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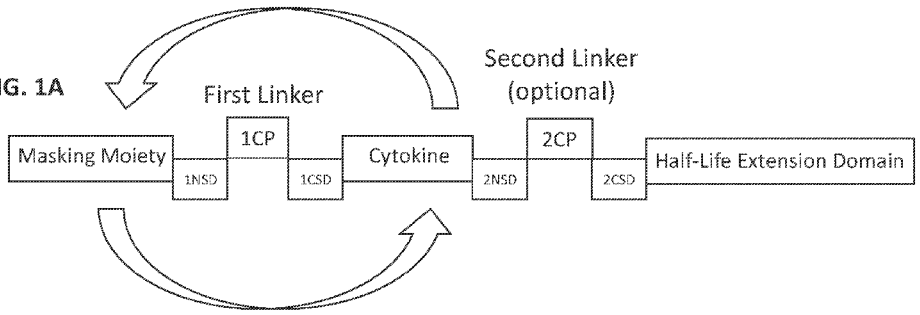
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(54) Title: MASKED CYTOKINE POLYPEPTIDES

FIG. 1A



(57) Abstract: Provided herein are cytokines or functional fragments thereof that, in some embodiments, are engineered to be masked by a masking moiety at one or more receptor binding site(s) of the cytokine or functional fragment thereof. In some embodiments, the cytokines are engineered to be activatable by a protease at a target site, such as in a tumor microenvironment, by including a proteolytically cleavable linker. In some embodiments, the proteolytically cleavable linker links the cytokine to the masking moiety, links the cytokine to a half-life extension domain, and/or links the masking moiety to a half-life extension domain. The masking moiety blocks, occludes, inhibits (e.g., decreases) or otherwise prevents (e.g., masks) the activity or binding of the cytokine to its cognate receptor or protein. Upon proteolytic cleavage of the cleavable linker at the target site, the cytokine becomes activated, which renders it capable of binding to its cognate receptor or protein with increased affinity.

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MASKED CYTOKINE POLYPEPTIDES

CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] This application claims priority to U.S. Provisional Application No. 62/737,803, filed September 27, 2018, U.S. Provisional Application No. 62/888,276, filed August 16, 2019, and U.S. Provisional Application No. 62/891,199, filed August 23, 2019. The contents of the above-listed applications are incorporated herein by this reference in their entirety for all purposes.

INCORPORATION BY REFERENCE OF SEQUENCE LISTING

[0002] The present application is being filed along with a Sequence Listing in electronic format. The Sequence Listing is provided as a file entitled 737762000940SeqList, created September 26, 2019, which is 1,024.111 KB in size. The information in the electronic format of the Sequence Listing is incorporated by reference in its entirety.

FIELD

[0003] This invention relates to masked cytokines and methods related to the use and manufacture of the same.

BACKGROUND

[0004] Cancer is the second leading cause of death in the United States, accounting for more deaths than the next five leading causes (chronic respiratory disease, stroke, accidents, Alzheimer's disease and diabetes). While great strides have been made especially with targeted therapies, there remains a great deal of work to do in this space. Immunotherapy and a branch of this field, immuno-oncology, is creating viable and exciting therapeutic options for treating malignancies. Specifically, it is now recognized that one hallmark of cancer is immune evasion and significant efforts have identified targets and developed therapies to these targets to reactivate the immune system to recognize and treat cancer.

[0005] Cytokine therapy is an effective strategy for stimulating the immune system to induce anti-tumor cytotoxicity. For example, aldesleukin, a recombinant form of interleukin-2 (IL-2), has been approved by the FDA for the treatment of metastatic renal cell carcinoma and melanoma. Unfortunately, cytokines that are administered to patients generally have a very short half-life, thereby requiring frequent dosing. For instance, the product label of aldesleukin, marketed under the brand name Proleukin, states that the drug was shown to have a half-life of 85 minutes in patients who received a 5-minute intravenous (IV) infusion. In addition, administration of high doses of cytokine can cause

adverse health outcomes, such as vascular leakage, through systemic immune activation. These findings illustrate the need for developing cytokine therapeutics that effectively target tumors without the side effects associated with systemic immune activation. Provided herein are masked cytokines, compositions thereof and methods of use thereof for addressing this need.

[0006] All references cited herein, including patent applications, patent publications, and scientific literature, are herein incorporated by reference in their entirety, as if each individual reference were specifically and individually indicated to be incorporated by reference.

[0006a] It is to be understood that if any prior art publication is referred to herein, such reference does not constitute an admission that the publication forms a part of the common general knowledge in the art in Australia or any other country.

SUMMARY

[0007] The disclosed invention relates to the engineering and use of masked cytokines or functional fragments thereof that, in some embodiments, are engineered to be masked by a masking moiety at one or more receptor binding site(s) of the cytokine or functional fragment thereof. In some embodiments, the cytokines are engineered to be activatable by a protease at a target site, such as in a tumor microenvironment, by including a proteolytically cleavable linker. In some embodiments, the proteolytically cleavable linker links the cytokine to the masking moiety, links the cytokine to a half-life extension domain, and/or links the masking moiety to a half-life extension domain. The masking moiety blocks, occludes, inhibits (e.g., decreases) or otherwise prevents (e.g., masks) the activity or binding of the cytokine to its cognate receptor or protein. Upon proteolytic cleavage of the cleavable linker at the target site, the cytokine becomes activated, which renders it capable of binding to its cognate receptor or protein with increased affinity.

[0008] One embodiment comprises a masked cytokine comprising a masking moiety; and a cytokine or functional fragment thereof, wherein the masking moiety is linked to the cytokine or functional fragment thereof via a linker. In one aspect, the masked cytokine further comprises a half-life extension domain that is linked to either the masking moiety or the cytokine or functional fragment thereof.

[0009] In one embodiment, the masked cytokine comprises in an N to C-terminal or in a C to N-terminal direction: a) a masking moiety; b) a first linker; c) a cytokine or functional fragment thereof; and d) a half-life extension domain. In another embodiment, the masked cytokine comprises in an N to C-terminal or in a C to N-terminal direction: a) a masking moiety; b) a first linker; c) a cytokine or functional fragment thereof; d) a second linker and e) a half-life extension domain. In another embodiment, the masked cytokine comprises in an N to C-terminal or in a C to N-terminal direction: a) a

cytokine or functional fragment thereof; b) a first linker; c) a masking moiety; and d) a half-life extension domain.

[0010] In another embodiment, the masked cytokine comprises in an N to C-terminal or in a C to N-terminal direction: a) a cytokine or functional fragment thereof; b) a first linker; c) a masking moiety; d) a second linker; and e) a half-life extension domain.

[0011] In one embodiment, the cytokine or functional fragment thereof is an IL-2 polypeptide or functional fragment thereof or an IL-15 polypeptide or functional fragment thereof.

[0012] In one embodiment, the masked cytokine one or more amino acid substitutions into the amino acid sequence of the IL-2 or IL-15 polypeptide or functional fragment thereof. In one embodiment, the amino acid substitutions reduce the affinity of the IL-2 polypeptide or functional fragment thereof for CD25 (IL-2Rα).

[0013] In one embodiment, the IL-2 polypeptide or functional fragment thereof comprises an amino acid sequence produced by introducing one or more amino acid substitutions into the amino acid sequence of the IL-2 polypeptide or functional fragment thereof that increases the affinity of the IL-2 polypeptide or functional fragment thereof for IL-2Rβ or IL-2Rγ.

[0014] In one embodiment, the half-life extension domain is an antibody or fragment thereof, and in some embodiments, one or more amino acid substitutions altering effector function.

[0015] In one embodiment, the antibody or fragment thereof is a Fragment crystallizable domain (Fc domain) or fragment thereof.

[0016] In one embodiment, the half-life extension domain is a polyamino acid sequence, such as a PAS polypeptide or an XTEN polypeptide.

[0017] In one embodiment the masked cytokine comprises a second masking moiety, wherein the second masking moiety is linked to the cytokine or functional fragment thereof via a second linker.

[0018] In one embodiment, the masked cytokine comprises in an N to C-terminal or in a C to N-terminal direction: a) a first masking moiety; b) a first linker; c) a cytokine or functional fragment thereof; d) a second linker; e) a second masking moiety; and f) a half-life extension domain.

[0019] In one embodiment, the masked cytokine comprises in an N to C-terminal or in a C to N-terminal direction: a) a first masking moiety; b) a first linker; c) a cytokine or functional fragment thereof; d) a second linker; e) a second masking moiety; f) a third linker; and g) a half-life extension domain.

[0020] In one embodiment, the masked cytokine comprises in an N to C-terminal or in a C to N-terminal direction: a) a second masking moiety; b) a second linker; c) a cytokine or functional fragment thereof; d) a first linker; e) a first masking moiety; and f) a half-life extension domain.

[0021] In one embodiment, the masked cytokine comprises in an N to C-terminal or in a C to N-terminal direction: a) a second masking moiety; b) a second linker; c) a cytokine or functional fragment thereof; d) a first linker; e) a first masking moiety; f) a third linker; and g) a half-life extension domain.

[0022] In one embodiment, the half-life extension domain is an albumin polypeptide or functional fragment thereof.

[0023] In one embodiment, the cleavable peptide is cleaved by one or more enzyme selected from the group consisting of: ABHD12, ADAM12, ABHD12B, ABHD13, ABHD17A, ADAM19, ADAM20,

ADAM21, ADAM28, ADAM30, ADAM33, ADAM8, ABHD17A, ADAMDEC1, ADAMTS1, ADAMTS10, ADAMTS12, ADAMTS13, ADAMTS14, ADAMTS15, ADAMTS16, ADAMTS17, ADAMTS18, ADAMTS19, ADAMTS2, ADAMTS20, ADAMTS3, ADAMTS4, ABHD17B, ADAMTS5, ADAMTS6, ADAMTS7, ADAMTS8, ADAMTS9, ADAMTSL1, ADAMTSL2, ADAMTSL3, ABHD17C, ADAMTSL5, ASTL, BMP1, CELA1, CELA2A, CELA2B, CELA3A, CELA3B, ADAM10, ADAM15, ADAM17, ADAM9, ADAMTS4, CTSE, CTSF, ADAMTSL4, CMA1, CTRB1, CTRC, CTSO, CTRl, CTSA, CTSW, CTSB, CTSC, CTSD, ESP1, CTSG, CTSH, GZMA, GZMB, GZMH, CTSK, GZMM, CTSL, CTSS, CTSV, CTSZ, HTRA4, KLK10, KLK11, KLK13, KLK14, KLK2, KLK4, DPP4, KLK6, KLK7, KLKB1, ECE1, ECE2, ECEL1, MASP2, MEP1A, MEP1B, ELANE, FAP, GZMA, MMP11, GZMK, HGFAC, HPN, HTRA1, MMP11, MMP16, MMP17, MMP19, HTRA2, MMP20, MMP21, HTRA3, HTRA4, KEL, MMP23B, MMP24, MMP25, MMP26, MMP27, MMP28, KLK5, MMP3, MMP7, MMP8, MMP9, LGMN, LNPEP, MASP1, PAPPA, PAPPA2, PCSK1, NAPSA, PCSK5, PCSK6, MME, MMP1, MMP10, PLAT, PLAU, PLG, PRSS1, PRSS12, PRSS2, PRSS21, PRSS3, PRSS33, PRSS4, PRSS55, PRSS57, MMP12, PRSS8, PRSS9, PRTN3, MMP13, MMP14, ST14, TMPRSS10, TMPRSS11A, TMPRSS11D, TMPRSS11E, TMPRSS11F, TMPRSS12, TMPRSS13, MMP15, TMPRSS15, MMP2, TMPRSS2, TMPRSS3, TMPRSS4, TMPRSS5, TMPRSS6, TMPRSS7, TMPRSS9, NRDC, OVCH1, PAMR1, PCSK3, PHEX, TINAG, TPSAB1, TPSD1, and TPSG1.

[0024] In one embodiment, the half-life extension domain is conjugated to an agent, such as an inhibitor of tubulin polymerization, a DNA damaging agent, or a DNA synthesis inhibitor, a maytansinoid, an auristatin, a pyrrolobenzodiazepine (PBD) dimer, a calicheamicin, a duocarmycin, a indo-linobenzodiazepine dimer or exatecan derivative Dxd.

[0025] In one embodiment, the half-life extension domain is conjugated to an immune stimulant, such as a stimulator of interferon genes (STING) agonist, such as a cyclic dinucleotide (CDN), such as cGAMP, c-di-AMP, c-di-GMP, cAIMP, c-di-IMP, or 4-(2-chloro-6-fluorobenzyl)-N-(furan-2-ylmethyl)-3-oxo-3,4-dihydro-2H-benzo[b][1,4]thiazine-6-carboxamide or a toll-like receptor (TLR) agonist, such as TLR1, TLR2, TLR3, TLR4, TLR5, TLR6, TLR7, TLR8, TLR9, or TLR10.

[0026] In one embodiment, the masked cytokine comprises a first half-life extension domain and a second half-life extension domain, wherein the masking moiety is linked to the first half-life extension domain, and wherein the cytokine or functional fragment thereof is linked to the second half-life extension domain,

[0027] In one embodiment, the first half-life extension domain and the second half-life extension domain contain modifications promoting the association of the first and the second half-life extension domain.

[0028] One embodiment comprises a nucleic acid encoding the masked cytokines described herein. Another embodiment encompasses a vector comprising the nucleic acid. In another embodiment a host

cell comprising the nucleic acid. Another embodiment comprises one or more nucleic acids encoding the masked cytokines described herein. Another embodiment encompasses a vector comprising the one or more nucleic acids. Another embodiment encompasses one or more vectors comprising the one or more nucleic acids.

[0029] In another embodiment is provided a method of producing a masked cytokine comprising culturing the host cell under a condition that produces the masked cytokine. In one embodiment, the masked cytokine produced by the host cell is recovered. One embodiment encompasses a masked cytokine produced by the disclosed methods.

[0030] In one embodiment, a composition comprising a disclosed masked cytokine is provided. In another embodiment, the composition further comprises an anti-inflammatory agent or an anti-cancer agent, such as a PD-1 inhibitor, an EGFR inhibitor, a HER2 inhibitor , a VEGFR inhibitor, a CTLA-4 inhibitor, a BTLA inhibitor, a B7H4 inhibitor, a B7H3 inhibitor, a CSFIR inhibitor, an HVEM inhibitor, a CD27 inhibitor, a KIR inhibitor, an NKG2A inhibitor, an NKG2D agonist, a TWEAK inhibitor, an ALK inhibitor, a CD52 targeting antibody, a CCR4 targeting antibody, a PD-L1 inhibitor, a KIT inhibitor, a PDGFR inhibitor, a BAFF inhibitor, an HDAC inhibitor, a VEGF ligand inhibitor, a CD19 targeting molecule, a FOLR1 targeting molecule, a DLL3 targeting molecule, a DKK1 targeting molecule, a MUC1 targeting molecule, a MUC16 targeting molecule, a PSMA targeting molecule, an MSLN targeting molecule, an NY-ES0-1 targeting molecule, a B7H3 targeting molecule, a B7H4 targeting molecule, a BCMA targeting molecule, a CD29 targeting molecule, a CD151targeting molecule, a CD123 targeting molecule, a CD33 targeting molecule, a CD37 targeting molecule, a CDH19 targeting molecule, a CEA targeting molecule, a Claudin 18.2 targeting molecule, a CLEC12A targeting molecule, an EGFRVIII targeting molecule, an EPCAM targeting molecule, an EPHA2 targeting molecule, an FCRH5 targeting molecule, an FLT3 targeting molecule, a GD2 targeting molecule, a glypican 3 targeting molecule, a gpA33 targeting molecule, a GPRC5D targeting molecule, an IL-23R targeting molecule, an IL-1RAP targeting molecule, a MCSP targeting molecule, a RON targeting molecule, a ROR1 targeting molecule, a STEAP2 targeting molecule, a TfR targeting molecule, a CD166 targeting molecule, a TPBG targeting molecule, a TROP2 targeting molecule, a proteasome inhibitor, an ABL inhibitor, a CD30 inhibitor, a FLT3 inhibitor, a MET inhibitor, a RET inhibitor, an IL-1β inhibitor, a MEK inhibitor, a ROS1 inhibitor, a BRAF inhibitor, a CD38 inhibitor, a RANKL inhibitor, a B4GALNT1 inhibitor, a SLAMF7 inhibitor, an IDH2 inhibitor, an mTOR inhibitor, a CD20 targeting antibody, a BTK inhibitor, a PI3K inhibitor, a FLT3 inhibitor, a PARP inhibitor, a CDK4 inhibitor, a CDK6 inhibitor, an FGFR inhibitor, a RAF inhibitor, a JAK1 inhibitor, a JAK2 inhibitor, a JAK3 inhibitor, an IL-6 inhibitor, a IL-17 inhibitor, a Smoothened inhibitor, an IL-6R inhibitor, a BCL2 inhibitor, a PTCH inhibitor, a PIGF inhibitor, a TGFB inhibitor, a CD28 agonist, a CD3 agonist, CD40 agonist, a GITR agonist, a OX40 agonist, a VISTA agonist, a CD137 agonist, a LAG3 inhibitor, a TIM3 inhibitor, a TIGIT inhibitor, or an IL-2R inhibitor.

[0031] In one embodiment, the anti-inflammatory agent is a cyclooxygenase (COX) inhibitor, such as a COX-1 and/or COX-2 inhibitor, such as SC-560, FR122047, P6, mofezolac, TFAP, flurbiprofen, ketoprofen, celecoxib, rofecoxib, meloxicam, piroxicam, deracoxib, parecoxib, valdecoxib, etoricoxib, a chromene derivative, a chroman derivative, N-(2-cyclohexyloxynitrophenyl) methane sulfonamide, parecoxib, lumiracoxib, RS 57067, T-614, BMS-347070, JTE-522, S-2474, SVT- 2016, CT-3, ABT-963, SC-58125, nimesulide, flosulide, NS-398, L- 745337, RWJ-63556, L-784512, darbufelone, CS-502, LAS-34475, LAS- 34555, S-33516, diclofenac, mefenamic acid, SD-8381, ibuprofen, naproxen, ketorolac, indomethacin, aspirin, naproxen, tolmetin, piroxicam, or meclofenamate.

[0032] In one embodiment, the anti-inflammatory agent is an NF-κB inhibitor, such as an IKK complex inhibitor, an IκB degradation inhibitor, an NF-κB nuclear translocation inhibitor, a p65 acetylation inhibitor, an NF-κB DNA binding inhibitor, an NF-κB transactivation inhibitor, or a p53 induction inhibitor.

[0033] In one embodiment, the NF-κB inhibitor is TPCA-1, NF-κB Activation Inhibitor VI (BOT-64), BMS-345541, amlexanox, SC-514 (GK-01140), IMD-0354, IKK-16, BAY-11-7082, MG-115, MG-132, lactacystin, epoxomicin, parthenolide, carfilzomib, MLN-4924 (pevonedistat), JSH-23 rolipram, gallic acid, anacardic acid, GYY-4137, p-XSC, CV-3988, prostaglandin E2 (PGE2), LY-294002, wortmannin, mesalamine, quinacrine, or flavopiridol.

[0034] One embodiment encompasses a pharmaceutical composition comprising a disclosed masked cytokine and a pharmaceutically acceptable carrier.

[0035] Another embodiment encompasses a kit comprising the disclosed masked cytokine.

[0036] Another embodiment comprises a method of treating or preventing a neoplastic disease in a subject, the method comprising administering to the subject an effective amount of a disclosed masked cytokine composition for the treatment of a disease or condition, such as a neoplastic disease, for example, cancer. In one embodiment the cancer is leukemia, lymphoma, head and neck cancer, colorectal cancer, prostate cancer, pancreatic cancer, melanoma, breast cancer, neuroblastoma, lung cancer, ovarian cancer, bone cancer (e.g., osteosarcoma, chondrosarcoma, Ewing sarcoma), bladder cancer, cervical cancer, liver cancer, kidney cancer, skin cancer, testicular cancer, adrenal cancer, adenoid cystic carcinoma, anal cancer, brain cancer, ductal carcinoma, endometrial cancer, esophageal cancer, gastric cancer, oral cancer, thyroid cancer, retinoblastoma, parathyroid cancer, pituitary cancer, bile duct cancer, or uterine cancer. In some embodiments, the cancer is selected from the group consisting of lymphoma, sarcoma, bladder cancer, bone cancer, brain tumor, cervical cancer, colon cancer, esophageal cancer, gastric cancer, head and neck cancer, kidney cancer, myeloma, thyroid cancer, leukemia, prostate cancer, breast cancer (e.g. triple negative, ER positive, ER negative, chemotherapy resistant, Herceptin resistant, HER2 positive, doxorubicin resistant, tamoxifen resistant, ductal carcinoma, lobular carcinoma, primary, metastatic), ovarian cancer, pancreatic cancer, liver cancer (e.g. hepatocellular carcinoma), lung cancer (e.g. non-small cell lung carcinoma, squamous cell lung

carcinoma, adenocarcinoma, large cell lung carcinoma, small cell lung carcinoma, carcinoid, sarcoma), glioblastoma multiforme, glioma, melanoma, prostate cancer, castration-resistant prostate cancer, breast cancer, triple negative breast cancer, glioblastoma, ovarian cancer, lung cancer, squamous cell carcinoma (e.g., head, neck, or esophagus), colorectal cancer, leukemia, acute myeloid leukemia, lymphoma, B cell lymphoma, or multiple myeloma. Additional examples include, cancer of the thyroid, endocrine system, brain, breast, cervix, colon, head & neck, esophagus, liver, kidney, lung, non-small cell lung, melanoma, mesothelioma, ovary, sarcoma, stomach, uterus or Medulloblastoma, Hodgkin's Disease, Non-Hodgkin's Lymphoma, multiple myeloma, neuroblastoma, glioma, glioblastoma multiforme, ovarian cancer, rhabdomyosarcoma, primary thrombocytosis, primary macroglobulinemia, primary brain tumors, cancer, malignant pancreatic insulanoma, malignant carcinoid, urinary bladder cancer, premalignant skin lesions, testicular cancer, lymphomas, thyroid cancer, neuroblastoma, esophageal cancer, genitourinary tract cancer, malignant hypercalcemia, endometrial cancer, adrenal cortical cancer, neoplasms of the endocrine or exocrine pancreas, medullary thyroid cancer, medullary thyroid carcinoma, melanoma, colorectal cancer, papillary thyroid cancer, hepatocellular carcinoma, Paget's Disease of the Nipple, Phyllodes Tumors, Lobular Carcinoma, Ductal Carcinoma, cancer of the pancreatic stellate cells, cancer of the hepatic stellate cells, or prostate cancer.

