
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10 15

<210> 172
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 172

Gly Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr
1   5   10   15

Lys Gly

<210> 173
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 173
Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
1   5   10   15

Gly Gly Gly Ser Gly Gly Gly Ser Leu Gln
            20   25

<210> 174
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 174
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1   5   10   15

His Ala Ala Arg Pro
            20

<210> 175
<211> 5
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 175
Gly Gly Gly Gly Ser
1 5

<210> 176
<211> 400
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<220>
<221> misc_feature
<222> (1)..(400)
<223> This sequence may encompass 10-400 nucleotides

<220>
<223> See specification as filed for detailed description of
substitutions and preferred embodiments

<400> 176
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 60

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 120

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 180

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 240

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 300

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 360

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 400

<210> 177
<211> 200
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

polynucleotide

<220>
<221> misc_feature
<222> (1)..(200)
<223> This sequence may encompass 10-200 nucleotides

<220>
<223> See specification as filed for detailed description of
substitutions and preferred embodiments

<400> 177
ccccccccc ccccccccc ccccccccc ccccccccc ccccccccc ccccccccc 60

ccccccccc ccccccccc ccccccccc ccccccccc ccccccccc ccccccccc 120

ccccccccc ccccccccc ccccccccc ccccccccc ccccccccc ccccccccc 180

ccccccccc ccccccccc 200