[0037] Another embodiment comprises a method of treating or preventing an inflammatory or autoimmune disease in a subject, the method comprising administering to the subject an effective amount of a disclosed masked cytokine composition, wherein the inflammatory or autoimmune disease is selected from the group consisting of atherosclerosis, obesity, inflammatory bowel disease (IBD), rheumatoid arthritis, allergic encephalitis, psoriasis, atopic skin disease, osteoporosis, peritonitis, hepatitis, lupus, celiac disease, Sjogren's syndrome, polymyalgia rheumatica, multiple sclerosis (MS), ankylosing spondylitis, type 1 diabetes mellitus, alopecia areata, vasculitis, and temporal arteritis, graft versus host disease (GVHD), asthma, COPD, a paraneoplastic autoimmune disease, cartilage inflammation, juvenile arthritis, juvenile rheumatoid arthritis, pauciarticular juvenile rheumatoid arthritis, polyarticular juvenile rheumatoid arthritis, systemic onset juvenile rheumatoid arthritis, juvenile ankylosing spondylitis, juvenile enteropathic arthritis, juvenile reactive arthritis, juvenile Reiter's Syndrome, SEA Syndrome (Seronegativity, Enthesopathy, Arthropathy Syndrome), juvenile dermatomyositis , juvenile psoriatic arthritis, juvenile Scleroderma, juvenile systemic lupus erythematosus, juvenile vasculitis, pauciarticular rheumatoid arthritis, systemic onset rheumatoid arthritis, enteropathic arthritis, reactive arthritis, Reiter's Syndrome, dermatomyositis, psoriatic arthritis, Scleroderma, vasculitis, myolitis, polymyolitis, dermatomyolitis, polyarteritis nodossa, Wegener's granulomatosis, arteritis, ploymyalgia rheumatica, sarcoidosis, Sclerosis, primary biliary Sclerosis, Sclerosing cholangitis, psoriasis, plaque psoriasis, guttate psoriasis, inverse psoriasis, pustular psoriasis, erythrodermic psoriasis, dermatitis, atopic dermatitis, atherosclerosis, Still's disease, Systemic Lupus Erythematosus (SLE), myasthenia gravis, Crohn's disease, ulcerative colitis, celiac disease,

rhinosinusitis, rhinosinusitis with polyps, eosinophilic esophogitis, eosinophilic bronchitis, Guillain-Barre disease, thyroiditis (e.g., Graves' disease), Addison's disease, Raynaud's phenomenon, autoimmune hepatitis, transplantation rejection, kidney damage, hepatitis C-induced vasculitis, or spontaneous loss of pregnancy.

BRIEF DESCRIPTION OF THE DRAWINGS

[0038] **FIG. 1A** and **FIG. 1B** show the structure of exemplary embodiments of a masked cytokine that includes a masking moiety, a cytokine or functional fragment thereof ("cytokine"), a half-life extension domain, and a first linker that includes a first cleavable peptide ("1CP"), a first N-terminal spacer domain ("1NSD"), and a first C-terminal spacer domain ("1CSD"). These exemplary embodiments also include a second linker that includes a second cleavable peptide ("2CP"), a second N-terminal spacer domain ("2NSD"), and a second C-terminal spacer domain ("2CSD"). As shown by the arrows, while the exemplary embodiments shows the masking moiety linked to the first linker, and the cytokine or functional fragment thereof is linked to the first linker and the second linker, the masking moiety and the cytokine or functional fragment thereof can be interchanged such that the cytokine or functional fragment thereof is linked to the first linker, and the masking moiety is linked to the first linker and the second linker. **FIG. 1A** shows the structure of an exemplary embodiment of a masked cytokine as a monomer. **FIG. 1B** shows the structure of an exemplary embodiment of a masked cytokine as a homodimer formed by disulfide bonds.

[0039] **FIG. 2A** and **FIG. 2B** show the structure of exemplary embodiments of a masked cytokine that includes a first masking moiety ("Mask 1"), a cytokine or functional fragment thereof ("cytokine"), a second masking moiety ("Mask 2"), a half-life extension domain, a first linker that includes a first cleavable peptide ("1CP"), a first N-terminal spacer domain ("1NSD"), and a first C-terminal spacer domain ("1CSD"), and a second linker that includes a second cleavable peptide ("2CP"), a second N-terminal spacer domain ("2NSD"), and a second C-terminal spacer domain ("2CSD"). These exemplary embodiments also include a third linker that includes a third cleavable peptide ("3CP"), a third N-terminal spacer domain ("3NSD"), and a third C-terminal spacer domain ("3CSD"). **FIG. 2A** shows the structure of an exemplary embodiment of a masked cytokine as a monomer. **FIG. 2B** shows the structure of an exemplary embodiment of a masked cytokine as a homodimer formed by disulfide bonds.

[0040] **FIG. 3A** shows the structure of an exemplary embodiment of a masked cytokine that includes a masking moiety, a cytokine or functional fragment thereof ("cytokine"), a first half-life extension domain, and a second half-life extension domain. The exemplary embodiment shown in **FIG. 3A** also includes a first linker that includes a first cleavable peptide ("1CP"), a first N-terminal spacer domain ("1NSD"), and a first C-terminal spacer domain ("1CSD"), and a second linker that includes a second cleavable peptide ("2CP"), a second N-terminal spacer domain ("2NSD"), and a second C-

terminal spacer domain ("2CSD"). The exemplary first and second half-life extension domains include "knobs into holes" modifications that promote the association of the first half-life extension domain with the second half-life extension domain, as shown by the "hole" in the first half-life extension domain and the "knob" in the second half-life extension domain. The first half-life extension domain and the second half-life extension domain are also shown as associating, at least in part, due to the formation of disulfide bonds. It is to be understood that although the "hole" is depicted as part of the first half-life extension domain (linked to the masking moiety) and the "knob" is depicted as part of the second half-life extension domain (linked to the cytokine), the "hole" and the "knob" can alternatively be included in the second half-life extension domain and the first half-life extension domain, respectively, so that the "hole" is a part of the second half-life extension domain (linked to the cytokine) and the "knob" is part of the first half-life extension domain (linked to masking moiety). **FIG. 3B** shows the structure of an exemplary embodiment of a masked cytokine that includes a masking moiety, a cytokine or functional fragment thereof ("cytokine"), a first half-life extension domain, a second half-life extension domain, and a third linker that includes a third N-terminal spacer domain ("3NSD") and a third C-terminal spacer domain ("3CSD"). The third linker links the first half-life extension domain to the second half-life extension domain. The exemplary embodiment shown in **FIG. 3B** also includes a first linker that includes a first cleavable peptide ("1CP"), a first N-terminal spacer domain ("1NSD"), and a first C-terminal spacer domain ("1CSD"), and a second linker that includes a second cleavable peptide ("2CP"), a second N-terminal spacer domain ("2NSD"), and a second C-terminal spacer domain ("2CSD").

[0041] **Figure 4** shows a dimer of the exemplary masked cytokine shown in **FIG. 3A** formed by disulfide bonds.

[0042] **FIG. 5A** shows the structure of an exemplary embodiment of a masked cytokine that includes a first masking moiety ("Mask 1"), a first half-life extension domain, a second masking moiety ("Mask 2"), a cytokine or functional fragment thereof ("cytokine"), and a second half-life extension domain. The exemplary embodiment shown in **FIG. 5A** also includes a first linker that includes a first cleavable peptide ("1CP"), a first N-terminal spacer domain ("1NSD"), and a first C-terminal spacer domain ("1CSD"), a second linker that includes a second cleavable peptide ("2CP"), a second N-terminal spacer domain ("2NSD"), and a second C-terminal spacer domain ("2CSD"), and a third linker that includes a third cleavable peptide ("3CP"), a third N-terminal spacer domain ("3NSD"), and a third C-terminal spacer domain ("3CSD"). It is to be understood that although the "hole" is depicted as part of the first half-life extension domain (linked to the masking moiety) and the "knob" is depicted as part of the second half-life extension domain (linked to the cytokine), the "hole" and the "knob" can alternatively be included in the second half-life extension domain and the first half-life extension domain, respectively, so that the "hole" is a part of the second half-life extension domain (linked to the cytokine) and the "knob" is part of the first half-life extension domain (linked to masking moiety). **FIG. 5B** shows the structure of an exemplary embodiment of a masked cytokine that includes a first masking moiety

("Mask 1"), a first half-life extension domain, a second masking moiety ("Mask 2"), a cytokine or functional fragment thereof ("cytokine"), a second half-life extension domain, and a fourth linker that includes a fourth N-terminal spacer domain ("4NSD") and a fourth C-terminal spacer domain ("4CSD"). The fourth linker links the first half-life extension domain to the second half-life extension domain. The exemplary embodiment shown in **FIG. 5B** also includes a first linker that includes a first cleavable peptide ("1CP"), a first N-terminal spacer domain ("1NSD"), and a first C-terminal spacer domain ("1CSD"), a second linker that includes a second cleavable peptide ("2CP"), a second N-terminal spacer domain ("2NSD"), and a second C-terminal spacer domain ("2CSD"), and a third linker that includes a third cleavable peptide ("3CP"), a third N-terminal spacer domain ("3NSD"), and a third C-terminal spacer domain ("3CSD"). As shown by the arrows in **FIGs. 5A** and **5B**, while the exemplary embodiment shows the second masking moiety linked to the third linker, and the cytokine or functional fragment thereof is linked to the third linker and the second linker, the first masking moiety and the cytokine or functional fragment thereof can be interchanged such that the cytokine or functional fragment thereof is linked to the third linker, and the first masking moiety is linked to the third linker and the second linker.

[0043] **Figure 6** shows a dimer of the exemplary masked cytokine shown in **FIG. 5A** formed by disulfide bonds.

[0044] **FIGs. 7A-7E** shows exemplary embodiments of masked cytokines prior to (left) and after (right) cleavage by a protease, such as at the tumor microenvironment. **FIGs. 7A-7D** show exemplary embodiments of a masked IL-2 cytokine, and **FIG. 7E** shows an exemplary embodiment of a masked IL-15 cytokine. Cleavage by a protease releases a masking moiety (e.g., IL-2Rβ, as shown in **FIGs. 7A**, **7B**, and **7D**), or releases an IL-2 (**FIG. 7C**), or releases IL-15 (**FIG. 7E**).

[0045] **Figure 8** shows SDS-PAGE analysis on flow-through (FT) samples (i.e., proteins that did not bind to the Protein A column) and the eluted (E) samples (i.e., proteins that bound to the Protein A column and were eluted from it) following production and purification of exemplary constructs (AK304, AK305, AK307, AK308, AK309, AK310, AK311, AK312, AK313, AK314, and AK315).

[0046] **FIGs. 9A-9D** shows results from SPR analysis that tested the binding of exemplary masked IL-2 polypeptide constructs (AK215 and AK216), or a rhIL2 control, to CD25-Fc. **FIG. 9A** shows the interaction between AK215 and CD25-Fc, **FIG. 9B** shows the interaction between AK216 and CD25-Fc, and **FIG. 9C** shows the interaction between a recombinant human IL2 (rhIL2) control and CD25-Fc. **FIG. 9D** provides a table summarizing the data obtained for the association constant (ka), dissociation constant (kd), equilibrium dissociation constant (KD), as well as the Chi^2 value and U-value for each interaction.

[0047] **FIGs. 10A-10D** shows results from SPR analysis that tested the binding of exemplary masked IL-2 polypeptide constructs (AK216 and AK218), or a rhIL2 control, to CD122-Fc. **FIG. 10A** shows the interaction between AK216 and CD122-Fc, **FIG. 10B** shows the interaction between AK218

and CD122-Fc, and **FIG. 10C** shows the interaction between a recombinant human IL2 (rhIL2) control and CD122-Fc. **FIG. 10D** provides a table summarizing the data obtained for the association constant (ka), dissociation constant (kd), equilibrium dissociation constant (KD), as well as the Chi^2 value and U-value for each interaction.

[0048] **FIG. 11A** shows an exemplary embodiment of a masked cytokines prior to (left) and after (right) cleavage by a protease, such as at the tumor microenvironment. **FIG. 11B** shows SDS-PAGE analysis of an exemplary masked IL-2 polypeptide construct that was incubated in the absence (left lane) or presence (right lane) of the MMP10 protease, which demonstrates the release of IL-2 from the Fc portion.

[0049] **FIGs. 12A-12D** shows STAT5 activation (%) in PBMCs treated with the construct AK032, AK035, AK041, or rhIL-2 as a control. The levels of STAT5 activation (%) are shown for NK cells, CD8+ T cells, effector T cells (Teff), and regulatory T cells (Treg), as determined following incubation with rhIL-2 (**FIG. 12A**), AK032 (**FIG. 12B**), AK035 (**FIG. 12C**), or AK041 (**FIG. 12D**).

[0050] **FIGs. 13A-13C** shows STAT5 activation (%) in PBMCs treated with the construct AK081 or AK032. The AK081 construct with and without prior exposure to MMP10 was tested. An isotype control as well as a no IL-2 negative control was also tested. The levels of STAT5 activation (%) are shown for NK cells (**FIG. 13A**), CD8+ T cells (**FIG. 13C**), and CD4+ T cells (**FIG. 13B**).

[0051] **FIGs. 14A-14D** shows the results from STAT5 activation studies in PBMCs using constructs AK081 and AK111, as well as controls that included an rhIL-2 and anti-RSV antibody. A no-treatment control was also tested. EC50 (pM) is also shown for the rhIL-2, AK081, and AK111 treatments. STAT5 activation (%) is shown for CD4+FoxP3+CD25+ cells (**FIG. 14A**), CD8+ cells (**FIG. 14B**), and CD4+FoxP3-CD25- cells (**FIG. 14C**). **FIG. 14D** provides EC50 (pM) and fold-change data for the AK081, AK111 constructs, as well as the rhIL-2 control.

[0052] **FIGs. 15A-15D** shows the results from STAT5 activation studies in PBMCs using constructs AK167 and AK168, as well as controls that included an rhIL-2 and anti-RSV antibody. A no-treatment control was also tested. EC50 (pM) is also shown for the rhIL-2, AK167, and AK168 treatments. STAT5 activation (%) is shown for CD4+FoxP3+CD25+ cells (**FIG. 15A**), CD8+ cells (**FIG. 15B**), and CD4+FoxP3-CD25- cells (**FIG. 15C**). **FIG. 15D** provides EC50 (pM) and fold-change data for the AK167 and AK168 constructs, as well as the rhIL-2 control.

[0053] **FIGs. 16A-16D** shows STAT5 activation (%) in PBMCs treated with the construct AK165 or AK166, or an isotype control or an IL-2-Fc control, that were (+ MMP10) or were not previously exposed to the MMP10 protease. The key as shown in **FIG. 16A** also applies to **FIG. 16B**, and the key as shown in **FIG. 16C** also applies to **FIG. 16D**. STAT5 activation (%) is shown for CD4+FoxP3+ T regulatory cells (**FIG. 16A**), CD4+FoxP3- T helper cells (**FIG. 16B**), CD8+ cytotoxic T cells (**FIG. 16C**), and CD56+ NK cells (**FIG. 16D**).

[0054] **FIGs. 17A-17C** shows STAT5 activation (%) in PBMCs treated with the construct AK109 or AK110, or an isotype control or an IL-2-Fc control, that were (+ MMP10) or were not previously exposed to the MMP10 protease. The key as shown in **FIG. 17B** also applies to **FIG. 17A**. STAT5 activation (%) is shown for NK cells (**FIG. 17A**), CD8 cells (**FIG. 17B**), and CD4 cells (**FIG. 17C**).

[0055] **FIGs. 18A-18D** shows the results from STAT5 activation studies in PBMCs using the constructs AK211, AK235, AK253, AK306, AK310, AK314, and AK316, as well as an an rhIL-2 control. STAT5 activation (%) is shown for CD3+CD4+FoxP3+ cells (**FIG. 18A**), CD3+CD4+FoxP3- cells (**FIG. 18B**), and CD3+CD8+ cells (**FIG. 18C**). **FIG. 18D** provides EC50 data for each of the tested constructs as well as the rhIL-2 control.

[0056] **FIGs. 19A-19D** shows the results from STAT5 activation studies in PBMCs using the constructs AK081, AK167, AK216, AK218, AK219, AK220, and AK223 that have been activated by protease, as well as an an rhIL-2 control. STAT5 activation (%) is shown for CD4+FoxP3+CD25+ regulatory T cells (**FIG. 19A**), CD4+FoxP3-CD25- cells (**FIG. 19B**), and CD8+ cells (**FIG. 19C**). **FIG. 19D** provides EC50 data for each of the tested constructs as well as the rhIL-2 control.

[0057] **FIGs. 20A-20C** shows STAT5 activation (%) in PBMCs treated with the construct AK081, AK189, AK190, or AK210, or an anti-RSV control. The key as shown in **FIG. 20A** also applies to **FIGs. 20B** and **20C**. STAT5 activation (%) is shown for regulatory T cells (**FIG. 20A**), CD4 helper T cells (**FIG. 20B**), and CD8 cells (**FIG. 20C**).

[0058] **FIGs. 21A-21C** shows STAT5 activation (%) in PBMCs treated with the construct AK167, AK191, AK192, or AK193, or an anti-RSV control. The key as shown in **FIG. 21A** also applies to **FIGs. 21B** and **21C**. STAT5 activation (%) is shown for regulatory T cells (**FIG. 21A**), CD4 helper T cells (**FIG. 21B**), and CD8 cells (**FIG. 21C**).

[0059] **FIGs. 22A** and **22B** show the results from reporter bioassays on an exemplary masked IL-15 polypeptide construct, AK248, with (+ MMP) or without prior exposure to an activating protease, or a rhIL-15 as a control. **FIG. 22A** shows results from a reporter bioassay using a HEK-Blue IL2 reporter cell line, and **FIG. 22B** shows results from a reporter bioassay using an IL-15 bioassay with a mouse CTLL2 cell line.

[0060] **FIGs. 23A-23D** show results from pharmacokinetic studies carried out in tumor-bearing mice using the construct AK032, AK081, AK111, AK167, or AK168, or an anti-RSV control. **FIG. 23A** provides a simplistic depiction of the structure of each of the constucts tested. **FIG. 23B** shows Fc levels in plasma (μg/mL) by detecting human IgG, **FIG. 23C** shows Fc-CD122 levels in plasma (μg/mL) by detecting human CD122, and **FIG. 23D** shows Fc-IL2 levels in plasma (μg/mL) by detecting human IL-2. Prior to the detection step, an anti-human IG was used as the capture antibody.

[0061] **FIGs. 24A-24D** show results from pharmacokinetic studies carried out in tumor-bearing mice using the construct AK167, AK191 AK197, AK203, AK209, or AK211, or an anti-RSV control. **FIG. 24A** provides a simplistic depiction of the structure of each of the constucts tested. **FIG. 24B**

shows Fc levels in plasma (μg/mL) by detecting human IgG, **FIG. 24C** shows Fc-IL2 levels in plasma (μg/mL) by detecting human IL-2, and **FIG. 24D** shows Fc-CD122 levels in plasma (μg/mL) by detecting human CD122. Prior to the detection step, an anti-human IG was used as the capture antibody.

[0062] **FIGs. 25A-25L** shows results from studies testing the in vivo responses of CD4, CD8, NK, and Treg percentages in spleen, blood, and tumor, using the AK032, AK081, AK111, AK167, or AK168 construct, or an anti-RSV IgG control. For spleen tissue, % CD8 cells of CD3 cells (**FIG. 25A**), % CD4 of CD3 cells (**FIG. 25B**), % NK cells of CD3- cells (**FIG. 25C**), % FoxP3 of CD4 cells (**FIG. 25D**) is shown. For blood, % CD8 cells of CD3 cells (**FIG. 25E**), % CD4 of CD3 cells (**FIG. 25F**), % NK cells of CD3- cells (**FIG. 25G**), % FoxP3 of CD4 cells (**FIG. 25H**) is shown. For tumor tissue, % CD8 cells of CD3 cells (**FIG. 25I**), % CD4 of CD3 cells (**FIG. 25J**), % NK cells of CD3- cells (**FIG. 25K**), % FoxP3 of CD4 cells (**FIG. 25L**) is shown.

[0063] **FIGs. 26A-26L** shows results from studies testing the in vivo responses of CD4, CD8, NK, and Treg percentages in spleen, blood, and tumor, using the AK167, AK168, AK191, AK197, AK203, AK209, or AK211 construct, or an anti-RSV IgG control. For spleen tissue, % CD8 cells of CD3 cells (**FIG. 26A**), % CD4 of CD3 cells (**FIG. 26B**), % NK cells of CD3- cells (**FIG. 26C**), % FoxP3 of CD4 cells (**FIG. 26D**) is shown. For blood, % CD8 cells of CD3 cells (**FIG. 26E**), % CD4 of CD3 cells (**FIG. 26F**), % NK cells of CD3- cells (**FIG. 26G**), % FoxP3 of CD4 cells (**FIG. 26H**) is shown. For tumor tissue, % CD8 cells of CD3 cells (**FIG. 26I**), % CD4 of CD3 cells (**FIG. 26J**), % NK cells of CD3- cells (**FIG. 26K**), % FoxP3 of CD4 cells (**FIG. 26L**) is shown.

[0064] **FIGs. 27A-27L** shows results from studies testing the in vivo responses of CD4, CD8, NK, and Treg percentages in spleen, blood, and tumor, using the AK235, AK191, AK192, AK193, AK210, AK189, AK190, or AK211 construct, or an anti-RSV IgG control. For spleen tissue, % CD8 cells of CD3 cells (**FIG. 27A**), % CD4 of CD3 cells (**FIG. 27B**), % NK cells of CD3- cells (**FIG. 27C**), % FoxP3 of CD4 cells (**FIG. 27D**) is shown. For blood, % CD8 cells of CD3 cells (**FIG. 27E**), % CD4 of CD3 cells (**FIG. 27F**), % NK cells of CD3- cells (**FIG. 27G**), % FoxP3 of CD4 cells (**FIG. 27H**) is shown. For tumor tissue, % CD8 cells of CD3 cells (**FIG. 27I**), % CD4 of CD3 cells (**FIG. 27J**), % NK cells of CD3- cells (**FIG. 27K**), % FoxP3 of CD4 cells (**FIG. 27L**) is shown.

[0065] **FIGs. 28A-28I** show results from in vivo T cell activation in spleen, blood, and tumor, using the AK235, AK191, AK192, AK193, AK210, AK189, AK190, or AK211 construct. T cell activation was measured as the mean fluorescence intensity (MFI) of CD25 in CD8+ T cells (**FIG. 28A; FIG. 28D; FIG. 28G**), CD4+ T cells (**FIG. 28B; FIG. 28E; FIG. 28H**), or Foxp3+ cells (**FIG. 28C; FIG. 28F; FIG. 28I**) in the spleen, blood, and tumor. Statistical analysis was performed using One-way ANOVA as compared to the non-cleavable AK211 construct.

[0066] **FIGs. 29A-29D** show the results from studies testing the in vivo cleavage of the exemplary masked IL-2 polypeptide constructs AK168 (cleavable peptide sequence: MPYDLYHP; SEQ ID NO: 96) and AK209 (cleavable peptide sequence: VPLSLY; SEQ ID NO: 135). **FIG. 29E** shows results from a

pharmacokinetic study of total plasma IgG concentration (μg/mL) for total levels of the AK167, AK168, and AK209 constructs, and for levels of non-cleaved forms of each construct.

[0067] **FIGs. 30A-30D** shows results from an in vivo study that assessed vascular leakage using the exemplary masked IL-2 polypeptide construct AK111 or AK168, or the non-masked IL-2 polypeptide construct AK081 or AK167, or an anti-RSV control. **FIG.30A** shows the percentage (%) of body weight loss, and **FIGs. 30B, 30C**, and **30D** shows the weight in grams of the liver, lung, and spleen, respectively, for each.

[0068] **FIGs. 31A** and **31B** shows results from an in vivo study that assessed vascular leakage as indicated by measuring the extent of dye leakage into liver and lung tissue following administration of the AK081, AK111, AK167, or AK168 construct, or an anti-RSV control. The extent of dye leakage into liver (**FIG. 31A**) and lung (**FIG. 31B**) was measured based on absorbance at 650nm.

[0069] **FIGs. 32A** and **32B** shows results from an in vivo study that assessed vascular leakage as indicated by measuring the extent of mononuclear cell perivascular invasion into into the liver and lung tissue following administration of the AK081, AK111, AK167, or AK168 construct, or an anti-RSV control. The average number of mononuclear cells in the liver (**FIG. 32A**) and the average number of mononuclear cells in the lung (**FIG. 32B**) depicted for each.

[0070] **FIGs. 33A** and **33B** show results from a syngeneic tumor model study that assessed tumor volume and body weight over the course of treatment with the AK032, AK081, AK111, AK167, or AK168 construct, or an anti-RSV control. **FIG. 33A** shows data on tumor volume over the course of treatment, and **FIG. 33B** shows data on the percentage (%) change in body weight over the course of the treatment.

DETAILED DESCRIPTION

[0071] Provided herein are cytokines or functional fragments thereof that, in some embodiments, are engineered to be masked by a masking moiety at one or more receptor binding site(s) of the cytokine or functional fragment thereof. In some embodiments, the cytokines are engineered to be activatable by a protease at a target site, such as in a tumor microenvironment, by including a proteolytically cleavable linker. In some embodiments, the proteolytically cleavable linker links the cytokine to the masking moiety, links the cytokine to a half-life extension domain, and/or links the masking moiety to a half-life extension domain. The masking moiety blocks, occludes, inhibits (e.g., decreases) or otherwise prevents (e.g., masks) the activity or binding of the cytokine to its cognate receptor or protein. Upon proteolytic cleavage of the cleavable linker at the target site, the cytokine becomes activated, which renders it capable of binding to its cognate receptor or protein with increased affinity.

[0072] By using a masking moiety, the systemic side effects of an administered cytokine can be reduced by interfering with the binding capability of the cytokine. For instance, high-dose recombinant

IL-2 (aldesleukin) has been approved by the FDA for the treatment of metastatic renal cell carcinoma and melanoma, but has been associated with severe cardiovascular, hepatic, pulmonary, gastrointestinal, neurologic, and hematological side effects. Preclinical studies showed, for instance, that IL-2-induced pulmonary edema is caused by the interaction between IL-2 and the IL-2Rα (CD25) subunit of the IL-2 receptor (IL-2R) on lung endothelial cells, and that this IL-2-mediated pulmonary adema could be abrogated by interfering with the ability of the IL-2 to bind IL-2Rα. *See* Krieg et al. (2010) PNAS, 107(26): 11906-11911. Thus, in some embodiments where the cytokine or functional fragment thereof is an IL-2 polypeptide, a masking moiety is employed that blocks, occludes, inhibits (e.g., decreases) or otherwise prevents (e.g., masks) the activity or binding of an IL-2 cytokine to IL-2Rα. To further reduce systemic effects of a masked IL-2 polypeptide, the masked IL-2 polypeptide can further include a masking moiety that blocks, occludes, inhibits (e.g., decreases) or otherwise prevents (e.g., masks) the activity or binding of the IL-2 cytokine to the IL-2Rβ and/or IL-2Rγ subunits of IL-2R. Similar strategies are likewise employed for other cytokines by interfering with their ability to bind certain proteins (e.g., a receptor subunit(s)) that are associated with causing detrimental systemic side effects. Moreover, by masking the cytokine using a linker that includes cleavable peptide, the binding capability that is interfered with by using the masking moiety can be restored by cleavage of the cleavable peptide at the tumor microenvironment. Thus, in some embodiments, the masked cytokines provided herein are engineered to precisely target pharmacological activity to the tumor microenvironment by exploiting one of the hallmarks of cancer, high local concentrations of active protease. This feature of the tumor microenvironment is used to transform a systemically inert molecule into a locally active cytokine. Activation of the cytokine at the tumor microenvironment significantly reduces systemic toxicities that can be associated with drugs that are administered to a subject in active form.

[0073] All publications, including patent documents, scientific articles and databases, referred to in this application are incorporated by reference in their entirety for all purposes to the same extent as if each individual publication were individually incorporated by reference. If a definition set forth herein is contrary to or otherwise inconsistent with a definition set forth in the patents, applications, published applications and other publications that are herein incorporated by reference, the definition set forth herein prevails over the definition that is incorporated herein by reference.

[0074] The section headings used herein are for organizational purposes only and are not to be construed as limiting the subject matter described.

I. Masked Cytokines

[0075] Provided herein, in some embodiments, is a masked cytokine comprising (a) a masking moiety; and (b) a cytokine or functional fragment thereof, wherein the masking moiety is linked to the cytokine or functional fragment thereof via a first linker. In some embodiments, the masked cytokine further comprises a half-life extension domain that is linked to either the masking moiety or the cytokine

or functional fragment thereof. In some embodiments, the half-life extension domain is linked to either the masking moiety or the IL-2 polypeptide or functional fragment thereof via a second linker.

[0076] In some embodiments, the masked cytokine comprises in an N to C-terminal direction: (a) the masking moiety; (b) the first linker; (c) the cytokine or functional fragment thereof; and (d) the half-life extension domain. In some embodiments, the masked cytokine comprises in a C to N-terminal direction: (a) the masking moiety; (b) the first linker; (c) the cytokine or functional fragment thereof; and (d) the half-life extension domain. In some embodiments, the masked cytokine comprises in an N to C-terminal direction: (a) the masking moiety; (b) the first linker; (c) the cytokine or functional fragment thereof; (d) the second linker and (e) the half-life extension domain. In some embodiments, the masked cytokine comprises in a C to N-terminal direction: (a) the masking moiety; (b) the first linker; (c) the cytokine or functional fragment thereof; (d) the second linker and (e) the half-life extension domain. In some embodiments, the masked cytokine comprises in an N to C-terminal direction: (a) the cytokine or functional fragment thereof; (b) the first linker; (c) the masking moiety; and (d) the half-life extension domain. In some embodiments, the masked cytokine comprises in a C to N-terminal direction: (a) the cytokine or functional fragment thereof; (b) the first linker; (c) the masking moiety; and (d) the half-life extension domain. In some embodiments, the masked cytokine comprises in an N to C-terminal direction: (a) the cytokine or functional fragment thereof; (b) the first linker; (c) the masking moiety; (d) the second linker; and (e) the half-life extension domain. In some embodiments, the masked cytokine comprises in a C to N-terminal direction: (a) the cytokine or functional fragment thereof; (b) the first linker; (c) the masking moiety; (d) the second linker; and (e) the half-life extension domain. In some embodiments, the masked cytokine comprises in an N to C-terminal direction: (a) the half-life extension domain; (b) the first linker; (c) the masking moiety; (d) the second linker; and (e) the cytokine or functional fragment thereof. In some embodiments, the masked cytokine comprises in an N to C-terminal direction: (a) the half-life extension domain; (b) the cytokine or functional fragment thereof; (c) the first linker; and (d) the masking moiety. In some embodiments, the masked cytokine comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NOs: 585-597, 602, 610-614, 627-636, 642, and 643. In some embodiments, the masked cytokine comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 585-597, 602, 610-614, 627-636, 642, and 643. In some embodiments, the masked cytokine is any of the exemplary constructs described in Table 4 or Table 5, or is variant created by modifying any of the exemplary constructs described in Table 4 or Table 5, such as by incorporating one or more additional components to the structure of the construct in accordance with the teachings herein.

[0077] Also provided herein, in some embodiments, is a masked cytokine comprising (a) a first masking moiety; (b) a cytokine or functional fragment thereof, wherein the first masking moiety is linked to the cytokine or functional fragment thereof via a first linker; and (c) a second masking moiety, wherein

the second masking moiety is linked to the cytokine or functional fragment thereof via a second linker. In some embodiments, the masked cytokine further comprises a half-life extension domain that is linked to either the first masking moiety or the second masking moiety. In some embodiments, the half-life extension domain is linked to either the first masking moiety or the second masking moiety via a third linker.

[0078] Also provided herein, in some embodiments, is a masked cytokine comprising (a) a first masking moiety, wherein the first masking moiety is linked to a first half-life extension domain; (b) a cytokine or functional fragment thereof, wherein the cytokine or functional fragment thereof is linked to a second half-life extension domain; and (c) a second masking moiety, wherein the second masking moiety is linked to the first masking moiety. In some embodiments, the first masking moiety is linked to the first half-life extension domain via a first linker. In some embodiments, the second masking moiety is linked to the first masking moiety via a second linker. In some embodiments, the cytokine or functional fragment thereof is linked to the second half-life extension domain via a third linker. In some embodiments, the first linker comprises a cleavable peptide. In some embodiments, the second linker comprises a cleavable peptide. In some embodiments, the third linker comprises a cleavable peptide.

[0079] In some embodiments, the masked cytokine comprises in an N to C-terminal direction: (a) the first masking moiety; (b) the first linker; (c) the cytokine or functional fragment thereof; (d) a second linker; (e) a second masking moiety; and (f) the half-life extension domain. In some embodiments, the masked cytokine comprises in a C to N-terminal direction: (a) the first masking moiety; (b) the first linker; (c) the cytokine or functional fragment thereof; (d) a second linker; (e) a second masking moiety; and (f) the half-life extension domain. In some embodiments, the masked cytokine comprises in an N to C-terminal direction: (a) the first masking moiety; (b) the first linker; (c) the cytokine or functional fragment thereof; (d) a second linker; (e) a second masking moiety; (f) the third linker; and (g) the half-life extension domain. In some embodiments, the masked cytokine comprises in a C to N-terminal direction: (a) the first masking moiety; (b) the first linker; (c) the cytokine or functional fragment thereof; (d) a second linker; (e) a second masking moiety; (f) the third linker; and (g) the half-life extension domain. In some embodiments, the masked cytokine comprises in an N to C-terminal direction: (a) the half-life extension domain; (b) a first linker; (c) the first masking moiety; (d) a second linker; (e) the cytokine or functional fragment thereof; (f) a third linker; and (g) the second masking moiety. In some embodiments, the masked cytokine comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 567 and 598-601. In some embodiments, the masked cytokine comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NOs: 567 and 598-601. In some embodiments, the masked cytokine is any of the exemplary constructs described in Table 6 or Table 7, or is variant created by modifying any of the exemplary

constructs described in Table 6 or Table 7, such as by incorporating one or more additional components to the structure of the construct in accordance with the teachings herein.

[0080] Also provided herein, in some embodiments, is a masked cytokine comprising (a) a first half-life extension domain and a second half-life extension domain; (b) a masking moiety; and (c) a cytokine or functional fragment thereof, wherein the masking moiety is linked to the first half-life extension domain, the cytokine or functional fragment thereof is linked to the second half-life extension domain, and the first half-life extension domain and the second half-life extension domain contain modifications promoting the association of the first and the second half-life extension domain. In some embodiments, the masking moiety is linked to the first half-life extension domain via a first linker, and/or the cytokine or functional fragment thereof is linked to the second half-life extension domain via a second linker. In some embodiments, the first half-life extension domain is linked to the second half-life extension domain, optionally by a third linker. In some embodiments, the masked cytokine comprises (a) a first half-life extension domain comprising the amino acid sequence of SEQ ID NO: 155 and a second half-life extension domain comprising the amino acid sequence of SEQ ID NO: 156; (b) a masking moiety comprising the amino acid sequence of SEQ ID NO: 261; and (c) a cytokine or functional fragment thereof comprising the amino acid sequence of SEQ ID NO: 3, wherein the masking moiety is linked to the first half-life extension domain via a first linker comprising the amino acid sequence of SEQ ID NO: 28, the cytokine or functional fragment thereof is linked to the second half-life extension domain via a second linker comprising the amino acid sequence of SEQ ID NO: 811, the first half-life extension domain and the second half-life extension domain contain modifications promoting the association of the first and the second half-life extension domain, and the masked cytokine comprises the amino acid sequences of SEQ ID NOs: 266 and 267. In some embodiments, the masked cytokine comprises (a) a first half-life extension domain comprising the amino acid sequence of SEQ ID NO: 155 and a second half-life extension domain comprising the amino acid sequence of SEQ ID NO: 156; (b) a masking moiety comprising the amino acid sequence of SEQ ID NO: 261; and (c) a cytokine or functional fragment thereof comprising the amino acid sequence of SEQ ID NO: 260, wherein the masking moiety is linked to the first half-life extension domain via a first linker comprising the amino acid sequence of SEQ ID NO: 28, the cytokine or functional fragment thereof is linked to the second half-life extension domain via a second linker comprising the amino acid sequence of SEQ ID NO: 262, the first half-life extension domain and the second half-life extension domain contain modifications promoting the association of the first and the second half-life extension domain, and the masked cytokine comprises the amino acid sequences of SEQ ID NOs: 266 and 267. In some embodiments, the masked cytokine comprises the amino acid sequence of SEQ ID NO: 266. In some embodiments, the masked cytokine comprises the amino acid sequence of SEQ ID NO: 267. In some embodiments, the masked cytokine comprises the amino acid sequences of SEQ ID NOs: 266 and 267. In some embodiments, the masked cytokine comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%,

90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 266. In some embodiments, the masked cytokine comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 267. In some embodiments, the masked cytokine comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 266, and comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 267.

[0081] In some embodiments, the masked cytokine comprises (a) a first half-life extension domain comprising the amino acid sequence of SEQ ID NO: 155 and a second half-life extension domain comprising the amino acid sequence of SEQ ID NO: 156; (b) a masking moiety comprising the amino acid sequence of SEQ ID NO: 261; and (c) a cytokine or functional fragment thereof comprising the amino acid sequence of SEQ ID NO: 3, wherein the masking moiety is linked to the first half-life extension domain via a first linker comprising the amino acid sequence of SEQ ID NO: 28, the cytokine or functional fragment thereof is linked to the second half-life extension domain via a second linker comprising the amino acid sequence of SEQ ID NO: 807, the first half-life extension domain and the second half-life extension domain contain modifications promoting the association of the first and the second half-life extension domain, and the masked cytokine comprises the amino acid sequences of SEQ ID NOs: 679 and 267. In some embodiments, the masked cytokine comprises (a) a first half-life extension domain comprising the amino acid sequence of SEQ ID NO: 156 and a second half-life extension domain comprising the amino acid sequence of SEQ ID NO: 155; (b) a masking moiety comprising the amino acid sequence of SEQ ID NO: 261; and (c) a cytokine or functional fragment thereof comprising the amino acid sequence of SEQ ID NO: 3, wherein the masking moiety is linked to the first half-life extension domain via a first linker comprising the amino acid sequence of SEQ ID NO: 28, the cytokine or functional fragment thereof is linked to the second half-life extension domain via a second linker comprising the amino acid sequence of SEQ ID NO: 807, the first half-life extension domain and the second half-life extension domain contain modifications promoting the association of the first and the second half-life extension domain, and the masked cytokine comprises the amino acid sequences of SEQ ID NOs: 679 and 267.

[0082] In some embodiments, the masked cytokine comprises (a) a first half-life extension domain comprising the amino acid sequence of SEQ ID NO: 155 and a second half-life extension domain comprising the amino acid sequence of SEQ ID NO: 156; (b) a masking moiety comprising the amino acid sequence of SEQ ID NO: 261; and (c) a cytokine or functional fragment thereof comprising the amino acid sequence of SEQ ID NO: 3, wherein the masking moiety is linked to the first half-life extension domain via a first linker, the cytokine or functional fragment thereof is linked to the second

half-life extension domain via a second linker, the first half-life extension domain and the second half-life extension domain contain modifications promoting the association of the first and the second half-life extension domain, wherein the first linker and/or the second linker comprises a cleavable peptide. In some embodiments, the masked cytokine comprises (a) a first half-life extension domain comprising the amino acid sequence of SEQ ID NO: 156 and a second half-life extension domain comprising the amino acid sequence of SEQ ID NO: 155; (b) a masking moiety comprising the amino acid sequence of SEQ ID NO: 261; and (c) a cytokine or functional fragment thereof comprising the amino acid sequence of SEQ ID NO: 3, wherein the masking moiety is linked to the first half-life extension domain via a first linker, the cytokine or functional fragment thereof is linked to the second half-life extension domain via a second linker, the first half-life extension domain and the second half-life extension domain contain modifications promoting the association of the first and the second half-life extension domain, wherein the first linker and/or the second linker comprises a cleavable peptide.

[0083] In some embodiments, the masked cytokine comprises (a) a first half-life extension domain comprising the amino acid sequence of SEQ ID NO: 155 and a second half-life extension domain comprising the amino acid sequence of SEQ ID NO: 156; (b) a masking moiety comprising the amino acid sequence of SEQ ID NO: 261; and (c) a cytokine or functional fragment thereof comprising the amino acid sequence of SEQ ID NO: 1, wherein the masking moiety is linked to the first half-life extension domain via a first linker comprising the amino acid sequence of SEQ ID NO: 28, the cytokine or functional fragment thereof is linked to the second half-life extension domain via a second linker comprising the amino acid sequence of SEQ ID NO: 812, the first half-life extension domain and the second half-life extension domain contain modifications promoting the association of the first and the second half-life extension domain, and the masked cytokine comprises the amino acid sequences of SEQ ID NOs: 689 and 267. In some embodiments, the masked cytokine comprises (a) a first half-life extension domain comprising the amino acid sequence of SEQ ID NO: 156 and a second half-life extension domain comprising the amino acid sequence of SEQ ID NO: 155; (b) a masking moiety comprising the amino acid sequence of SEQ ID NO: 261; and (c) a cytokine or functional fragment thereof comprising the amino acid sequence of SEQ ID NO: 1, wherein the masking moiety is linked to the first half-life extension domain via a first linker comprising the amino acid sequence of SEQ ID NO: 28, the cytokine or functional fragment thereof is linked to the second half-life extension domain via a second linker comprising the amino acid sequence of SEQ ID NO: 812, the first half-life extension domain and the second half-life extension domain contain modifications promoting the association of the first and the second half-life extension domain, and the masked cytokine comprises the amino acid sequences of SEQ ID NOs: 689 and 267.

[0084] In some embodiments, the masked cytokine comprises (a) a first half-life extension domain comprising the amino acid sequence of SEQ ID NO: 155 and a second half-life extension domain comprising the amino acid sequence of SEQ ID NO: 156; (b) a masking moiety comprising the amino

acid sequence of SEQ ID NO: 261; and (c) a cytokine or functional fragment thereof comprising the amino acid sequence of SEQ ID NO: 1, wherein the masking moiety is linked to the first half-life extension domain via a first linker, the cytokine or functional fragment thereof is linked to the second half-life extension domain via a second linker, the first half-life extension domain and the second half-life extension domain contain modifications promoting the association of the first and the second half-life extension domain, wherein the first linker and/or the second linker comprises a cleavable peptide. In some embodiments, the masked cytokine comprises (a) a first half-life extension domain comprising the amino acid sequence of SEQ ID NO: 156 and a second half-life extension domain comprising the amino acid sequence of SEQ ID NO: 155; (b) a masking moiety comprising the amino acid sequence of SEQ ID NO: 261; and (c) a cytokine or functional fragment thereof comprising the amino acid sequence of SEQ ID NO: 1, wherein the masking moiety is linked to the first half-life extension domain via a first linker, the cytokine or functional fragment thereof is linked to the second half-life extension domain via a second linker, the first half-life extension domain and the second half-life extension domain contain modifications promoting the association of the first and the second half-life extension domain, wherein the first linker and/or the second linker comprises a cleavable peptide.

[0085] In some embodiments, the masked cytokine comprises the amino acid sequences of SEQ ID NOs: 562 and 563. In some embodiments, the masked cytokine comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 562, and comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 563.

[0086] In some embodiments, the masked cytokine comprises the amino acid sequences of SEQ ID NOs: 608 and 603. In some embodiments, the masked cytokine comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 608, and comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 603.

[0087] In some embodiments, the masked cytokine comprises the amino acid sequences of SEQ ID NOs: 604 and 603. In some embodiments, the masked cytokine comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 604, and comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 603.

[0088] In some embodiments, the masked cytokine comprises the amino acid sequences of SEQ ID NOs: 605 and 603. In some embodiments, the masked cytokine comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%,

98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 605, and comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 603.

[0089] In some embodiments, the masked cytokine comprises the amino acid sequences of SEQ ID NOs: 606 and 603. In some embodiments, the masked cytokine comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 606, and comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 603.

[0090] In some embodiments, the masked cytokine comprises the amino acid sequences of SEQ ID NOs: 615 and 617. In some embodiments, the masked cytokine comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 615, and comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 617.

[0091] In some embodiments, the masked cytokine comprises the amino acid sequences of SEQ ID NOs: 618 and 620. In some embodiments, the masked cytokine comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 618, and comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 620.

[0092] In some embodiments, the masked cytokine comprises the amino acid sequences of SEQ ID NOs: 621 and 623. In some embodiments, the masked cytokine comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 621, and comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 623.

[0093] In some embodiments, the masked cytokine comprises the amino acid sequences of SEQ ID NOs: 624 and 626. In some embodiments, the masked cytokine comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 624, and comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 626.

[0094] In some embodiments, the masked cytokine comprises the amino acid sequences of SEQ ID NOs: 608 and 267. In some embodiments, the masked cytokine comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%,

98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 608, and comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 267.

[0095] In some embodiments, the masked cytokine comprises the amino acid sequences of SEQ ID NOs: 663 and 664. In some embodiments, the masked cytokine comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 663, and comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 664.

[0096] In some embodiments, the masked cytokine comprises the amino acid sequences of SEQ ID NOs: 665 and 666. In some embodiments, the masked cytokine comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 665, and comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 666.

[0097] In some embodiments, the masked cytokine comprises the amino acid sequences of SEQ ID NOs: 667 and 267. In some embodiments, the masked cytokine comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 667, and comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 267.

[0098] In some embodiments, the masked cytokine comprises the amino acid sequences of SEQ ID NOs: 669 and 267. In some embodiments, the masked cytokine comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 669, and comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 267.

[0099] In some embodiments, the masked cytokine comprises the amino acid sequences of SEQ ID NOs: 670 and 671. In some embodiments, the masked cytokine comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 670, and comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 671.

[0100] In some embodiments, the masked cytokine comprises the amino acid sequences of SEQ ID NOs: 672 and 267. In some embodiments, the masked cytokine comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%,

98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 672, and comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 267.

[0101] In some embodiments, the masked cytokine comprises the amino acid sequences of SEQ ID NOs: 673 and 267. In some embodiments, the masked cytokine comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 673, and comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 267.

[0102] In some embodiments, the masked cytokine comprises the amino acid sequences of SEQ ID NOs: 674 and 267. In some embodiments, the masked cytokine comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 674, and comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 267.

[0103] In some embodiments, the masked cytokine comprises the amino acid sequences of SEQ ID NOs: 675 and 267. In some embodiments, the masked cytokine comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 675, and comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 267.

[0104] In some embodiments, the masked cytokine comprises the amino acid sequences of SEQ ID NOs: 676 and 267. In some embodiments, the masked cytokine comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 676, and comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 267.

[0105] In some embodiments, the masked cytokine comprises the amino acid sequences of SEQ ID NOs: 677 and 267. In some embodiments, the masked cytokine comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 677, and comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 267.

[0106] In some embodiments, the masked cytokine comprises the amino acid sequences of SEQ ID NOs: 678 and 267. In some embodiments, the masked cytokine comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%,

98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 678, and comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 267.

[0107] In some embodiments, the masked cytokine comprises the amino acid sequences of SEQ ID NOs: 679 and 267. In some embodiments, the masked cytokine comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 679, and comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 267.

[0108] In some embodiments, the masked cytokine comprises the amino acid sequences of SEQ ID NOs: 680 and 267. In some embodiments, the masked cytokine comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 680, and comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 267.

[0109] In some embodiments, the masked cytokine comprises the amino acid sequences of SEQ ID NOs: 681 and 267. In some embodiments, the masked cytokine comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 681, and comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 267.

[0110] In some embodiments, the masked cytokine comprises the amino acid sequences of SEQ ID NOs: 682 and 267. In some embodiments, the masked cytokine comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 682, and comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 267.

[0111] In some embodiments, the masked cytokine comprises the amino acid sequences of SEQ ID NOs: 683 and 267. In some embodiments, the masked cytokine comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 683, and comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 267.

[0112] In some embodiments, the masked cytokine comprises the amino acid sequences of SEQ ID NOs: 684 and 267. In some embodiments, the masked cytokine comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%,

98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 684, and comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 267.

[0113] In some embodiments, the masked cytokine comprises the amino acid sequences of SEQ ID NOs: 685 and 267. In some embodiments, the masked cytokine comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 685, and comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 267.

[0114] In some embodiments, the masked cytokine comprises the amino acid sequences of SEQ ID NOs: 686 and 267. In some embodiments, the masked cytokine comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 686, and comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 267.

[0115] In some embodiments, the masked cytokine comprises the amino acid sequences of SEQ ID NOs: 687 and 267. In some embodiments, the masked cytokine comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 687, and comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 267.

[0116] In some embodiments, the masked cytokine comprises the amino acid sequences of SEQ ID NOs: 688 and 267. In some embodiments, the masked cytokine comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 688, and comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 267.

[0117] In some embodiments, the masked cytokine comprises the amino acid sequences of SEQ ID NOs: 689 and 267. In some embodiments, the masked cytokine comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 689, and comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 267.

[0118] In some embodiments, the masked cytokine comprises the amino acid sequences of SEQ ID NOs: 690 and 267. In some embodiments, the masked cytokine comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%,

98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 690, and comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 267.

[0119] In some embodiments, the masked cytokine comprises the amino acid sequences of SEQ ID NOs: 266 and 267. In some embodiments, the masked cytokine comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 266, and comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 267.

[0120] In some embodiments, the masked cytokine comprises the amino acid sequences of SEQ ID NOs: 692 and 267. In some embodiments, the masked cytokine comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 692, and comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 267.

[0121] In some embodiments, the masked cytokine comprises the amino acid sequences of SEQ ID NOs: 693 and 267. In some embodiments, the masked cytokine comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 693, and comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 267.

[0122] In some embodiments, the masked cytokine comprises the amino acid sequences of SEQ ID NOs: 694 and 267. In some embodiments, the masked cytokine comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 694, and comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 267.

[0123] In some embodiments, the masked cytokine comprises the amino acid sequences of SEQ ID NOs: 695 and 267. In some embodiments, the masked cytokine comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 695, and comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 267.

[0124] In some embodiments, the masked cytokine comprises the amino acid sequences of SEQ ID NOs: 696 and 267. In some embodiments, the masked cytokine comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%,

98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 696, and comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 267.

[0125] In some embodiments, the masked cytokine comprises the amino acid sequences of SEQ ID NOs: 697 and 267. In some embodiments, the masked cytokine comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 697, and comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 267.

[0126] In some embodiments, the masked cytokine comprises the amino acid sequences of SEQ ID NOs: 698 and 267. In some embodiments, the masked cytokine comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 698, and comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 267.

[0127] In some embodiments, the masked cytokine comprises the amino acid sequences of SEQ ID NOs: 699 and 267. In some embodiments, the masked cytokine comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 699, and comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 267.

[0128] In some embodiments, the masked cytokine comprises the amino acid sequences of SEQ ID NOs: 700 and 267. In some embodiments, the masked cytokine comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 700, and comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 267.

[0129] In some embodiments, the masked cytokine comprises the amino acid sequences of SEQ ID NOs: 701 and 267. In some embodiments, the masked cytokine comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 701, and comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 267.

[0130] In some embodiments, the masked cytokine comprises the amino acid sequences of SEQ ID NOs: 702 and 267. In some embodiments, the masked cytokine comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%,

98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 702, and comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 267.

[0131] In some embodiments, the masked cytokine comprises the amino acid sequences of SEQ ID NOs: 703 and 267. In some embodiments, the masked cytokine comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 703, and comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 267.

[0132] In some embodiments, the masked cytokine comprises the amino acid sequences of SEQ ID NOs: 704 and 267. In some embodiments, the masked cytokine comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 704, and comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 267.

[0133] In some embodiments, the masked cytokine comprises the amino acid sequences of SEQ ID NOs: 705 and 267. In some embodiments, the masked cytokine comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 705, and comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 267.

[0134] In some embodiments, the masked cytokine comprises the amino acid sequences of SEQ ID NOs: 706 and 267. In some embodiments, the masked cytokine comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 706, and comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 267.

[0135] In some embodiments, the masked cytokine comprises the amino acid sequences of SEQ ID NOs: 707 and 267. In some embodiments, the masked cytokine comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 707, and comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 267.

[0136] In some embodiments, the masked cytokine comprises the amino acid sequences of SEQ ID NOs: 708 and 267. In some embodiments, the masked cytokine comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%,

98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 708, and comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 267.

[0137] In some embodiments, the masked cytokine comprises the amino acid sequences of SEQ ID NOs: 709 and 267. In some embodiments, the masked cytokine comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 709, and comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 267.

[0138] In some embodiments, the masked cytokine comprises the amino acid sequences of SEQ ID NOs: 710 and 267. In some embodiments, the masked cytokine comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 710, and comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 267.

[0139] In some embodiments, the masked cytokine comprises the amino acid sequences of SEQ ID NOs: 711 and 267. In some embodiments, the masked cytokine comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 711, and comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 267.

[0140] In some embodiments, the masked cytokine comprises the amino acid sequences of SEQ ID NOs: 712 and 667. In some embodiments, the masked cytokine comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 712, and comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 667.

[0141] In some embodiments, the masked cytokine comprises the amino acid sequences of SEQ ID NOs: 713 and 267. In some embodiments, the masked cytokine comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 713, and comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 267.

[0142] In some embodiments, the masked cytokine comprises the amino acid sequences of SEQ ID NOs: 714 and 267. In some embodiments, the masked cytokine comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%,

98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 714, and comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 267.

[0143] In some embodiments, the masked cytokine comprises the amino acid sequences of SEQ ID NOs: 716 and 699. In some embodiments, the masked cytokine comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 716, and comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 699.

[0144] In some embodiments, the masked cytokine comprises the amino acid sequences of SEQ ID NOs: 717 and 267. In some embodiments, the masked cytokine comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 717, and comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 267.

[0145] In some embodiments, the masked cytokine comprises the amino acid sequences of SEQ ID NOs: 718 and 267. In some embodiments, the masked cytokine comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 718, and comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 267.

[0146] In some embodiments, the masked cytokine comprises the amino acid sequences of SEQ ID NOs: 719 and 267. In some embodiments, the masked cytokine comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 719, and comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 267.

[0147] In some embodiments, the masked cytokine comprises the amino acid sequences of SEQ ID NOs: 720 and 267. In some embodiments, the masked cytokine comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 720, and comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 267.

[0148] In some embodiments, the masked cytokine comprises the amino acid sequences of SEQ ID NOs: 722 and 267. In some embodiments, the masked cytokine comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%,

98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 722, and comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 267.

[0149] In some embodiments, the masked cytokine comprises the amino acid sequences of SEQ ID NOs: 723 and 267. In some embodiments, the masked cytokine comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 723, and comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 267.

[0150] In some embodiments, the masked cytokine comprises the amino acid sequences of SEQ ID NOs: 726 and 267. In some embodiments, the masked cytokine comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 720, and comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 267.

[0151] In some embodiments, the masked cytokine comprises the amino acid sequences of SEQ ID NOs: 728 and 267. In some embodiments, the masked cytokine comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 728, and comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 267.

[0152] In some embodiments, the masked cytokine comprises the amino acid sequences of SEQ ID NOs: 729 and 267. In some embodiments, the masked cytokine comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 729, and comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 267.

[0153] In some embodiments, the masked cytokine comprises the amino acid sequences of SEQ ID NOs: 730 and 267. In some embodiments, the masked cytokine comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 730, and comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 267.

[0154] In some embodiments, the masked cytokine comprises the amino acid sequences of SEQ ID NOs: 731 and 267. In some embodiments, the masked cytokine comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%,

98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 731, and comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 267.

[0155] In some embodiments, the masked cytokine comprises the amino acid sequences of SEQ ID NOs: 732 and 267. In some embodiments, the masked cytokine comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 732, and comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 267.

[0156] In some embodiments, the masked cytokine comprises the amino acid sequences of SEQ ID NOs: 733 and 267. In some embodiments, the masked cytokine comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 733, and comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 267.

[0157] In some embodiments, the masked cytokine comprises the amino acid sequences of SEQ ID NOs: 734 and 267. In some embodiments, the masked cytokine comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 734, and comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 267.

[0158] In some embodiments, the masked cytokine comprises the amino acid sequences of SEQ ID NOs: 735 and 267. In some embodiments, the masked cytokine comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 735, and comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 267.

[0159] In some embodiments, the masked cytokine comprises the amino acid sequences of SEQ ID NOs: 736 and 267. In some embodiments, the masked cytokine comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 736, and comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 267.

[0160] In some embodiments, the masked cytokine comprises the amino acid sequences of SEQ ID NOs: 737 and 267. In some embodiments, the masked cytokine comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%,

98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 737, and comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 267.

[0161] In some embodiments, the masked cytokine comprises the amino acid sequences of SEQ ID NOs: 738 and 267. In some embodiments, the masked cytokine comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 738, and comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 267.

[0162] In some embodiments, the masked cytokine comprises the amino acid sequences of SEQ ID NOs: 739 and 267. In some embodiments, the masked cytokine comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 739, and comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 267.

[0163] In some embodiments, the masked cytokine comprises the amino acid sequences of SEQ ID NOs: 740 and 267. In some embodiments, the masked cytokine comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 740, and comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 267.

[0164] In some embodiments, the masked cytokine comprises the amino acid sequences of SEQ ID NOs: 741 and 267. In some embodiments, the masked cytokine comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 741, and comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 267.

[0165] In some embodiments, the masked cytokine comprises the amino acid sequences of SEQ ID NOs: 742 and 267. In some embodiments, the masked cytokine comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 742, and comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 267.

[0166] In some embodiments, the masked cytokine comprises the amino acid sequences of SEQ ID NOs: 743 and 267. In some embodiments, the masked cytokine comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%,

98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 743, and comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 267.

[0167] In some embodiments, the masked cytokine comprises the amino acid sequences of SEQ ID NOs: 744 and 267. In some embodiments, the masked cytokine comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 744, and comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 267.

[0168] In some embodiments, the masked cytokine comprises the amino acid sequences of SEQ ID NOs: 745 and 267. In some embodiments, the masked cytokine comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 745, and comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 267.

[0169] In some embodiments, the masked cytokine comprises the amino acid sequences of SEQ ID NOs: 746 and 267. In some embodiments, the masked cytokine comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 746, and comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 267.

[0170] In some embodiments, the masked cytokine comprises the amino acid sequences of SEQ ID NOs: 674 and 828. In some embodiments, the masked cytokine comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 674, and comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 828.

[0171] In some embodiments, the masked cytokine comprises the amino acid sequences of SEQ ID NOs: 674 and 829. In some embodiments, the masked cytokine comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 674, and comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 829.

[0172] In some embodiments, the masked cytokine comprises the amino acid sequences of SEQ ID NOs: 726 and 830. In some embodiments, the masked cytokine comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%,

98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 726, and comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 830.

[0173] In some embodiments, the masked cytokine comprises the amino acid sequences of SEQ ID NOs: 726 and 829. In some embodiments, the masked cytokine comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 726, and comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 829.

[0174] In some embodiments, the masked cytokine comprises the amino acid sequences of SEQ ID NOs: 747 and 671. In some embodiments, the masked cytokine comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 747, and comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 671.

[0175] In some embodiments, the masked cytokine comprises the amino acid sequences of SEQ ID NOs: 715 and 267. In some embodiments, the masked cytokine comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 715, and comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 267.

[0176] In some embodiments, the masked cytokine comprises the amino acid sequences of SEQ ID NOs: 715 and 671. In some embodiments, the masked cytokine comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 715, and comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 671.

[0177] In some embodiments, the masked cytokine comprises the amino acid sequences of SEQ ID NOs: 748 and 671. In some embodiments, the masked cytokine comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 748, and comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 671.

[0178] In some embodiments, the masked cytokine comprises the amino acid sequences of SEQ ID NOs: 749 and 671. In some embodiments, the masked cytokine comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%,

98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 749, and comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 671.

[0179] In some embodiments, the masked cytokine comprises the amino acid sequences of SEQ ID NOs: 750 and 671. In some embodiments, the masked cytokine comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 750, and comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 671.

[0180] In some embodiments, the masked cytokine comprises the amino acid sequences of SEQ ID NOs: 751 and 671. In some embodiments, the masked cytokine comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 751, and comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 671.

[0181] In some embodiments, the masked cytokine comprises the amino acid sequences of SEQ ID NOs: 752 and 671. In some embodiments, the masked cytokine comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 752, and comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 671.

[0182] In some embodiments, the masked cytokine comprises the amino acid sequences of SEQ ID NOs: 753 and 671. In some embodiments, the masked cytokine comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 753, and comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 671.

[0183] In some embodiments, the masked cytokine comprises the amino acid sequences of SEQ ID NOs: 754 and 671. In some embodiments, the masked cytokine comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 754, and comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 671.

[0184] In some embodiments, the masked cytokine comprises the amino acid sequences of SEQ ID NOs: 758 and 671. In some embodiments, the masked cytokine comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%,

98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 758, and comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 671.

[0185] In some embodiments, the masked cytokine comprises the amino acid sequences of SEQ ID NOs: 759 and 671. In some embodiments, the masked cytokine comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 759, and comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 671.

[0186] In some embodiments, the masked cytokine comprises the amino acid sequences of SEQ ID NOs: 760 and 671. In some embodiments, the masked cytokine comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 760, and comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 671.

[0187] In some embodiments, the masked cytokine comprises the amino acid sequences of SEQ ID NOs: 761 and 671. In some embodiments, the masked cytokine comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 761, and comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 671.

[0188] In some embodiments, the masked cytokine is an exemplary masked cytokine construct as described in any of Tables 8-11, or is a variant created by modifying any of the exemplary constructs described in Tabls 8-11, such as by incorporating one or more additional components to the structure of the construct in accordance with the teachings herein.

[0189] Also provided herein, in some embodiments, is a masked cytokine comprising (a) a first half-life extension domain and a second half-life extension domain; (b) a first masking moiety and a second masking moiety; and (c) a cytokine or functional fragment thereof, wherein the first masking moiety is linked to the first half-life extension domain, the second masking moiety is linked to the cytokine or functional fragment thereof, either the second masking moiety or the cytokine or functional fragment thereof is linked to the second half-life extension domain, and the first half-life extension domain and the second half-life extension domain contain modifications promoting the association of the first and the second half-life extension domain. In some embodiments, the first masking moiety is linked to the first half-life extension domain via a first linker, and/or either the second masking moiety or the cytokine or functional fragment thereof is linked to the second half-life extension domain via a second linker. In some embodiments, the second masking moiety is linked to the cytokine or functional fragment thereof

via a third linker. In some embodiments, the first half-life extension domain is linked to the second half-life extension domain, optionally by a fourth linker. In some embodiments, the masked cytokine comprises the amino acid sequences of SEQ ID NOs: 755 and 616. In some embodiments, the masked cytokine comprises the amino acid sequences of SEQ ID NOs: 756 and 616. In some embodiments, the masked cytokine comprises the amino acid sequences of SEQ ID NOs: 757 and 616. In some embodiments, the masked cytokine comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 755, and an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 616. In some embodiments, the masked cytokine comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 756, and an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 616. In some embodiments, the masked cytokine comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 757, and an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 616.

[0190] In some embodiments, the masked cytokine comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 265-267, 556-720, 722, 723, 726, 728-761, and 828-830. In some embodiments, the masked cytokine comprises two different amino acid sequences selected from the group consisting of SEQ ID NOs: 265-267, 556-720, 722, 723, 726, 728-761, and 828-830. In some embodiments, the masked cytokine comprises the amino acid sequences associated with any of the exemplary constructs as described in Tables 4-11.

[0191] Each component of the masked cytokines provided herein is discussed in greater detail below.

A. Cytokines

[0192] Provided herein is a cytokine or functional fragment thereof. The cytokine or functional fragment thereof can be any cytokine, any functional fragment of any cytokine, or any natural or non-natural variant of any cytokine. A cytokine is a small polypeptide that plays a role in cellular signaling, particularly in cells of the immune system. Examples of cytokines may include chemokines, interferons, interleukins, lymphokines, and tumor necrosis factors.

[0193] Cytokines can be classified in a variety of ways, such as based on their three-dimensional structure. Examples include the β-trefoil fold class, the short-chain four-helix bundle class, and the long-chain four-helix bundle class.

[0194] The β-trefoil fold class includes cytokines that are characterized by three βββ-loop-β units (12 β strands total) that form a barrel structure with a hairpin cap for the barrel. Examples of cytokines in the β-trefoil fold class include IL-1α, IL-1β, IL-1 receptor antagonist (IL-1RA), IL-18, IL-33, IL-36 α, IL-36 β, IL-36γ, IL-36 receptor antagonist (IL-36RA), IL-37, and IL-38.

[0195] Short-chain and long-chain four-helix bundle classes are characterized by a monomeric helical bundle having four amphipathic helices oriented in a unique up-up-down-down topology. The short-chain four-helix bundle class is characterized by shorter helices, such as those 10-20 amino acid residues in length, while the long-chain four-helix bundle class is characterized by longer helices, such as those 20-30 amino acid residues in length. Examples of cytokines in the short-chain four-helix bundle class include IL-2, IL-3, IL-4, IL-5, IL-7, IL-9, IL-13, IL-15, IL-21, granulocyte-macrophage colony-stimulating factor (GM-CSF), and macrophage colony-stimulating factor (M-CSF). Examples of cytokine in the long-chain four-helix bundle class include IL-6, IL-11, IL-12, growth hormone (GH), erythropoietin (EPO), prolactin (PRL), leukemia inhibitory factor (LIF), oncostatin (OSM), and thrombopoietin (TPO).

[0196] In contrast to the short- and long-chain four-helix bundle classes, which are monomeric, some cytokines are homodimeric. Examples of dimeric cytokines include IL-10 and IFN-γ (gamma).

[0197] Some cytokines are classified as being heterodimeric. Examples of heterodimeric cytokines include IL-12 and IL-23.

[0198] Some cytokines, such as IL-15, also function by binding to, and being presented by, a membrane-bound cytokine receptor.

[0199] In some embodiments, the cytokine or functional fragment thereof is IL-2, or is a functional fragment or variant of IL-2. In some embodiments, the cytokine or functional fragment thereof is IL-15, or is a functional fragment or variant of IL-15. In some embodiments, the cytokine or functional fragment thereof is selected from the group consisting of IL-2, IL-10, IL-12, IL-15, IL-18, interferon (IFN)-α (alpha), IFN-β (beta), and IFN-γ (gamma). In some embodiments, the cytokine or functional fragment thereof is a functional fragment or variant of IL-2, IL-10, IL-12, IL-15, IL-18, IFN-α (alpha), IFN-β (beta), or IFN-γ (gamma).

[0200] In some embodiments, the cytokine or functional fragment thereof is selected from the group consisting of IL-1α, IL-1β, IL-1 receptor antagonist (IL-1RA), IL-18, IL-33, IL-36 α, IL-36 β, IL-36γ, IL-36 receptor antagonist (IL-36RA), IL-37, and IL-38.

[0201] In some embodiments, the cytokine or functional fragment thereof is selected from the group consisting of IL-2, IL-3, IL-4, IL-5, IL-7, IL-9, IL-13, IL-15, IL-21, granulocyte-macrophage colony-

stimulating factor (GM-CSF), macrophage colony-stimulating factor (M-CSF), IL-6, IL-11, IL-12, growth hormone (GH), erythropoietin (EPO), prolactin (PRL), leukemia inhibitory factor (LIF), oncostatin (OSM), and thrombopoietin (TPO).

[0202] In some embodiments, the cytokine or functional fragment thereof is selected from the group consisting of CXCL1, CXCL2, CXCL3, CXCL4, CXCL5, CXCL6, CXCL7, CXCL8, CXCL9, CXCL10, CXCL11, CXCL12, CXCL13, CXCL14, CXCL15, CXCL16, CCL1e, CCL2, CCL3, CCL3L1, CCL4, CCL5, CCL6, CCL7, CCL8, CCL9/10, CCL11, CCL12, CCL13, CCL14, CCL15, CCL16, CCL17, CCL18, CCL19, CCL20, CCL21, CCL22, CCL23, CCL24, CCL25, CCL26, CCL27, CCL28, CX3CL1, XCL1, and XCL2. In some embodiments, the cytokine or functional fragment thereof is a functional fragment or variant of CXCL1, CXCL2, CXCL3, CXCL4, CXCL5, CXCL6, CXCL7, CXCL8, CXCL9, CXCL10, CXCL11, CXCL12, CXCL13, CXCL14, CXCL15, CXCL16, CCL1e, CCL2, CCL3, CCL3L1, CCL4, CCL5, CCL6, CCL7, CCL8, CCL9/10, CCL11, CCL12, CCL13, CCL14, CCL15, CCL16, CCL17, CCL18, CCL19, CCL20, CCL21, CCL22, CCL23, CCL24, CCL25, CCL26, CCL27, CCL28, CX3CL1, XCL1, or XCL2.

[0203] In some embodiments, the cytokine or functional fragment thereof is selected from the group consisting of IFN-α (alpha), IFN-β (beta), IFN-γ (gamma), IFN-ε (epsilon), IFN-κ (kappa), IFN-ώ (omega), IFN-τ (tau), IFN-ζ (zeta), IFN-δ (delta), and IFN-λ (lambda). In some embodiments, the cytokine or functional fragment thereof is a functional fragment or variant of IFN-α (alpha), IFN-β (beta), IFN-γ (gamma), IFN-ε (epsilon), IFN-κ (kappa), IFN-ώ (omega), IFN-τ (tau), IFN-ζ (zeta), IFN-δ (delta), or IFN-λ (lambda).

[0204] In some embodiments, the cytokine or functional fragment thereof is selected from the group consisting of IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, IL-13, IL-14, IL-15, IL-16, IL-17, IL-18, IL-19, IL-20, IL-21, IL-22, IL-23, IL-24, IL-25, IL-26, IL-27, IL-28A, IL-28B, IL-29, IL-30, IL-31, IL-32, IL-33, IL-34, IL-35, IL-36, and IL-37. In some embodiments, the cytokine or functional fragment thereof is a functional fragment or variant of IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, IL-13, IL-14, IL-15, IL-16, IL-17A, IL-17C, IL-17D, IL-17F, IL-17A/F, IL-18, IL-19, IL-20, IL-21, IL-22, IL-23, IL-24, IL-25, IL-26, IL-27, IL-28A, IL-28B, IL-29, IL-30, IL-31, IL-32, IL-33, IL-34, IL-35, IL-36, or IL-37.

[0205] In some embodiments, the cytokine or functional fragment thereof is selected from the group consisting of granulocyte-macrophage colony-stimulating factor (GM-CSF), macrophage colony-stimulating factor (M-CSF), tumor necrosis factor alpha (TNF-α), transforming growth factor beta (TGF-β), IFN-γ (gamma), IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, and IL-12. In some embodiments, the cytokine or functional fragment thereof is a functional fragment or variant of granulocyte-macrophage colony-stimulating factor (GM-CSF), macrophage colony-stimulating factor (M-CSF), tumor necrosis factor alpha (TNF-α), transforming growth factor beta (TGF-β), IFN-γ (gamma), IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, or IL-12.

[0206] In some embodiments, the cytokine or functional fragment thereof is selected from the group consisting of TNF-α (alpha), TNF-β (beta), TNF-γ (gamma), CD252, CD154, CD178, CD70, CD153, 4-1BB-L, TRAIL, RANKL, APO3L, CD256, CD257, CD258, TL1, AITRL, and EDA1. In some embodiments, the cytokine or functional fragment thereof is a functional fragment or variant of TNF-α (alpha), TNF-β (beta), TNF-γ (gamma), CD252, CD154, CD178, CD70, CD153, 4-1BB-L, TRAIL, RANKL, APO3L, CD256, CD257, CD258, TL1, AITRL, and EDA1.

[0207] The cytokine or functional fragment thereof comprises an amino-terminus and a carboxy-terminus. In some embodiments, a half-life extension domain is linked to the amino-terminus or the carboxy-terminus of the cytokine or functional fragment thereof. In some embodiments, a masking moiety is linked to the amino-terminus or the carboxy-terminus of the cytokine or functional fragment thereof. In some embodiments, a linker is linked to the amino-terminus or the carboxy-terminus of the cytokine or functional fragment thereof. In some embodiments, a cleavable peptide of a linker is linked to the amino-terminus or the carboxy-terminus of the cytokine or functional fragment thereof. In some embodiments, an N-terminal spacer domain or a C-terminal spacer domain of a linker is linked to the amino-terminus or the carboxy-terminus of the cytokine or functional fragment thereof.

[0208] Exemplary embodiments of the cytokine or functional fragment thereof in the form of IL-2 polypeptides or functional fragments thereof, and IL-15 polypeptides or functional fragments thereof, are provided below in detail.

1. IL-2 Polypeptides

[0209] In some embodiments, the cytokine or functional fragment thereof is an IL-2 polypeptide or functional fragment thereof. In eukaryotic cells, IL-2 is synthesized as a precursor polypeptide of 153 amino acids, which is then processed into mature IL-2 by the removal of amino acid residues 1-20. This results in a mature form of IL-2 consisting of 133 amino acids (amino acid residues 21-153) that is secreted in a mature, active form.

[0210] In some embodiments, the IL-2 polypeptide or functional fragment thereof is any naturally occurring interleukin-2 (IL-2) protein or modified variant thereof capable of binding to, or otherwise exhibiting affinity for, an interleukin-2 receptor (IL-2R) or component thereof (e.g., the IL-2Rα chain). In some embodiments, the IL-2 polypeptide or functional fragment thereof is a mature form of IL-2 that consists of amino acid residues 21-153 of SEQ ID NO: 159. In some embodiments, the IL-2 polypeptide or functional fragment thereof comprises the amino acid sequence of SEQ ID NO: 160. In some embodiments, the IL-2 polypeptide or functional fragment thereof comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 1-8 and 260. In some embodiments, the IL-2 polypeptide or functional fragment thereof comprises the amino acid sequence of SEQ ID NO: 260. In some embodiments, the IL-2 polypeptide or functional fragment thereof comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 1-8, 160, 230, 243-251, 260, 775-792, and

813-822. In some embodiments, the IL-2 polypeptide or functional fragment thereof comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NOs: 1-8, 160, 243-251, 260, 775-792, and 813-822. In some embodiments, the IL-2 polypeptide or functional fragment thereof comprises the amino acid sequence of SEQ ID NO: 230. In some embodiments, the IL-2 polypeptide or functional fragment thereof comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 230. In some embodiments, the IL-2 polypeptide or functional fragment thereof comprises the amino acid sequence of SEQ ID NO: 3. In some embodiments, the IL-2 polypeptide or functional fragment thereof comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 3.

[0211] In some embodiments, the IL-2 polypeptide or functional fragment thereof comprises an amino acid sequence produced by at least one amino acid modification to an amino acid sequence selected from the group consisting of SEQ ID NOs: 1-8, 160, 230, 243-251, 260, 775-792, and 813-822. Each of the at least one amino acid modifications can be any amino acid modification, such as a substitution, insertion, or deletion. In some embodiments, the IL-2 polypeptide or functional fragment thereof comprises an amino acid sequence produced by at least 1, at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, or at least 10 amino acid substitutions in the amino acid sequence of any one of SEQ ID NOs: 1-8, 160, 230, 243-251, 260, 775-792, and 813-822. In some embodiments, the IL-2 peptide or functional fragment thereof comprises an amino acid sequence that comprises a serine (S), glycine (G), or alanine (A) residue at amino acid residue 125. In some embodiments the IL-2 peptide or functional fragment thereof comprises an amino acid sequence that comprises an alanine (A) residue at amino acid residue 3. For example, in some embodiments, the IL-2 peptide or functional fragment thereof comprises an amino acid sequence produced by introducing a T3A amino acid substitution to an amino acid sequence selected from the group consisting of SEQ ID NOs: 1-8 and 160. In some embodiments, the IL-2 peptide or functional fragment thereof comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 243-251 and 260. In some embodiments, the IL-2 peptide or functional fragment thereof comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 775-792, and 813-822.

[0212] In some embodiments, the IL-2 peptide or functional fragment thereof comprises an amino acid sequence having one or more amino acid substitutions compared to the amino acid sequence of wildtype IL-2 that reduces the affinity of the IL-2 peptide or functional fragment thereof for IL-2Rα (CD25). In some embodiments, the IL-2 polypeptide or functional fragment thereof comprises an amino acid sequence produced by one or more amino acid substitutions in the amino acid sequence of any one of SEQ ID NOs: 1-8, 160, 243-251, 260, 775-792, and 813-822, such that one or more of amino acid

residues 38, 42, 45, and 62 is an alanine (A). In some embodiments, the IL-2 polypeptide or functional fragment thereof comprises an amino acid sequence produced by one or more amino acid substitutions in the amino acid sequence of any one of SEQ ID NOs: 1-8, 160, 243-251, 260, 775-792, and 813-822, such that amino acid residues 38, 42, 45, and 62 are an alanine (A). In some embodiments, the IL-2 polypeptide or functional fragment thereof comprises an amino acid sequence produced by one or more amino acid substitutions in the amino acid sequence of any one of SEQ ID NOs: 1-8, 160, 243-251, 260, 775-792, and 813-822, such that amino acid residues 38, 42, 45, and 62 are an alanine (A) and amino acid residue 125 is a serine (S), glycine (G), or alanine (A). In some embodiments, the IL-2 polypeptide or functional fragment thereof comprises an amino acid sequence produced by one or more amino acid substitutions in the amino acid sequence of any one of SEQ ID NOs: 1-8, 160, 243-251, 260, 775-792, and 813-822, such that amino acid residues 38 and 42 are an alanine (A) and amino acid residue 125 is a serine (S), glycine (G), or alanine (A). In some embodiments, the IL-2 polypeptide or functional fragment thereof comprises an amino acid sequence produced by substituting amino acid residues R38, F42, Y45, and E62 for alanine in the amino acid sequence of SEQ ID NO: 160 or 251. In some embodiments, the IL-2 polypeptide or functional fragment thereof comprises an amino acid sequence produced by substituting amino acid residues R38, F42, Y45, and E62 for alanine (A) and by substituting amino acid residue C125 for serine (S), glycine (G), or alanine (A) in the amino acid sequence of SEQ ID NO: 160 or 251. In some embodiments, the IL-2 polypeptide or functional fragment thereof comprises an amino acid sequence produced by one or more amino acid substitutions in the amino acid sequence of any one of SEQ ID NOs: 1-8, 160, 243-251, 260, 775-792, and 813-822, such that amino acid residue 42 is lysine (K). In some embodiments, the IL-2 polypeptide or functional fragment thereof comprises an amino acid sequence produced by one or more amino acid substitutions in the amino acid sequence of any one of SEQ ID NOs: 1-8, 160, 243-251, 260, 775-792, and 813-822, such that amino acid residue 42 is lysine (K) and amino acid residue 125 is a serine (S), glycine (G), or alanine (A). In some embodiments, the IL-2 polypeptide or functional fragment thereof comprises an amino acid sequence produced by one or more amino acid substitutions in the amino acid sequence of any one of SEQ ID NOs: 1-8, 160, 243-251, 260, 775-792, and 813-822, such that amino acid residues 42 and 45 are alanine (A) and amino acid residue 72 is glycine (G). In some embodiments, the IL-2 polypeptide or functional fragment thereof comprises an amino acid sequence produced by one or more amino acid substitutions in the amino acid sequence of any one of SEQ ID NOs: 1-8, 160, 243-251, 260, 775-792, and 813-822, such that amino acid residues 42 and 45 are alanine (A), amino acid residue 72 is glycine (G), and amino acid residue 125 is a serine (S), glycine (G), or alanine (A). In some embodiments, the IL-2 polypeptide or functional fragment thereof comprises an amino acid sequence produced by one or more amino acid substitutions in the amino acid sequence of any one of SEQ ID NOs: 1-8, 160, 243-251, 260, 775-792, and 813-822, such that amino acid residue 62 is an arginine (R) or serine (S). In some embodiments, the IL-2 polypeptide or functional fragment thereof comprises an amino acid sequence produced by one or

more amino acid substitutions in the amino acid sequence of any one of SEQ ID NOs: 1-8, 160, 243-251, 260, 775-792, and 813-822, such that amino acid residue 42 is glutamic acid (E). In some embodiments, the IL-2 polypeptide or functional fragment thereof comprises an amino acid sequence produced by one or more amino acid substitutions in the amino acid sequence of any one of SEQ ID NOs: 1-8, 160, 243-251, 260, 775-792, and 813-822, such that amino acid residue 43 is alanine (A). In some embodiments, the IL-2 polypeptide or functional fragment thereof comprises an amino acid sequence produced by one or more amino acid substitutions in the amino acid sequence of any one of SEQ ID NOs: 1-8, 160, 243-251, 260, 775-792, and 813-822, such that amino acid residue 45 is asparagine (N), arginine (R), or alanine (A). In some embodiments, the IL-2 polypeptide or functional fragment thereof comprises an amino acid sequence produced by one or more amino acid substitutions in the amino acid sequence of any one of SEQ ID NOs: 1-8, 160, 243-251, 260, 775-792, and 813-822, such that amino acid residue 45 is alanine (A) and amino acid residue 62 is serine (S). In some embodiments, the IL-2 polypeptide or functional fragment thereof comprises an amino acid sequence produced by one or more amino acid substitutions in the amino acid sequence of any one of SEQ ID NOs: 1-8, 160, 243-251, 260, 775-792, and 813-822, such that amino acid residue 42 is serine (S), amino acid residue 62 is serine (S). In some embodiments, the IL-2 polypeptide or functional fragment thereof comprises an amino acid sequence produced by one or more amino acid substitutions in the amino acid sequence of any one of SEQ ID NOs: 1-8, 160, 243-251, 260, 775-792, and 813-822, such that amino acid residue 38 is glycine (G), amino acid residue 45 is alanine (A), and amino acid residue 62 is serine (S).

[0213] In some embodiments, the IL-2 peptide or functional fragment thereof comprises an amino acid sequence produced by introducing one or more of the following amino acid substitutions into any one of SEQ ID NOs: 1-8, 160, 243-251, 260, 775-792, and 813-822: R38A, F42A, F42E, F42K, K43A, Y45A, Y45N, Y45R, E62A, E62R, E62S, L72G, C125S, C125G, and C125A.

[0214] In some embodiments, the IL-2 polypeptide or functional fragment thereof comprises an amino acid sequence having one or more amino acid substitutions compared to the amino acid sequence of wildtype IL-2 that enhances the affinity of the IL-2 polypeptide or functional fragment thereof for IL-2Rβ (CD122). In some embodiments, the IL-2 polypeptide or functional fragment thereof comprises an amino acid sequence produced by one or more amino acid substitutions in the amino acid sequence of any one of SEQ ID NOs: 1-8, 160, 243-251, 260, 775-792, and 813-822, such that amino acid residue 80 is phenylalanine (F), amino acid residue 81 is aspartic acid (D), amino acid residue 85 is valine (V), amino acid residue 86 is valine (V), or amino acid residue 92 is phenylalanine (F), or combinations thereof. In some embodiments, the IL-2 polypeptide or functional fragment thereof comprises an amino acid sequence produced by one or more amino acid substitutions in the amino acid sequence of any one of SEQ ID NOs: 1-8, 160, 243-251, 260, 775-792, and 813-822, such that amino acid residue 80 is phenylalanine (F), amino acid residue 81 is aspartic acid (D), amino acid residue 85 is valine (V), amino acid residue 86 is valine (V), or amino acid residue 92 is phenylalanine (F), or combinations thereof, and

amino acid residue 125 is serine (S), glycine (G), or alanine (A). In some embodiments, the IL-2 polypeptide or functional fragment thereof comprises an amino acid sequence produced by one or more amino acid substitutions in the amino acid sequence of any one of SEQ ID NOs: 1-8, 160, 243-251, 260, 775-792, and 813-822, such that amino acid residue 80 is phenylalanine (F), amino acid residue 81 is aspartic acid (D), amino acid residue 85 is valine (V), amino acid residue 86 is valine (V), and amino acid residue 92 is phenylalanine (F). In some embodiments, the IL-2 polypeptide or functional fragment thereof comprises an amino acid sequence produced by one or more amino acid substitutions in the amino acid sequence of any one of SEQ ID NOs: 1-8, 160, 243-251, 260, 775-792, and 813-822, such that amino acid residue 80 is phenylalanine (F), amino acid residue 81 is aspartic acid (D), amino acid residue 85 is valine (V), amino acid residue 86 is valine (V), amino acid residue 92 is phenylalanine (F), and amino acid residue 125 is serine (S), glycine (G), or alanine (A). In some embodiments, the IL-2 polypeptide or functional fragment thereof comprises an amino acid sequence produced by one or more amino acid substitutions in the amino acid sequence of any one of SEQ ID NOs: 1-8, 160, 243-251, 260, 775-792, and 813-822, such that amino acid residue 18 is a cysteine (C). In some embodiments, the IL-2 polypeptide or functional fragment thereof comprises an amino acid sequence produced by one or more amino acid substitutions in the amino acid sequence of any one of SEQ ID NOs: 1-8, 160, 243-251, 260, 775-792, and 813-822, such that amino acid residue 20 is an alanine (A), leucine (L), or phenylalanine (F). In some embodiments, the IL-2 polypeptide or functional fragment thereof comprises an amino acid sequence produced by one or more amino acid substitutions in the amino acid sequence of any one of SEQ ID NOs: 1-8, 160, 243-251, 260, 775-792, and 813-822, such that amino acid residue 16 is an isoleucine. In some embodiments, the IL-2 polypeptide or functional fragment thereof comprises an amino acid sequence produced by one or more amino acid substitutions in the amino acid sequence of any one of SEQ ID NOs: 1-8, 160, 243-251, 260, 775-792, and 813-822, such that amino acid residue 29 is a leucine (L).

[0215] In some embodiments, the IL-2 peptide or functional fragment thereof comprises an amino acid sequence produced by introducing one or more of the following amino acid substitutions into any one of SEQ ID NOs: 1-8, 160, 243-251, 260, 775-792, and 813-822: L18C, D20A, D20L, D20F, H16I, N29L, L80F, R81D, L85V, I86V, I92F, C125S, C125G, and C125A.

[0216] In some embodiments, the IL-2 polypeptide or functional fragment thereof comprises an amino acid sequence having one or more amino acid substitutions compared to the amino acid sequence of wildtype IL-2 that reduces the affinity of the IL-2 peptide or functional fragment thereof for IL-2Rα (CD25), and one or more amino acid substitutions compared to the amino acid sequence of wildtype IL-2 that enhances the affinity of the IL-2 polypeptide or functional fragment thereof for IL-2Rβ (CD122). In some embodiments, the IL-2 polypeptide or functional fragment thereof comprises an amino acid sequence produced by one or more amino acid substitutions in the amino acid sequence of any one of SEQ ID NOs: 1-8, 160, 243-251, 260, 775-792, and 813-822, such that one or more of amino acid

residues 38, 42, 45, and 62 is an alanine (A), amino acid residue 42 is lysine (K), amino acid residue 72 is glycine (G), amino acid residue 80 is phenylalanine (F), amino acid residue 81 is aspartic acid (D), amino acid residue 85 is valine (V), amino acid residue 86 is valine (V), or amino acid residue 92 is phenylalanine (F), or combinations thereof. As such, in some embodiments, the IL-2 polypeptide or functional fragment thereof comprises an amino acid sequence that comprises one or more of the following amino acid substitutions compared to the mature form of wildtype IL-2: D20A, D20L, D20F, H16I, L18C, N29L, R38A, F42A, F42E, F42K, K43A, Y45A, Y45N, Y45R, E62A, E62R, E62S, L72G, L80F, R81D, L85V, I86V, I92F, C125S, C125G, and C125A.

[0217] In some embodiments, the IL-2 polypeptide or functional fragment thereof comprises an amino acid sequence produced by one or more amino acid substitutions in the amino acid sequence of any one of SEQ ID NOs: 1-8, 160, 243-251, 260, 775-792, and 813-822, such that amino acid residue 38 is a glycine (G), alanine (A), lysine (K), or tryptophan (W), amino acid residue 42 is an alanine (A), lysine (K), or isoleucine (I), amino acid residue 45 is an alanine (A) or asparagine (N), amino acid residue 62 is an alanine (A) or a leucine (L), or amino acid residue 68 is a valine (V), or combinations thereof. In some embodiments, the IL-2 polypeptide or functional fragment thereof comprises an amino acid sequence produced by one or more amino acid substitutions in the amino acid sequence of any one of SEQ ID NOs: 1-8, 160, 243-251, 260, 775-792, and 813-822, such that amino acid residue 38 is a lysine (K), amino acid residue 42 is a glutamine (Q), amino acid residue 45 is a glutamic acid (E), or amino acid residue 68 is a valine (V), or combinations thereof. In some embodiments, the IL-2 polypeptide or functional fragment thereof comprises an amino acid sequence produced by one or more amino acid substitutions in the amino acid sequence of any one of SEQ ID NOs: 1-8, 160, 243-251, 260, 775-792, and 813-822, such that amino acid residue 38 is an alanine (A), amino acid residue 42 is an isoleucine (I), amino acid residue 45 is an asparagine (N), amino acid residue 62 is a leucine (L), or amino acid residue 68 is a valine (V), or combinations thereof. In some embodiments, the IL-2 polypeptide or functional fragment thereof comprises an amino acid sequence produced by one or more amino acid substitutions in the amino acid sequence of any one of SEQ ID NOs: 1-8, 160, 243-251, 260, 775-792, and 813-822, such that amino acid residue 38 is a lysine (K), amino acid residue 42 is a lysine (K), amino acid residue 45 is an arginine (R), amino acid residue 62 is a leucine (L), or amino acid residue 68 is a valine (V), or combinations thereof. In some embodiments, the IL-2 polypeptide or functional fragment thereof comprises an amino acid sequence produced by one or more amino acid substitutions in the amino acid sequence of any one of SEQ ID NOs: 1-8, 160, 243-251, 260, 775-792, and 813-822, such that amino acid residue 38 is an alanine (A) or lysine (K), amino acid residue 42 is an alanine (A), amino acid residue 45 is an alanine (A), or amino acid residue 62 is an alanine (A), or combinations thereof. In some embodiments, the IL-2 polypeptide or functional fragment thereof comprises an amino acid sequence produced by one or more amino acid substitutions in the amino acid sequence of any one of SEQ ID NOs: 1-8, 160, 243-251, 260, 775-792, and 813-822, such that amino

acid residue 42 is an isoleucine (I), amino acid residue 45 is a glutamic acid (E), or amino acid residue 68 is a valine (V), or combinations thereof.

[0218] In some embodiments, the IL-2 polypeptide or functional fragment thereof comprises an amino acid sequence produced by introducing, or further introducing, a C125S, C125G, or C125A substitution into any one of the amino acid sequences for an IL-2 polypeptide or functional fragment thereof described herein.

[0219] In some embodiments, one or more amino acid residues are removed from the amino acid sequence of the IL-2 polypeptide or functional fragment thereof for the purpose of removing an O-glycosylation site. In some embodiments, the IL-2 polypeptide or functional fragment thereof comprises an amino acid sequence produced by deleting the first three amino acid residues (residues 1-3) of the amino acid sequence of any of the IL-2 polypeptides or functional fragments thereof disclosed herein. In some embodiments, one or more amino acid residues are substituted into the amino acid sequence of the IL-2 polypeptide or functional fragment thereof for the purpose of removing an O-glycosylation site. In some embodiments, the IL-2 polypeptide or functional fragment thereof comprises an amino acid sequence produced by introducing amino acid substitutions into one or more of the first three amino acid residues (residues 1-3) of the amino acid sequence of any of the IL-2 polypeptides or functional fragments thereof disclosed herein.

[0220] The IL-2 polypeptide or functional fragment thereof comprises an amino-terminus and a carboxy-terminus. In some embodiments, a half-life extension domain is linked to the amino-terminus or the carboxy-terminus of the IL-2 polypeptide or functional fragment thereof. In some embodiments, a masking moiety is linked to the amino-terminus or the carboxy-terminus of the IL-2 polypeptide or functional fragment thereof. In some embodiments, a linker is linked to the amino-terminus or the carboxy-terminus of the IL-2 polypeptide or functional fragment thereof. In some embodiments, a cleavable peptide of a linker is linked to the amino-terminus or the carboxy-terminus of the IL-2 polypeptide or functional fragment thereof. In some embodiments, an N-terminal spacer domain or a C-terminal spacer domain of a linker is linked to the amino-terminus or the carboxy-terminus of the IL-2 polypeptide or functional fragment thereof.

2. IL-15 Polypeptides

[0221] In some embodiments, the cytokine or functional fragment thereof is an IL-15 polypeptide or functional fragment thereof. In eukaryotic cells, IL-15 is synthesized as a precursor polypeptide of 162 amino acids, which is then processed into mature IL-15 by the removal of amino acid residues 1-48. This results in a mature form of IL-15 consisting of 114 amino acids (amino acid residues 49-162) that is secreted in a mature, active form (*see* SEQ ID NO: 167).

[0222] In some embodiments, the IL-15 polypeptide or functional fragment thereof is any naturally occurring interleukin-15 (IL-15) protein or modified variant thereof capable of binding to, or otherwise exhibiting affinity for, an interleukin-15 receptor (IL-15R) or component thereof (e.g., the IL-15Rα, IL-2Rβ, and/or IL-2Rγ chain). In some embodiments, the IL-15 polypeptide or functional fragment thereof is a mature form of IL-15 that consists of amino acid residues 49-162 of SEQ ID NO: 166. In some embodiments, the IL-15 polypeptide or functional fragment thereof comprises the amino acid sequence of SEQ ID NO: 167. In some embodiments, the IL-15 polypeptide or functional fragment thereof comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 166 or 167.

[0223] In some embodiments, the IL-15 polypeptide or functional fragment thereof comprises an amino acid sequence produced by at least one amino acid modification to the amino acid sequence of SEQ ID NO: 167. Each of the at least one amino acid modifications can be any amino acid modification, such as a substitution, insertion, or deletion. In some embodiments, the IL-15 polypeptide or functional fragment thereof comprises an amino acid sequence produced by at least 1, at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, or at least 10 amino acid substitutions in the amino acid sequence of SEQ ID NO: 167.

[0224] The IL-15 polypeptide or functional fragment thereof comprises an amino-terminus and a carboxy-terminus. In some embodiments, a half-life extension domain is linked to the amino-terminus or the carboxy-terminus of the IL-15 polypeptide or functional fragment thereof. In some embodiments, a masking moiety is linked to the amino-terminus or the carboxy-terminus of the IL-15 polypeptide or functional fragment thereof. In some embodiments, a linker is linked to the amino-terminus or the carboxy-terminus of the IL-15 polypeptide or functional fragment thereof. In some embodiments, a cleavable peptide of a linker is linked to the amino-terminus or the carboxy-terminus of the IL-15 polypeptide or functional fragment thereof. In some embodiments, an N-terminal spacer domain or a C-terminal spacer domain of a linker is linked to the amino-terminus or the carboxy-terminus of the IL-15 polypeptide or functional fragment thereof.

B. Masking Moieties

[0225] A masking moiety as provided herein refers to a moiety capable of binding to, or otherwise exhibiting an affinity for, a cytokine or functional fragment thereof such that, in some embodiments, the binding decreases the affinity of the cytokine or functional fragment thereof for its cognate receptor or protein. For example, a masking moiety for an IL-2 polypeptide or functional fragment thereof is capable of binding to, or otherwise exhibiting an affinity for, an IL-2 polypeptide or functional fragment thereof such that, in some embodiments, the binding decreases the affinity of the IL-2 polypeptide or functional fragment thereof for its cognate receptor or protein (e.g., IL-2R or a component thereof, such

as the IL-2Rα and/or IL-2Rβ chain). When bound to the cytokine or functional fragment thereof, the masking moiety blocks, occludes, inhibits (e.g. decreases) or otherwise prevents (e.g., masks) the activity or binding of the cytokine or functional fragment thereof to its cognate receptor or protein. In some embodiments that include a first masking moiety and a second masking moiety, the presence of one of the masking moieties (e.g., the first masking moiety) blocks, occludes, inhibits (e.g. decreases) or otherwise prevents (e.g., masks) the activity or binding of the cytokine or functional fragment thereof to its cognate receptor or protein, while the other masking moiety (e.g., the second masking moiety) can, in some embodiments, remain associated with the cytokine or functional fragment thereof following cleavage of the first masking moiety and still allow, or possibly even promote, binding of the cytokine or functional fragment thereof to its cognate receptor or protein at the site where the first masking moiety was bound. *See, e.g.*, FIG. 7B. Methods for determining the extent of binding of a protein (e.g., cytokine) to a cognate protein (e.g., cytokine receptor), is well known in the art.

[0226] The masked cytokines provided herein comprise a masking moiety. The masking moiety comprises an amino-terminus and a carboxy-terminus. In some embodiments, the masked cytokine comprises a single masking moiety. In some embodiments, the masked cytokine comprises more than one masking moiety, each of which can be any of the masking moieties described herein. In some embodiments, the masked cytokine comprises a first masking moiety and a second masking moiety. It is understood, for instance, that reference to "a masking moiety" or "the masking moiety" can refer to the masking moiety in a masked cytokine comprising a single masking moiety, or it can refer to the first masking moiety in a masked cytokine comprising a first masking moiety and a second masking moiety, or it can refer to the second masking moiety in a masked cytokine comprising a first masking moiety and a second masking moiety, or it can refer to the first masking moiety and the second masking moiety in a masked cytokine comprising a first masking moiety and a second masking moiety.

[0227] In some embodiments, the masking moiety is linked to the cytokine or functional fragment thereof. In some embodiments, the masking moiety is linked to the cytokine or functional fragment thereof via a first linker. In some embodiments, the masked cytokine comprises a half-life extension domain that is linked to the masking moiety. In some embodiments, the masked cytokine comprises a half-life extension domain that is linked to the masking moiety via a second linker. In some embodiments, the masking moiety is linked to the cytokine or functional fragment thereof, and is linked to the half-life extension domain. In some embodiments, the cytokine or functional fragment thereof is linked to the amino-terminus of the masking peptide, and the half-life extension domain is linked to the carboxy-terminus of the masking peptide. In some embodiments, the cytokine or functional fragment thereof is linked to the carboxy-terminus of the masking peptide, and the half-life extension domain is linked to the amino-terminus of the masking peptide. In some embodiments, the half-life extension domain is linked to the amino-terminus or the carboxy-terminus of the masking moiety. In some embodiments, the second linker is linked to the amino-terminus or the carboxy-terminus of the masking

moiety. In some embodiments, the masking moiety is linked to the first linker, and is linked to the second linker. In some embodiments, the first linker is linked to the amino-terminus of the masking peptide, and the second linker is linked to the carboxy-terminus of the masking peptide. In some embodiments, the first linker is linked to the carboxy-terminus of the masking peptide, and the second linker is linked to the amino-terminus of the masking peptide.

[0228] In some embodiments comprising a first masking moiety and a second masking moiety, the first masking moiety is linked to the cytokine or functional fragment thereof, and the second masking moiety is linked to the cytokine or functional fragment thereof. In some embodiments comprising a first masking moiety and a second masking moiety, the first masking moiety is linked to the cytokine or functional fragment thereof via a first linker, and the second masking moiety is linked to the cytokine or functional fragment thereof via a second linker. In some embodiments, the masked cytokine comprises a half-life extension domain that is linked to either the first masking moiety or the second masking moiety. In some embodiments, the masked cytokine comprises a half-life extension domain that is linked to either the first masking moiety or the second masking moiety via a third linker. In some embodiments, the first linker is linked to the amino-terminus or the carboxy-terminus of the first masking moiety. In some embodiments, the second linker is linked to the amino-terminus or the carboxy-terminus of the second masking moiety. In some embodiments, the half-life extension domain is linked to the amino-terminus or the carboxy-terminus of the first masking moiety. In some embodiments, the half-life extension domain is linked to the amino-terminus or the carboxy-terminus of the second masking moiety. In some embodiments, the third linker is linked to the amino-terminus or the carboxy-terminus of the first masking moiety. In some embodiments, the third linker is linked to the amino-terminus or the carboxy-terminus of the second masking moiety.

[0229] In some embodiments comprising a first masking moiety and a second masking moiety, the first masking moiety is linked to the first half-life extension domain, the second masking moiety is linked to the first masking moiety, and the cytokine or functional fragment thereof is linked to the second half-life extension domain. In some embodiments comprising a first masking moiety and a second masking moiety, the first masking moiety is linked to the first half-life extension domain via a first linker, the second masking moiety is linked to the first masking moiety via a second linker, and the cytokine or functional fragment thereof is linked to the second half-life extension domain via a third linker. In some embodiments, the first linker is linked to the amino-terminus or the carboxy-terminus of the first half-life extension domain. In some embodiments, the second linker is linked to the amino-terminus or the carboxy-terminus of the second masking moiety. In some embodiments, the second half-life extension domain is linked to the amino-terminus or the carboxy-terminus of the cytokine or functional fragment thereof. In some embodiments, the first half-life extension domain is linked to the amino-terminus or the carboxy-terminus of the first masking moiety. In some embodiments, the third linker is linked to the amino-terminus or the carboxy-terminus of the second half-life extension domain. In some

embodiments, the third linker is linked to the amino-terminus or the carboxy-terminus of the cytokine or functional fragment thereof.

[0230] In some embodiments comprising a first masking moiety and a second masking moiety, the second masking moiety is linked to the first half-life extension domain, the first masking moiety is linked to the second masking moiety, and the cytokine or functional fragment thereof is linked to the second half-life extension domain. In some embodiments comprising a first masking moiety and a second masking moiety, the second masking moiety is linked to the first half-life extension domain via a first linker, the first masking moiety is linked to the second masking moiety via a second linker, and the cytokine or functional fragment thereof is linked to the second half-life extension domain via a third linker. In some embodiments, the first linker is linked to the amino-terminus or the carboxy-terminus of the first half-life extension domain. In some embodiments, the second linker is linked to the amino-terminus or the carboxy-terminus of the first masking moiety. In some embodiments, the second half-life extension domain is linked to the amino-terminus or the carboxy-terminus of the cytokine or functional fragment thereof. In some embodiments, the first half-life extension domain is linked to the amino-terminus or the carboxy-terminus of the second masking moiety. In some embodiments, the third linker is linked to the amino-terminus or the carboxy-terminus of the second half-life extension domain. In some embodiments, the third linker is linked to the amino-terminus or the carboxy-terminus of the cytokine or functional fragment thereof.

[0231] In some embodiments comprising a first half-life extension domain and a second half-life extension domain, the masking moiety is linked to the first half-life extension domain. In some embodiments, the first half-life extension domain is linked to the amino-terminus or the carboxy-terminus of the masking moiety. In some embodiments, the masking moiety is linked to the first half-life extension domain via a first linker. In some embodiments, the first linker is linked to the amino-terminus or the carboxy-terminus of the masking moiety.

[0232] In some embodiments comprising a first half-life extension domain, a second half-life extension domain, a first masking moiety, and a second masking moiety, the first masking moiety is linked to the first half-life extension domain and the second masking moiety is linked to the cytokine or functional fragment thereof. In some embodiments, the second masking moiety is further linked to the second half-life extension domain. In some embodiments, the first masking moiety is linked to the first half-life extension domain via a first linker, and/or either the second masking moiety or the cytokine or functional fragment thereof is linked to the second half-life extension domain via a second linker. In some embodiments, the second masking moiety is linked to the cytokine or functional fragment thereof via a third linker.

[0233] In some embodiments, the first half-life extension domain is linked to the amino-terminus or the carboxy-terminus of the first masking moiety. In some embodiments, the cytokine or functional fragment thereof is linked to the amino-terminus or the carboxy-terminus of the second masking moiety.

In some embodiments, the first linker is linked to the amino-terminus or the carboxy-terminus of the first masking moiety. In some embodiments, the second linker is linked to the amino-terminus or the carboxy-terminus of the second masking moiety. In some embodiments, the third linker is linked to the amino-terminus or the carboxy-terminus of the second masking moiety. In some embodiments, the second linker is linked to the amino-terminus of the second masking moiety and the third linker is linked to the carboxy-terminus of the second masking moiety. In some embodiments, the second linker is linked to the carboxy-terminus of the second masking moiety and the third linker is linked to the amino-terminus of the second masking moiety.

[0234] In some embodiments, the masking moiety comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 9, 10, 161-165, 187-218, 221-229, 231, and 261. In some embodiments, the masking moiety comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NOs: 9, 10, 161-165, 187-218, 221-229, 231, and 261. In some embodiments, the masking moiety comprises the amino acid sequence of SEQ ID NO: 261. In some embodiments, the masking moiety comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 261.

[0235] In some embodiments, the masked cytokine comprises a first masking moiety and a second masking moiety. In some embodiments, the first masking moiety comprises the amino acid sequence of SEQ ID NO: 9 or 231, and the second masking moiety comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 10, 161-165, 187-218, 221-229, and 261. In some embodiments, the first masking moiety comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 9 or 231, and the second masking moiety comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NOs: 10, 161-165, 187-218, 221-229, and 261. In some embodiments, the first masking moiety comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 10, 161-165, 187-218, 221-229, and 261, and the second masking moiety comprises the amino acid sequence of SEQ ID NO: 9 or 231. In some embodiments, the first masking moiety comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NOs: 10, 161-165, 187-218, 221-229, and 261, and the second masking moiety comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 9 or 231. In some embodiments, the first masking moiety comprises the amino acid sequence of SEQ ID NO:

9 or 231, and the second masking moiety comprises the amino acid sequence of SEQ ID NO: 261. In some embodiments, the second masking moiety comprises the amino acid sequence of SEQ ID NO: 9 or 231, and the first masking moiety comprises the amino acid sequence of SEQ ID NO: 261. In some embodiments, the first masking moiety comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 261, and the second masking moiety comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 9 or 231. In some embodiments, the second masking moiety comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 261, and the first masking moiety comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 9 or 231.

[0236] In some embodiments, the first masking moiety comprises the amino acid sequence of SEQ ID NO: 9 or 231, and the second masking moiety comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 10, 161-165, 221-226, and 261. In some embodiments, the first masking moiety comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 9 or 231, and the second masking moiety comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NOs: 10, 161-165, 221-226, and 261. In some embodiments, the first masking moiety comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 10, 161-165, 221-226, and 261, and the second masking moiety comprises the amino acid sequence of SEQ ID NO: 9 or 231. In some embodiments, the first masking moiety comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NOs: 10, 161-165, 221-226, and 261, and the second masking moiety comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 9 or 231. In some embodiments, the first masking moiety comprises the amino acid sequence of SEQ ID NO: 9 or 231, and the second masking moiety comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 10, 161-165, 221-226, 261, 826, and 827. In some embodiments, the first masking moiety comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 9 or 231, and the

second masking moiety comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NOs: 10, 161-165, 221-226, 261, 826, and 827. In some embodiments, the second masking moiety comprises the amino acid sequence of SEQ ID NO: 9 or 231, and the first masking moiety comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 10, 161-165, 221-226, 261, 826, and 827. In some embodiments, the second masking moiety comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 9 or 231, and the first masking moiety comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NOs: 10, 161-165, 221-226, 261, 826, and 827.

[0237] In some embodiments, the first masking moiety comprises the amino acid sequence of SEQ ID NO: 9 or 231, and the second masking moiety comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 187-218. In some embodiments, the first masking moiety comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 9 or 231, and the second masking moiety comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NOs: 187-218. In some embodiments, the first masking moiety comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 187-218, and the second masking moiety comprises the amino acid sequence of SEQ ID NO: 9 or 231. In some embodiments, the first masking moiety comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NOs: 187-218, and the second masking moiety comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 9 or 231.

[0238] In some embodiments, the first masking moiety comprises the amino acid sequence of SEQ ID NO: 9 or 231, and the second masking moiety comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 227-229. In some embodiments, the first masking moiety comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 9 or 231, and the second masking moiety comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NOs: 227-229. In some

embodiments, the first masking moiety comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 227-229, and the second masking moiety comprises the amino acid sequence of SEQ ID NO: 9 or 231. In some embodiments, the first masking moiety comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NOs: 227-229, and the second masking moiety comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 9 or 231.

[0239] In some embodiments, the first masking moiety comprises the amino acid sequence of SEQ ID NO: 9, and the second masking moiety comprises the amino acid sequence of SEQ ID NO: 10. In some embodiments, the first masking moiety comprises the amino acid sequence of SEQ ID NO: 10, and the second masking moiety comprises the amino acid sequence of SEQ ID NO: 9. In some embodiments, the first masking moiety comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 9, and the second masking moiety comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 10. In some embodiments, the first masking moiety comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 10, and the second masking moiety comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 9. In some embodiments, the masking moiety comprises an amino acid sequence produced by one or more of the following amino acid substitutions to SEQ ID NO: 10 or 261: C122S, C168S, R42A, K71A, T73A, T74A, V75A, H133A, Y134A, R137D, Q162W, E170A, and Q188A. In some embodiments, the masking moiety comprising an amino acid sequence that is produced by one or more amino acid substitutions comprises the amino acid sequence of SEQ ID NO: 826.

[0240] In some embodiments, the masking moiety comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 10, 161-165, 219-229, 232-234, 261, and 823-825. In some embodiments, the masking moiety comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NOs: 10, 161-165, 219-229, 232-234, 261, and 823-825. In some embodiments, the masking moiety comprises the amino acid sequence of SEQ ID NO: 261. In some embodiments, the masking moiety comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 261. In some embodiments,

the masking moiety comprises the amino acid sequence of SEQ ID NO: 826 or 827, or comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 826 or 827.

[0241] In some embodiments, the masked cytokine comprises a first masking moiety and a second masking moiety. In some embodiments, the first masking moiety comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 232-234, and 823-825, and the second masking moiety comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 10, 161-165, 219-229, and 261. In some embodiments, the first masking moiety comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 10, 161-165, 219-229, and 261, and the second masking moiety comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 232-234, and 823-825. In some embodiments, the first masking moiety comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NOs: 10, 161-165, 219-229, and 261, and the second masking moiety comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NOs: 232-234, and 823-825. In some embodiments, the second masking moiety comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NOs: 10, 161-165, 219-229, and 261, and the first masking moiety comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NOs: 232-234, and 823-825.

[0242] In some embodiments, the first masking moiety comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 232-234, and 823-825, and the second masking moiety comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 10, 161-165, 219-229, 261, 826, and 827. In some embodiments, the second masking moiety comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 232-234, and 823-825, and the first masking moiety comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 10, 161-165, 219-229, 261, 826, and 827. In some embodiments, the first masking moiety comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NOs: 10, 161-165, 219-229, 261, 826, and 827, and the second masking moiety comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to an amino acid sequence selected

from the group consisting of SEQ ID NOs: 232-234, and 823-825. In some embodiments, the second masking moiety comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NOs: 10, 161-165, 219-229, 261, 826, and 827, and the first masking moiety comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NOs: 232-234, and 823-825. In some embodiments, the first masking moiety comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 232-234, and 823-825, and the second masking moiety comprises the amino acid sequence of SEQ ID NO: 826 or 827. In some embodiments, the second masking moiety comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 232-234, and 823-825, and the first masking moiety comprises the amino acid sequence of SEQ ID NO: 826 or 827.

[0243] In some embodiments, the first masking moiety comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 232-234, and 823-825, and the second masking moiety comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 10, 161-165, 221-226, and 261. In some embodiments, the first masking moiety comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 10, 161-165, 221-226, and 261, and the second masking moiety comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 232-234, and 823-825. In some embodiments, the first masking moiety comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NOs: 10, 161-165, 221-226, and 261, and the second masking moiety comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NOs: 232-234, and 823-825. In some embodiments, the second masking moiety comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NOs: 10, 161-165, 221-226, and 261, and the first masking moiety comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NOs: 232-234, and 823-825.

[0244] In some embodiments, the first masking moiety comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 232-234, and 823-825, and the second masking moiety comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 227-229. In some embodiments, the first masking moiety comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 227-229, and the second masking moiety comprises an amino acid sequence

selected from the group consisting of SEQ ID NOs: 232-234, and 823-825. In some embodiments, the first masking moiety comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NOs: 227-229, and the second masking moiety comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NOs: 232-234, and 823-825. In some embodiments, the second masking moiety comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NOs: 227-229, and the first masking moiety comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NOs: 232-234, and 823-825.

[0245] In some embodiments, the first masking moiety comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 232-234, and 823-825, and the second masking moiety comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 219 and 220. In some embodiments, the first masking moiety comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 219 and 220, and the second masking moiety comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 232-234, and 823-825. In some embodiments, the first masking moiety comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NOs: 219 and 220, and the second masking moiety comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NOs: 232-234, and 823-825. In some embodiments, the second masking moiety comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NOs: 219 and 220, and the first masking moiety comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NOs: 232-234, and 823-825.

[0246] In some embodiments, the masking moiety comprises an amino acid sequence produced by introducing one or more of the following amino acid substitutions into the amino acid sequence of any one of SEQ ID NOs: 232-234, and 823-825: R24A, R26A, K34A, S40A, L42A, and P67A. In some embodiments, the masking moiety comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to

an amino acid sequence selected from the group consisting of SEQ ID NOs: 232-234, and 823-825 and is further modified by introducing one or more of the following amino acid substitutions into the amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence selected from the group consisting of SEQ ID NOs: 232-234, and 823-825: R24A, R26A, K34A, S40A, L42A, and P67A.

[0247] In some embodiments, the masking moiety comprises IL-2Rα (also referred to as CD25) or a fragment, portion, or variant thereof that retains or otherwise demonstrates an affinity to IL-2. In some embodiments, the masking moiety comprises IL-2Rα (also referred to as CD25) or a fragment, portion, or variant thereof and comprises the amino acid sequence of SEQ ID NO: 9 or 231. In some embodiments, the masking moiety comprises IL-2Rβ (also referred to as CD122) or a fragment, portion, or variant thereof that retains or otherwise demonstrates an affinity to IL-2 and/or IL-15. In some embodiments, the masking moiety comprises IL-2Rβ (also referred to as CD122) or a fragment, portion, or variant thereof and comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 10, 161-165, 221-226, 261, 826, and 827. In some embodiments, the masking moiety comprises IL-2Rγ (also referred to as CD132) or a fragment, portion, or variant thereof that retains or otherwise demonstrates an affinity to IL-2 and/or IL-15. In some embodiments, the masking moiety comprises IL-15Rα (also referred to as CD215) or a fragment, portion, or variant thereof that retains or otherwise demonstrates an affinity to IL-15. In some embodiments, the masking moiety comprises IL-15Rα (also referred to as CD215) or a fragment, portion, or variant thereof and comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 232-234, and 823-825. In some embodiments, the masking moiety comprises an antigen-binding domain of an antibody or fragment thereof. In some embodiments, the masking moiety comprises an antigen-binding domain of an anti-IL-2 antibody or fragment thereof. In some embodiments, the masking moiety comprises an antigen-binding domain of an anti-IL-15 antibody or fragment thereof.

[0248] In some embodiments comprising a first masking moiety and a second masking moiety, the first masking moiety comprises IL-2Rα or a fragment, portion, or variant thereof that retains or otherwise demonstrates an affinity to IL-2, and the second masking moiety comprises IL-2Rβ or a fragment, portion, or variant thereof that retains or otherwise demonstrates an affinity to IL-2. In some embodiments comprising a first masking moiety and a second masking moiety, the first masking moiety comprises IL-2Rβ or a fragment, portion, or variant thereof that retains or otherwise demonstrates an affinity to IL-2, and the second masking moiety comprises IL-2Rα or a fragment, portion, or variant thereof that retains or otherwise demonstrates an affinity to IL-2. In some embodiments comprising a first masking moiety and a second masking moiety, the first masking moiety comprises IL-2Rα or a fragment, portion, or variant thereof that retains or otherwise demonstrates an affinity to IL-2, and the second masking moiety comprises IL-2Rγ or a fragment, portion, or variant thereof that retains or otherwise demonstrates an affinity to IL-2. In some embodiments comprising a first masking moiety and

a second masking moiety, the first masking moiety comprises IL-2Rγ or a fragment, portion, or variant thereof that retains or otherwise demonstrates an affinity to IL-2, and the second masking moiety comprises IL-2Rα or a fragment, portion, or variant thereof that retains or otherwise demonstrates an affinity to IL-2. In some embodiments comprising a first masking moiety and a second masking moiety, the first masking moiety comprises IL-2Rα or a fragment, portion, or variant thereof that retains or otherwise demonstrates an affinity to IL-2, and the second masking moiety comprises an antigen-binding domain of an anti-IL-2 antibody or fragment thereof. In some embodiments comprising a first masking moiety and a second masking moiety, the first masking moiety comprises an antigen-binding domain of an anti-IL-2 antibody or fragment thereof, and the second masking moiety comprises IL-2Rα or a fragment, portion, or variant thereof that retains or otherwise demonstrates an affinity to IL-2.

[0249] In some embodiments comprising a first masking moiety and a second masking moiety, the first masking moiety comprises IL-15Rα or a fragment, portion, or variant thereof that retains or otherwise demonstrates an affinity to IL-15, and the second masking moiety comprises IL-2Rβ or a fragment, portion, or variant thereof that retains or otherwise demonstrates an affinity to IL-15. In some embodiments comprising a first masking moiety and a second masking moiety, the first masking moiety comprises IL-2Rβ or a fragment, portion, or variant thereof that retains or otherwise demonstrates an affinity to IL-15, and the second masking moiety comprises IL-15Rα or a fragment, portion, or variant thereof that retains or otherwise demonstrates an affinity to IL-15. In some embodiments comprising a first masking moiety and a second masking moiety, the first masking moiety comprises IL-15Rα or a fragment, portion, or variant thereof that retains or otherwise demonstrates an affinity to IL-15, and the second masking moiety comprises IL-2Rγ or a fragment, portion, or variant thereof that retains or otherwise demonstrates an affinity to IL-15. In some embodiments comprising a first masking moiety and a second masking moiety, the first masking moiety comprises IL-2Rγ or a fragment, portion, or variant thereof that retains or otherwise demonstrates an affinity to IL-15, and the second masking moiety comprises IL-15Rα or a fragment, portion, or variant thereof that retains or otherwise demonstrates an affinity to IL-15. In some embodiments comprising a first masking moiety and a second masking moiety, the first masking moiety comprises IL-15Rα or a fragment, portion, or variant thereof that retains or otherwise demonstrates an affinity to IL-15, and the second masking moiety comprises an antigen-binding domain of an anti-IL-15 antibody or fragment thereof. In some embodiments comprising a first masking moiety and a second masking moiety, the first masking moiety comprises an antigen-binding domain of an anti-IL-15 antibody or fragment thereof, and the second masking moiety comprises IL-15Rα or a fragment, portion, or variant thereof that retains or otherwise demonstrates an affinity to IL-15.

C. Linkers

[0250] A linker as provided herein refers to a peptide of two more amino acids that is used to link two components together, such as two components of any of the masked cytokines described herein. In

some embodiments, the linker comprises a cleavable peptide. In some embodiments, the linker comprises an amino-terminal spacer domain (N-terminal spacer domain) and/or a carboxy-terminal spacer domain (C-terminal spacer domain). In some embodiments, the linker comprises an N-terminal spacer domain, a cleavable peptide, and/or a C-terminal spacer domain. In some embodiments, the linker consists of an N-terminal spacer domain. In some embodiments, the linker consists of a C-terminal spacer domain. In some embodiments, the linker consists of an N-terminal spacer domain and a C-terminal spacer domain. In some embodiments, the linker consists of a cleavable peptide. In some embodiments, the linker consists of an N-terminal spacer domain, a cleavable peptide, and a C-terminal spacer domain. In some embodiments, the linker consists of an N-terminal spacer domain and a cleavable peptide. In some embodiments, the linker consists of a cleavable peptide and a C-terminal spacer domain. In some embodiments, the linker consists of a cleavable peptide.

[0251] In some embodiments, the masked cytokine comprises a linker. In some embodiments, the masked cytokine comprises a single linker. In some embodiments, the masked cytokine comprises more than one linker, each of which can be any of the linkers described herein. In some embodiments, the masked cytokine comprises a first linker and a second linker. In some embodiments, the masked cytokine comprises a first linker, a second linker, and a third linker. In some embodiments, the masked cytokine comprises a first linker, a second linker, a third linker, and a fourth linker. For example, reference to "a linker" or "the linker" can refer to the linker in a masked cytokine comprising a single linker, or it can refer to the first linker in a masked cytokine comprising a first linker and a second linker, or it can refer to the second linker in a masked cytokine comprising a first linker and a second linker, or it can refer to the first linker and the second linker in a masked cytokine comprising a first linker and a second linker, or it can refer to the first linker, the second linker, and/or the third linker in a masked cytokine comprising a first linker, a second linker, and a third linker, or it can refer to the first linker, the second linker, the third linker, and/or the fourth linker in a masked cytokine comprising a first linker, a second linker, a third linker, and a fourth linker.

[0252] It is understood that each of the following terms are considered a "linker" as described herein: a linker, a first linker, a second linker, a third linker, and a fourth linker, as well as any other numbered linker (e.g., a fifth linker, a sixth linker, etc.). As such, in some embodiments, the masked cytokine may comprise a linker, a first linker, a second linker, a third linker, and/or a fourth linker, each of which is considered "a linker" as described herein, and any of the linkers described herein may be a linker, a first linker, a second linker, a third linker, and/or a fourth linker as described herein.

[0253] It is also understood that two components "linked" together includes embodiments in which the two components are directly linked together as well as embodiments in which the two components are linked together via a linker as described herein. For example, "a half-life extension domain that is linked to the masking moiety" is interpreted to mean either that the amino acid sequence of the half-life extension domain is linked directly to the amino acid sequence of the masking moiety, or that the amino

acid sequence of the half-life extension domain is linked to the amino acid sequence of the masking moiety via a linker, such as any of the linkers described herein.

[0254] The linker comprises an amino-terminus and a carboxy-terminus. In some embodiments, a masking moiety is linked to the amino-terminus or the carboxy-terminus of the linker. In some embodiments, a cytokine or functional fragment thereof is linked to the amino-terminus or the carboxy-terminus of the linker. In some embodiments, a cytokine or functional fragment thereof is linked to the amino-terminus of the linker, and a masking moiety is linked to the carboxy-terminus of the linker. In some embodiments, a cytokine or functional fragment thereof is linked to the carboxy-terminus of the linker, and a masking moiety is linked to the amino-terminus of the linker. In some embodiments, a half-life extension domain is linked to the amino-terminus or the carboxy-terminus of the linker. In some embodiments, a half-life extension domain is linked to the amino-terminus of the linker, and a masking moiety is linked to the carboxy-terminus of the linker. In some embodiments, a half-life extension domain is linked to the carboxy-terminus of the linker, and a masking moiety is linked to the amino-terminus of the linker. In some embodiments, a half-life extension domain is linked to the amino-terminus of the linker, and a cytokine or functional fragment thereof is linked to the carboxy-terminus of the linker. In some embodiments, a half-life extension domain is linked to the carboxy-terminus of the linker, and a cytokine or functional fragment thereof is linked to the amino-terminus of the linker.

[0255] In some embodiments comprising a first masking moiety and a second masking moiety that are each linked to a cytokine or functional fragment thereof, the first masking moiety or the second masking moiety is linked to the amino-terminus of a linker, and the cytokine or functional fragment thereof is linked to the carboxy-terminus of the linker. In some embodiments comprising a first masking moiety and a second masking moiety that are each linked to a cytokine or functional fragment thereof, the first masking moiety or the second masking moiety is linked to the carboxy-terminus of a linker, and the cytokine or functional fragment thereof is linked to the amino-terminus of the linker.

[0256] In some embodiments comprising a first half-life extension domain and a second half-life extension domain, a masking moiety is linked to the amino-terminus of a linker, and either the first half-life extension domain or the second half-life extension domain is linked to the carboxy-terminus of the linker. In some embodiments comprising a first half-life extension domain and a second half-life extension domain, a masking moiety is linked to the carboxy-terminus of the linker, and either the first half-life extension domain or the second half-life extension domain is linked to the amino-terminus of the linker. In some embodiments comprising a first half-life extension domain and a second half-life extension domain, a cytokine or functional fragment thereof is linked to the amino-terminus of the linker, and either the first half-life extension domain or the second half-life extension domain is linked to the carboxy-terminus of the linker. In some embodiments comprising a first half-life extension domain and a second half-life extension domain, a cytokine or functional fragment thereof is linked to the carboxy-

terminus of the linker, and either the first half-life extension domain or the second half-life extension domain is linked to the amino-terminus of the linker.

[0257] In some embodiments comprising a first masking moiety linked to a first half-life extension domain, a second masking moiety linked to a cytokine or functional fragment thereof, and where either the second masking moiety or the cytokine or functional fragment thereof is linked to the second half-life extension domain, the first masking moiety is linked to the amino-terminus of the linker and the first half-life extension domain is linked to the carboxy-terminus of the linker. In some embodiments comprising a first masking moiety linked to a first half-life extension domain, a second masking moiety linked to a cytokine or functional fragment thereof, and where either the second masking moiety or the cytokine or functional fragment thereof is linked to the second half-life extension domain, the first masking moiety is linked to the carboxy-terminus of the linker and the first half-life extension domain is linked to the amino-terminus of the linker. In some embodiments comprising a first masking moiety linked to a first half-life extension domain, a second masking moiety linked to a cytokine or functional fragment thereof, and where either the second masking moiety or the cytokine or functional fragment thereof is linked to the second half-life extension domain, the second masking moiety is linked to the amino-terminus of the linker and the cytokine or functional fragment thereof is linked to the carboxy-terminus of the linker. In some embodiments comprising a first masking moiety linked to a first half-life extension domain, a second masking moiety linked to a cytokine or functional fragment thereof, and where either the second masking moiety or the cytokine or functional fragment thereof is linked to the second half-life extension domain, the second masking moiety is linked to the carboxy-terminus of the linker and the cytokine or functional fragment thereof is linked to the amino-terminus of the linker. In some embodiments comprising a first masking moiety linked to a first half-life extension domain, a second masking moiety linked to a cytokine or functional fragment thereof, and where either the second masking moiety or the cytokine or functional fragment thereof is linked to the second half-life extension domain, the second masking moiety is linked to the amino-terminus of the linker and the second half-life extension domain is linked to the carboxy-terminus of the linker. In some embodiments comprising a first masking moiety linked to a first half-life extension domain, a second masking moiety linked to a cytokine or functional fragment thereof, and where either the second masking moiety or the cytokine or functional fragment thereof is linked to the second half-life extension domain, the second masking moiety is linked to the carboxy-terminus of the linker and the second half-life extension domain is linked to the amino-terminus of the linker. In some embodiments comprising a first masking moiety linked to a first half-life extension domain, a second masking moiety linked to a cytokine or functional fragment thereof, and where either the second masking moiety or the cytokine or functional fragment thereof is linked to the second half-life extension domain, the cytokine or functional fragment thereof is linked to the amino-terminus of the linker and the second half-life extension domain is linked to the carboxy-terminus of the linker. In some embodiments comprising a first masking moiety linked to a first half-life

extension domain, a second masking moiety linked to a cytokine or functional fragment thereof, and where either the second masking moiety or the cytokine or functional fragment thereof is linked to the second half-life extension domain, the cytokine or functional fragment thereof is linked to the carboxy-terminus of the linker and the second half-life extension domain is linked to the amino-terminus of the linker.

[0258] In some embodiments comprising a first masking moiety linked to a first half-life extension domain via a first linker, a second masking moiety linked to the first masking moiety via second linker, and a cytokine or functional fragment thereof linked to a second half-life extension domain via a third linker, the first masking moiety is linked to the carboxy-terminus of the first linker and the first half-life extension domain is linked to the amino-terminus of the first linker, the second masking moiety is linked to the carboxy-terminus of the second linker and the first masking moiety is linked to the amino-terminus of the second linker, and the cytokine or functional fragment thereof is linked to the carboxy-terminus of the third linker and the second half-life extension domain is linked to the amino-terminus of the third linker.

[0259] In some embodiments comprising a first masking moiety linked to a first half-life extension domain via a first linker, a second masking moiety linked to the first masking moiety via second linker, and a cytokine or functional fragment thereof linked to a second half-life extension domain via a third linker, the first masking moiety is linked to the amino-terminus of the first linker and the first half-life extension domain is linked to the carboxy-terminus of the first linker, the second masking moiety is linked to the amino-terminus of the second linker and the first masking moiety is linked to the carboxy-terminus of the second linker, and the cytokine or functional fragment thereof is linked to the amino-terminus of the third linker and the second half-life extension domain is linked to the carboxy-terminus of the third linker.

[0260] In some embodiments comprising a second masking moiety linked to a first half-life extension domain via a first linker, a first masking moiety linked to the second masking moiety via second linker, and a cytokine or functional fragment thereof linked to a second half-life extension domain via a third linker, the second masking moiety is linked to the carboxy-terminus of the first linker and the first half-life extension domain is linked to the amino-terminus of the first linker, the first masking moiety is linked to the carboxy-terminus of the second linker and the second masking moiety is linked to the amino-terminus of the second linker, and the cytokine or functional fragment thereof is linked to the carboxy-terminus of the third linker and the second half-life extension domain is linked to the amino-terminus of the third linker.

[0261] In some embodiments comprising a second masking moiety linked to a first half-life extension domain via a first linker, a first masking moiety linked to the second masking moiety via second linker, and a cytokine or functional fragment thereof linked to a second half-life extension domain via a third linker, the second masking moiety is linked to the amino-terminus of the first linker and the

first half-life extension domain is linked to the carboxy-terminus of the first linker, the first masking moiety is linked to the amino-terminus of the second linker and the second masking moiety is linked to the carboxy-terminus of the second linker, and the cytokine or functional fragment thereof is linked to the amino-terminus of the third linker and the second half-life extension domain is linked to the carboxy-terminus of the third linker.

[0262] In some embodiments comprising a first half-life extension domain and a second half-life extension domain, the first half-life extension domain is linked to the second half-life extension domain. In some embodiments comprising a first half-life extension domain and a second half-life extension domain, the first half-life extension domain is linked to the second half-life extension domain via a linker.

[0263] In some embodiments, the linker comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 11-153, 235-242, 262-264, 268-320, 323-338, 340-354, 356-555, 668, 691, 724, 725, 727, 762-771, 794, and 797-812. In some embodiments, the linker comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 20-153, 235-242, 264, 268-317, 323-338, 340-347, 356-415, 420-491, 494-501, 504-535, 538-555, 727, 794, and 799. In some embodiments, the linker comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 11-19, 262, 263, 318-320, 348-354, 416-419, 492, 493, 502, 503, 536, 537, 668, 691, 724, 725, 762-771, 797, 798, and 800-812, . In some embodiments, the linker comprises the amino acid sequence of SEQ ID NO: 262. In some embodiments, the linker comprises the amino acid sequence of SEQ ID NO: 28. In some embodiments, the linker comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 20-95, 235, 268, and 269. In some embodiments, the linker comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 20-33. In some embodiments, the linker comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 34-44. In some embodiments, the linker comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 45-95. In some embodiments, the linker comprises the amino acid sequence of SEQ ID NO: 235. In some embodiments, the linker comprises the amino acid sequence of SEQ ID NO: 28. In some embodiments, the linker comprises the amino acid sequence of SEQ ID NO: 268. In some embodiments, the linker comprises the amino acid sequence of SEQ ID NO: 269. In some embodiments, the linker comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 263, 318-322, 339, 348-355, 416-419, 492, 493, 502, 503, 536, 537, 668, 691, 724, 725, 727, 762-771, 794, 795, and 797-812.

[0264] In some embodiments, the linker comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 794, 795, and 797-812. In some embodiments, the linker comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 270-302, 306-317, 342-347, 356-415, 420-491, 494-501, 504-535, and 538-555.

[0265] In some embodiments, the linker comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NOs: 11-153, 235-242, 262-264, 268-320, 323-338, 340-354, 356-555, 668, 691, 724, 725, 727, 762-771, 794, and 797-812. In some embodiments, the linker comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NOs: 11-19, 262, 263, 318-320, 348-354, 416-419, 492, 493, 502, 503, 536, 537, 668, 691, 724, 725, 762-771, 797, 798, and 800-812. In some embodiments, the linker comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NOs: 20-33. In some embodiments, the linker comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NOs: 34-44. In some embodiments, the linker comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NOs: 45-95. In some embodiments, the linker comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 235. In some embodiments, the linker comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 262. In some embodiments, the linker comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NOs: 263, 318-320, 348-354, 416-419, 492, 493, 502, 503, 536, 537, 668, 691, 724, 725, 762-771, 797, 798, and 800-812. In some embodiments, the linker comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NOs: 318-320. In some embodiments, the linker comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NOs: 348-354. In some embodiments, the linker comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NOs: 416-419. In some embodiments, the linker comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to an

amino acid sequence selected from the group consisting of SEQ ID NOs: 492, 493, 502, 503, 536, 537. In some embodiments, the linker comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NOs: 668, 691, 724, 725, 762-771, 797, 798, and 800-812. In some embodiments, the linker comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NOs: 762-771, 797, 798, and 800-812. In some embodiments, the linker comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NOs: 762-771. In some embodiments, the linker comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NOs: 797, 798, and 800-812. In some embodiments, the linker comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NOs: 800-812.

[0266] The cleavable peptides and spacer domains of some embodiments of the linker are described in more detail below.

1. Cleavable Peptides

[0267] In some embodiments, the linker comprises a cleavable peptide. In some embodiments having more than one linker that comprises a cleavable peptide, a cleavable peptide may be referred to as a first cleavable peptide, a second cleavable peptide, or a third cleavable peptide, each of which is considered "a cleavable peptide" and may be any of the cleavable peptides described herein. For example, reference to "a cleavable peptide" or "the cleavable peptide" can refer to the cleavable peptide in a masked cytokine comprising a single cleavable peptide, or it can refer to the first cleavable peptide in a masked cytokine comprising a first cleavable peptide and a second cleavable peptide, or it can refer to the second cleavable peptide in a masked cytokine comprising a first cleavable peptide and a second cleavable peptide, or it can refer to the first cleavable peptide and the second cleavable peptide in a masked cytokine comprising a first cleavable peptide and a second cleavable peptide, or it can refer to the first cleavable peptide, the second cleavable peptide, and/or the third cleavable peptide in a masked cytokine comprising a first cleavable peptide, a second cleavable peptide, and a third cleavable peptide. It is conceivable that, in some embodiments, more than three cleavable peptides may be present in accordance with the teachings herein.

[0268] A cleavable peptide is a polypeptide that includes a cleavage site, such as a protease cleavage site. In some embodiments, the cleavable peptide comprises more than one cleavage site. A "cleavage site" as used herein refers to a recognizable site for cleavage of a portion of the cleavable peptide found in any of the linkers that comprise a cleavable peptide described herein. Thus, a cleavage site may be found in the sequence of a cleavable peptide as described herein. In some embodiments, the cleavage site is an amino acid sequence that is recognized and cleaved by a cleaving agent. Exemplary cleaving agents include proteins, enzymes, DNAzymes, RNAzymes, metals, acids, and bases.

[0269] In some embodiments, the cleavable peptide comprises a protease cleavage site. In some embodiments, the protease cleavage site is a tumor-associated protease cleavage site. A "tumor-associated protease cleavage site" as provided herein is an amino acid sequence recognized by a protease whose expression is specific or upregulated for a tumor cell or tumor cell environment thereof. In some embodiments, the protease cleavage site is a cleavage site recognized by one or more enzyme selected from the group consisting of: ABHD12, ADAM12, ABHD12B, ABHD13, ABHD17A, ADAM19, ADAM20, ADAM21, ADAM28, ADAM30, ADAM33, ADAM8, ABHD17A, ADAMDEC1, ADAMTS1, ADAMTS10, ADAMTS12, ADAMTS13, ADAMTS14, ADAMTS15, ADAMTS16, ADAMTS17, ADAMTS18, ADAMTS19, ADAMTS2, ADAMTS20, ADAMTS3, ADAMTS4, ABHD17B, ADAMTS5, ADAMTS6, ADAMTS7, ADAMTS8, ADAMTS9, ADAMTSL1, ADAMTSL2, ADAMTSL3, ABHD17C, ADAMTSL5, ASTL, BMP1, CELA1, CELA2A, CELA2B, CELA3A, CELA3B, ADAM10, ADAM15, ADAM17, ADAM9, ADAMTS4, CTSE, CTSF, ADAMTSL4, CMA1, CTRB1, CTRC, CTSO, CTRl, CTSA, CTSW, CTSB, CTSC, CTSD, ESP1, CTSG, CTSH, GZMA, GZMB, GZMH, CTSK, GZMM, CTSL, CTSS, CTSV, CTSZ, HTRA4, KLK10, KLK11, KLK13, KLK14, KLK2, KLK4, DPP4, KLK6, KLK7, KLKB1, ECE1, ECE2, ECEL1, MASP2, MEP1A, MEP1B, ELANE, FAP, GZMA, MMP11, GZMK, HGFAC, HPN, HTRA1, MMP11, MMP16, MMP17, MMP19, HTRA2, MMP20, MMP21, HTRA3, HTRA4, KEL, MMP23B, MMP24, MMP25, MMP26, MMP27, MMP28, KLK5, MMP3, MMP7, MMP8, MMP9, LGMN, LNPEP, MASP1, PAPPA, PAPPA2, PCSK1, NAPSA, PCSK5, PCSK6, MME, MMP1, MMP10, PLAT, PLAU, PLG, PRSS1, PRSS12, PRSS2, PRSS21, PRSS3, PRSS33, PRSS4, PRSS55, PRSS57, MMP12, PRSS8, PRSS9, PRTN3, MMP13, MMP14, ST14, TMPRSS10, TMPRSS11A, TMPRSS11D, TMPRSS11E, TMPRSS11F, TMPRSS12, TMPRSS13, MMP15, TMPRSS15, MMP2, TMPRSS2, TMPRSS3, TMPRSS4, TMPRSS5, TMPRSS6, TMPRSS7, TMPRSS9, NRDC, OVCH1, PAMR1, PCSK3, PHEX, TINAG, TPSAB1, TPSD1, and TPSG1. In some embodiments, the protease cleavage site is a cleavage site recognized by one or more enzyme selected from the group consisting of: ADAM17, HTRA1, PRSS1, FAP, GZMK, NAPSA, MMP1, MMP2, MMP9, MMP10, MMP7, MMP12, MMP28, ADAMTS9, HGFAC, and HTRA3.

[0270] In embodiments, the protease cleavage site is a matrix metalloprotease (MMP) cleavage site, a disintegrin and metalloprotease domain-containing (ADAM) metalloprotease cleavage site, a prostate

specific antigen (PSA) protease cleavage site, a urokinase-type plasminogen activator (uPA) protease cleavage site, a membrane type serine protease 1 (MT-SP1) protease cleavage site, a matriptase protease cleavage site (ST14) or a legumain protease cleavage site. In embodiments, the matrix metalloprotease (MMP) cleavage site is a MMP9 cleavage site, a MMP13 cleavage site or a MMP2 cleavage site. In embodiments, the disintegrin and metalloprotease domain-containing (ADAM) metalloprotease cleavage site is an ADAM9 metalloprotease cleavage site, a ADAM10 metalloprotease cleavage site or a ADAM17 metalloprotease cleavage site. Protease cleavage sites may be designated by a specific amino acid sequence.

[0271] In some embodiments, the cleavable peptide is cleaved by one or more enzyme selected from the group consisting of: ABHD12, ADAM12, ABHD12B, ABHD13, ABHD17A, ADAM19, ADAM20, ADAM21, ADAM28, ADAM30, ADAM33, ADAM8, ABHD17A, ADAMDEC1, ADAMTS1, ADAMTS10, ADAMTS12, ADAMTS13, ADAMTS14, ADAMTS15, ADAMTS16, ADAMTS17, ADAMTS18, ADAMTS19, ADAMTS2, ADAMTS20, ADAMTS3, ADAMTS4, ABHD17B, ADAMTS5, ADAMTS6, ADAMTS7, ADAMTS8, ADAMTS9, ADAMTSL1, ADAMTSL2, ADAMTSL3, ABHD17C, ADAMTSL5, ASTL, BMP1, CELA1, CELA2A, CELA2B, CELA3A, CELA3B, ADAM10, ADAM15, ADAM17, ADAM9, ADAMTS4, CTSE, CTSF, ADAMTSL4, CMA1, CTRB1, CTRC, CTSO, CTRl, CTSA, CTSW, CTSB, CTSC, CTSD, ESP1, CTSG, CTSH, GZMA, GZMB, GZMH, CTSK, GZMM, CTSL, CTSS, CTSV, CTSZ, HTRA4, KLK10, KLK11, KLK13, KLK14, KLK2, KLK4, DPP4, KLK6, KLK7, KLKB1, ECE1, ECE2, ECEL1, MASP2, MEP1A, MEP1B, ELANE, FAP, GZMA, MMP11, GZMK, HGFAC, HPN, HTRA1, MMP11, MMP16, MMP17, MMP19, HTRA2, MMP20, MMP21, HTRA3, HTRA4, KEL, MMP23B, MMP24, MMP25, MMP26, MMP27, MMP28, KLK5, MMP3, MMP7, MMP8, MMP9, LGMN, LNPEP, MASP1, PAPPA, PAPPA2, PCSK1, NAPSA, PCSK5, PCSK6, MME, MMP1, MMP10, PLAT, PLAU, PLG, PRSS1, PRSS12, PRSS2, PRSS21, PRSS3, PRSS33, PRSS4, PRSS55, PRSS57, MMP12, PRSS8, PRSS9, PRTN3, MMP13, MMP14, ST14, TMPRSS10, TMPRSS11A, TMPRSS11D, TMPRSS11E, TMPRSS11F, TMPRSS12, TMPRSS13, MMP15, TMPRSS15, MMP2, TMPRSS2, TMPRSS3, TMPRSS4, TMPRSS5, TMPRSS6, TMPRSS7, TMPRSS9, NRDC, OVCH1, PAMR1, PCSK3, PHEX, TINAG, TPSAB1, TPSD1, and TPSG1. In some embodiments, the cleavable peptide is cleaved by one or more enzyme selected from the group consisting of: ADAM17, HTRA1, PRSS1, FAP, GZMK, NAPSA, MMP1, MMP2, MMP9, MMP10, MMP7, MMP12, MMP28, ADAMTS9, HGFAC, and HTRA3. In some embodiments, the cleavable peptide is cleaved by one or more enzyme selected from the group consisting of uPA and MMP14. In some embodiments, the cleavable peptide is cleaved by one or more enzyme selected from the group consisting of matriptase and MMP14. In some embodiments, the cleavable peptide is cleaved by one or more enzyme selected from the group consisting of legumain and MMP14. In some embodiments, the cleavable peptide is cleaved by one or more enzyme selected from the group consisting of matriptase and uPA. In some embodiments, the cleavable peptide is cleaved by one or

more enzyme selected from the group consisting of uPA and legumain. In some embodiments, the cleavable peptide is cleaved by one or more enzyme selected from the group consisting of matriptase and legumain. In some embodiments, the cleavable peptide is cleaved by one or more enzyme selected from the group consisting of uPA, matriptase, and MMP14. In some embodiments, the cleavable peptide is cleaved by one or more enzyme selected from the group consisting of uPA, legumain, and MMP14. In some embodiments, the cleavable peptide is cleaved by one or more enzyme selected from the group consisting of matriptase, legumain, and MMP14. In some embodiments, the cleavable peptide is cleaved by one or more enzyme selected from the group consisting of matriptase, legumain, and uPA.

[0272] In some embodiments, the cleavable peptide is a substrate for a protease that is co-localized in a region or a tissue expressing a cytokine receptor. The cytokine receptor can be any cytokine receptor. In some embodiments, the cytokine receptor is selected from the group consisting of CXCR1, CXCR2, CXCR3, CXCR4, CXCR5, CXCR6, CXCR7, CCR1, CCR2, CCR3, CCR4, CCR5, CCR6, CCR7, CCR8, CCR9, CCR10, CCR11, XCR1, CX3CR1, IL-1RAP, IL-1RAPL1, IL-1RAPL2, IL-1RL1, IL-1RL2, IL-1R1, IL-1R2, IL-2R, IL-2Rα, IL-2Rβ, IL-2Rγ, IL-3Rα, IL-4R, IL-5Rα, IL-6R, IL-6ST, IL-7R, IL-9R, IL-10Rα, IL-10Rβ, IL-11Rα, IL-12Rβ1, IL-12Rβ2, IL-13Rα1, IL-13Rα2, IL-15Rα, IL-17RA, IL-17RB, IL-17RC, IL-17RD, IL-17RE, IL-18RAP, IL-18R1, IL-20Rα, IL-20Rβ, IL-21R, IL-22Rα1, IL-22Rα2, IL-23R, IL-27Rα, IL-28Rα, IL-31RA, IFNAR1, IFNAR2, IFNGR1, IFNGR2, IFNLR1, GMRα (CD116), CD131, GHR, PRLR, EPOR, LIFR (CD118), OSMRβ, TPO-R (CD110), CSF-1R, EDAR, TNFRSF1A, TNFRSF1B, LTBR, TNFRSF4, CD40, FAS, TNFRSF6B, CD27, TNFRSF8, TNFRSF9, TNFRSF10A, TNFRSF10B, TNFRSF10C, TNFRSF10D, TNFRSF11A, TNFRSF11B, TNFRSF12A, TNFRSF13B, TNFRSF13C, TNFRSF14, NGFR, TNFRSF17, TNFRSF18, TNFRSF19, RELT, TNFRSF21, TNFRSF25, and EDA2R.

[0273] In some embodiments, the cleavable peptide is a 5-mer (i.e. peptide 5 amino acids in length), 6-mer (i.e. peptide 6 amino acids in length), 7-mer (i.e. peptide 7 amino acids in length), 8-mer (i.e. peptide 8 amino acids in length), 9-mer (i.e. peptide 9 amino acids in length), 10-mer (i.e. peptide 10 amino acids in length), 11-mer (i.e. peptide 11 amino acids in length), 12-mer (i.e. peptide 12 amino acids in length), 13-mer (i.e. peptide 13 amino acids in length), 14-mer (i.e. peptide 14 amino acids in length), 15-mer (i.e. peptide 15 amino acids in length), 16-mer (i.e. peptide 16 amino acids in length), 17-mer (i.e. peptide 17 amino acids in length), or 18-mer (i.e. peptide 18 amino acids in length). Exemplary cleavable peptide sequences are shown in Table 1.

Table 1. Exemplary cleavable peptide sequences

Exemplary cleavable peptide sequences	
MPYDLYHP (SEQ ID NO: 96)	GGIGQLTSVLMAAP (SEQ ID NO: 129)
GGIGQLTA (SEQ ID NO: 97)	DSGGFMLTLVLPVLP (SEQ ID NO: 130)
DLGRFQTF (SEQ ID NO: 98)	TSEFVFAPDLGRFQTF (SEQ ID NO: 131)
DSGGFMLT (SEQ ID NO: 99)	TSTSGRSANPR (SEQ ID NO: 132)

Exemplary cleavable peptide sequences	
TSVLMAAP (SEQ ID NO: 100)	TSTSGRSANPG (SEQ ID NO: 133)
TSEFVFAPDQ (SEQ ID NO: 101)	TSTSGRSANPH (SEQ ID NO: 134)
KLVLPVLP (SEQ ID NO: 102)	VPLSLY (SEQ ID NO: 135)
KPILFFRL (SEQ ID NO: 103)	TSASGASASAA (SEQ ID NO: 136)
ANQLKG (SEQ ID NO: 104)	PSSPGGGSSP (SEQ ID NO: 137)
QSQLKE (SEQ ID NO: 105)	ISSGLLSGRSDNH (SEQ ID NO: 138)
HEQLTV (SEQ ID NO: 106)	ISSGLLSGRSDDH (SEQ ID NO: 139)
PANLVAPDP (SEQ ID NO: 107)	ISSGLLSGRSDIH (SEQ ID NO: 140)
PAPGVYPGP (SEQ ID NO: 108)	ISSGLLSGRSDQH (SEQ ID NO: 141)
APAGLIVPYN (SEQ ID NO: 109)	ISSGLLSGRSDTH (SEQ ID NO: 142)
PQALVA (SEQ ID NO: 110)	ISSGLLSGRSANP (SEQ ID NO: 143)
VGNLNF (SEQ ID NO: 111)	ISSGLLSGRSDNP (SEQ ID NO: 144)
VANLLYE (SEQ ID NO: 112)	ISSGLLSGRSANPRG (SEQ ID NO: 145)
VYNLMD (SEQ ID NO: 113)	AVGLLAPPGGLSGRSDNH (SEQ ID NO: 146)
TFNIKQ (SEQ ID NO: 114)	AVGLLAPPGGLSGRSDDH (SEQ ID NO: 147)
DLWKLLP (SEQ ID NO: 115)	AVGLLAPPGGLSGRSDIH (SEQ ID NO: 148)
PGSTKRA (SEQ ID NO: 116)	AVGLLAPPGGLSGRSDQH (SEQ ID NO: 149)
QQYRALKS (SEQ ID NO: 117)	AVGLLAPPGGLSGRSDTH (SEQ ID NO: 150)
YVPRAVL (SEQ ID NO: 118)	AVGLLAPPGGLSGRSANP (SEQ ID NO: 151)
GVNKWPT (SEQ ID NO: 119)	AVGLLAPPGGLSGRSDNP (SEQ ID NO: 152)
LAQAVRSS (SEQ ID NO: 120)	AVGLLAPPSGRSANPRG (SEQ ID NO: 153)
RAAAVKSP (SEQ ID NO: 121)	SGRSA (SEQ ID NO: 236)
DLLAVVAAS (SEQ ID NO: 122)	SGRSANA (SEQ ID NO: 237)
VQTVTWPD (SEQ ID NO: 123)	SGRNAQ (SEQ ID NO: 238)
AIPMSIPP (SEQ ID NO: 124)	SGRNAQVR (SEQ ID NO: 239)
GYEVHHQK (SEQ ID NO: 125)	SGRSDN (SEQ ID NO: 240)
VHHQKLVF (SEQ ID NO: 126)	SGRSDNPN (SEQ ID NO: 241)
IRRVSYSF (SEQ ID NO: 127)	GSGKSA (SEQ ID NO: 242)
MPYDLYHPILFFRL (SEQ ID NO: 128)	DSGGFMLTS (SEQ ID NO: 264)
ISSGLLGGLSGRSDQP (SEQ ID NO: 270)	IYDQKT (SEQ ID NO: 342)
ISSGLLSGRSDQG (SEQ ID NO: 271)	AHNYKT (SEQ ID NO: 343)
ISSGLLSGRSDQA (SEQ ID NO: 272)	MMDQAN (SEQ ID NO: 344)
ISSGLLSGRSDSP (SEQ ID NO: 273)	MLGEFVSE (SEQ ID NO: 345)
ISSGLLSGRSDTP (SEQ ID NO: 274)	GLVALRGA (SEQ ID NO: 346)
ISSGLLSGRSDMP (SEQ ID NO: 275)	KEHKYKAE (SEQ ID NO: 347)
ISSGLLSGRSD (SEQ ID NO: 276)	RQARVVG (SEQ ID NO: 356)
ISSGLLSGRSDQP (SEQ ID NO: 277)	LGGSGRSNAQVRLE (SEQ ID NO: 357)
ISSGLLGGLSGRSDNP (SEQ ID NO: 278)	LGGSGRKASLSLE (SEQ ID NO: 358)
ISSGLLSSGGLSGRSDQP (SEQ ID NO: 279)	SGRIGFLRTA (SEQ ID NO: 359)
ISSGLLSSGGLSGRSDNP (SEQ ID NO: 280)	SGAIGFLRTA (SEQ ID NO: 360)
ISSGLLSGRS (SEQ ID NO: 281)	RPARSGRSAGGSVA (SEQ ID NO: 361)
ISSGLLSGRSESP (SEQ ID NO: 282)	VTGRGDSPASS (SEQ ID NO: 362)
ISSGLLSGRSEQP (SEQ ID NO: 283)	PRFKIIGG (SEQ ID NO: 363)
ISSGLLSGRSEQH (SEQ ID NO: 284)	LSGRIGFLRTA (SEQ ID NO: 364)

Exemplary cleavable peptide sequences	
LSSGLLSGRSDQP (SEQ ID NO: 285)	LSGRSNAMPYDLYHP (SEQ ID NO: 365)
LSSGLLGGLSGRSDQP (SEQ ID NO: 286)	LSGRSNAGGIGQLTA (SEQ ID NO: 366)
LSSGLLSGRSDQG (SEQ ID NO: 287)	LSGRSNAVPLSLY (SEQ ID NO: 367)
LSSGLLSGRSDQA (SEQ ID NO: 288)	LSGRSNADSGGFMLT (SEQ ID NO: 368)
LSSGLLSGRSDSP (SEQ ID NO: 289)	LSGRSNAHEQLTA (SEQ ID NO: 369)
LSSGLLSGRSDTP (SEQ ID NO: 290)	LSGRSNARAAAVKSP (SEQ ID NO: 370)
LSSGLLSGRSDMP (SEQ ID NO: 291)	LSGRSNATSVLMAAP (SEQ ID NO: 371)
LSSGLLSGRSD (SEQ ID NO: 292)	VPLSLYLSGRSNA (SEQ ID NO: 372)
GKQLRVVNEYSSMDNMLLG (SEQ ID NO: 293)	DSGGFMLTLSGRSNA (SEQ ID NO: 373)
LSSGLLGGLSGRSDNP (SEQ ID NO: 294)	GGIGQLTALSGRSNA (SEQ ID NO: 374)
LSSGLLSSGGLSGRSDQP (SEQ ID NO: 295)	MPYDLYHPLSGRSNA (SEQ ID NO: 375)
LSSGLLSSGGLSGRSDNP (SEQ ID NO: 296)	HEQLTVLSGRSNA (SEQ ID NO: 376)
GKQLRVVNEYSSEDNMLLG (SEQ ID NO: 297)	RAAAVKSPLSGRSNA (SEQ ID NO: 377)
LSSGLLSGRSESP (SEQ ID NO: 298)	TSVLMAAPLSGRSNA (SEQ ID NO: 378)
LSSGLLSGRSEQP (SEQ ID NO: 299)	IPVSLRSGRSNAQRLE (SEQ ID NO: 379)
LSSGLLSGRSEQH (SEQ ID NO: 300)	VPLSLYRQARVVG (SEQ ID NO: 380)
MPYDLYH (SEQ ID NO: 301)	DSGGFMLTRQARVVG (SEQ ID NO: 381)
LSGRSDNH (SEQ ID NO: 302)	GGIGQLTARQARVVG (SEQ ID NO: 382)
GSIPVSLRSG (SEQ ID NO: 306)	MPYDLYHPRQARVVG (SEQ ID NO: 383)
GPSGPAGLKGAPG (SEQ ID NO: 307)	HEQLTVRQARVVG (SEQ ID NO: 384)
GPPGPAGMKGLPG (SEQ ID NO: 308)	RAAAVKSPRQARVVG (SEQ ID NO: 385)
GYVADAPK (SEQ ID NO: 309)	TSVLMAAPRQARVVG (SEQ ID NO: 386)
KKLADEPE (SEQ ID NO: 310)	KQLRVVNEYSSMDNMLLG (SEQ ID NO: 387)
GGSRPAHLRDSGK (SEQ ID NO: 311)	KQLRVVNEYSSEDNMLLG (SEQ ID NO: 388)
SFTQARVVGG (SEQ ID NO: 312)	KQLRVVNGYSSEDNMLLG (SEQ ID NO: 389)
VHMPLGFLGPRQARVVN (SEQ ID NO: 313)	KQLRVVGGLVHLKNTMET (SEQ ID NO: 390)
LSGRSDNHSPLGLAGS (SEQ ID NO: 314)	TRDRLDEVNFKQLRVVNG (SEQ ID NO: 391)
VPLSLYSG (SEQ ID NO: 315)	TRDRLDEVNFKLLRVVNG (SEQ ID NO: 392)
IPESLRAG (SEQ ID NO: 316)	TRDRLDPVNFKQLRVVNG (SEQ ID NO: 393)
IPVSLRSG (SEQ ID NO: 317)	TRDRLDPVNFKLLRVVNG (SEQ ID NO: 394)
TYSRSKYLATA (SEQ ID NO: 399)	NPMGSEPVNFKQLRVVNG (SEQ ID NO: 395)
TYSRSRYLATA (SEQ ID NO: 400)	NPMGSEPVNFKLLRVVNG (SEQ ID NO: 396)
KQLRVVNEYSSE (SEQ ID NO: 401)	NPMGSDPVNFKQLRVVNG (SEQ ID NO: 397)
KQLRVVNGYSSE (SEQ ID NO: 402)	NPMGSDPVNFKLLRVVNG (SEQ ID NO: 398)
KQLRVVGGLVAL (SEQ ID NO: 403)	AGQPKQLRVVNG (SEQ ID NO: 494)
KQLRVVNGLVAL (SEQ ID NO: 404)	AGQPLQLRVVNG (SEQ ID NO: 495)
SPGRVVGGLVAL (SEQ ID NO: 405)	AGQPLQERVVNG (SEQ ID NO: 496)

Exemplary cleavable peptide sequences	
PQPRTYSRSRYL (SEQ ID NO: 406)	AGQPKQERVVNG (SEQ ID NO: 497)
PQPRTTSRSRYL (SEQ ID NO: 407)	GTANKQLRVVNG (SEQ ID NO: 498)
VVNEYSSSRGPYH (SEQ ID NO: 408)	GTANKQLHVVNG (SEQ ID NO: 499)
VVNEYSSERGPYH (SEQ ID NO: 409)	GTANIQLRVVNG (SEQ ID NO: 500)
NKVSMSSSRGPYH (SEQ ID NO: 410)	GTANIQLHVVNG (SEQ ID NO: 501)
NKVSMSSTRGPYH (SEQ ID NO: 411)	KQLRTVAGLAGK (SEQ ID NO: 504)
APAMMRGSVILTV (SEQ ID NO: 412)	KQLRTVNGLAGK (SEQ ID NO: 505)
APAMMEGSVILTV (SEQ ID NO: 413)	KQLRVVAGLAGK (SEQ ID NO: 506)
RGSVIITVQTVTW (SEQ ID NO: 414)	KQLRVVNGLAGK (SEQ ID NO: 507)
RGSVILTVQTVTW (SEQ ID NO: 415)	GIKYKQLRVVNG (SEQ ID NO: 508)
RKGKALAAYRLE (SEQ ID NO: 420)	GIKYKYLRVVNG (SEQ ID NO: 509)
RKGKAGAAYRLE (SEQ ID NO: 421)	GIKYLQLRVVNG (SEQ ID NO: 510)
RQARVVGGLVAL (SEQ ID NO: 422)	GIKYLYLRVVNG (SEQ ID NO: 511)
GGVRGPRFKIIGG (SEQ ID NO: 423)	THLDLTYSRSKYLATA (SEQ ID NO: 512)
GGVRGPRVKIIGG (SEQ ID NO: 424)	THLDLTPSRSKYLATA (SEQ ID NO: 513)
VTGRGDSHSLTTN (SEQ ID NO: 425)	THLDLTYSRSRYLATA (SEQ ID NO: 514)
VTGRGDSPSLTTN (SEQ ID NO: 426)	THLDLTPSRSRYLATA (SEQ ID NO: 515)
TGHGQASQGLLDR (SEQ ID NO:427)	TYSRSKYLAPANGNAE (SEQ ID NO: 516)
TGHGQASSGLLDR (SEQ ID NO: 428)	TYSRSKYLATANGNAE (SEQ ID NO: 517)
KQLRVVNENLENY (SEQ ID NO: 429)	TYSRSRYLAPANGNAE (SEQ ID NO: 518)
KQLRVVNGNLENY (SEQ ID NO: 430)	TYSRSRYLATANGNAE (SEQ ID NO: 519)
SNVNDVANYNFF (SEQ ID NO: 431)	DPVNFKQLRVVNEYSSE (SEQ ID NO: 520)
SNVNDVSNYNFF (SEQ ID NO: 432)	DPVNFKQLRVVNGYSSE (SEQ ID NO: 521)
IDFNAAQNLYEK (SEQ ID NO: 433)	DPVNFKKLRVVNEYSSE (SEQ ID NO: 522)
IDFNAAYNLYEK (SEQ ID NO: 434)	DPVNFKKLRVVNGYSSE (SEQ ID NO: 523)
IQWNAGQPLQER (SEQ ID NO: 435)	RKGKAGAAKNLNEKDY (SEQ ID NO: 524)
IQWNAPQPLQER (SEQ ID NO: 436)	RKGKAGAAKNLYEKDY (SEQ ID NO: 525)
SMDNRLLGLFGE (SEQ ID NO: 437)	RKGKAGAAQNLNEKDY (SEQ ID NO: 526)
SMDNMLLGLFGE (SEQ ID NO: 438)	RKGKAGAAQNLYEKDY (SEQ ID NO: 527)
VPIDDPQDLLEG (SEQ ID NO: 439)	VTGRGDSHSLTKNQVSL (SEQ ID NO: 528)
VPIDDPEDLLEG (SEQ ID NO: 440)	VTGRGDSHSLTTNQVSL (SEQ ID NO: 529)
IPENLPPGLPLT (SEQ ID NO: 441)	VTGRGDSPSLTKNQVSL (SEQ ID NO: 530)
IPENLPPLLPLT (SEQ ID NO: 442)	VTGRGDSPSLTTNQVSL (SEQ ID NO: 531)
QPPSLTKNQVSL (SEQ ID NO: 443)	TGHGQASSERSSNIRTS (SEQ ID NO: 532)
QPPSLTRNQVSL (SEQ ID NO: 444)	TGHGQASSERSSNSRTS (SEQ ID NO: 533)
DSHSLTKNQVSL (SEQ ID NO: 445)	TGHGQASSERSSTIRTS (SEQ ID NO: 534)
DSHSLTTNQVSL (SEQ ID NO: 446)	TGHGQASSERSSTSRTS (SEQ ID NO: 535)
KAIQLTKNQVSL (SEQ ID NO: 447)	DPVNFKLLRVVNEYSSE (SEQ ID NO: 538)
KAIQLTYNQVSL (SEQ ID NO: 448)	DPVNFKLLRVVNGYSSE (SEQ ID NO: 539)
AEPWTNRNTDGS (SEQ ID NO: 449)	DPVNFKQLRVVGGLVAL (SEQ ID NO: 540)
AEPWTVRNTDGS (SEQ ID NO: 450)	DPVNFKQLRVVNGLVAL (SEQ ID NO: 541)
KQLRVVNG (SEQ ID NO: 451)	DPVNFKLLRVVGGLVAL (SEQ ID NO: 542)
KQLRVVTGRGDSP (SEQ ID NO: 452)	DPVNFKLLRVVNGLVAL (SEQ ID NO: 543)
KQLRVVNGRGDSP (SEQ ID NO: 453)	KQLRVQNGDSTE (SEQ ID NO: 544)
PSSRRRVVRKGVS (SEQ ID NO: 454)	KQLRVVNNDATE (SEQ ID NO: 545)
PSSRRRVNRKGVS (SEQ ID NO: 455)	KQLRVVNGDSTE (SEQ ID NO: 546)
SPGRVVTGRGDSP (SEQ ID NO: 456)	ISNNKQLRVVNG (SEQ ID NO: 547)

Exemplary cleavable peptide sequences	
SPGRVVGGRGDSP (SEQ ID NO: 457)	ISNNKQLPVVNG (SEQ ID NO: 548)
NSGRAVTGRGDSP (SEQ ID NO: 458)	ISNNEQLRVVNG (SEQ ID NO: 549)
NSGRAVTYRGDSP (SEQ ID NO: 459)	ISNNEQLPVVNG (SEQ ID NO: 550)
TGHGQPSSRRRVN (SEQ ID NO: 460)	KVSNKQLRVVNG (SEQ ID NO: 551)
TGHGQASSRRRVN (SEQ ID NO: 461)	KVSNKQLPVVNG (SEQ ID NO: 552)
TGHGQSSSRGPYH (SEQ ID NO: 462)	KVSNKALRVVNG (SEQ ID NO: 553)
TGHGQASSRGPYH (SEQ ID NO: 463)	KVSNKALPVVNG (SEQ ID NO: 554)
RGSVILTKNQVSL (SEQ ID NO: 464)	KQLRVQNNDATE (SEQ ID NO: 555)
RGSVILTVNQVSL (SEQ ID NO: 465)	TGHGQRSSNIRTS (SEQ ID NO: 480)
SPGRVVGINYWLA (SEQ ID NO: 466)	TGHGQASSNIRTS (SEQ ID NO: 481)
SPGRVVGGNYWLA (SEQ ID NO: 467)	TGHGQHSSNIANI (SEQ ID NO: 482)
SPGRVVGSNKGAI (SEQ ID NO: 468)	TGHGQASSNIANI (SEQ ID NO: 483)
SPGRVVGGNKGAI (SEQ ID NO: 469)	TGHGQASRNDYSY (SEQ ID NO: 484)
PGARGRAPNHAVV (SEQ ID NO: 470)	TGHGQASSNDYSY (SEQ ID NO: 485)
PGARGRAFNHAVV (SEQ ID NO: 471)	KALHVTNRNTDGS (SEQ ID NO:486)
PGARGNAFNNLDR (SEQ ID NO: 472)	KALHVTNINTDGS (SEQ ID NO: 487)
PGARGRAFNNLDR (SEQ ID NO: 473)	RVVRKKVSNKALP (SEQ ID NO: 488)
VSNKYISNNEQLP (SEQ ID NO: 474)	RVVRKGVSNKALP (SEQ ID NO: 489)
VSNKYFSNNEQLP (SEQ ID NO: 475)	RQARVVGINYWLA (SEQ ID NO: 490)
KVSNKALHVTNI (SEQ ID NO: 476)	RQARVVGGNYWLA (SEQ ID NO: 491)
KVSNKALPVTNI (SEQ ID NO: 477)	
VTGRGPSPDVPLT (SEQ ID NO: 478)	
VTGRGDSPDVPLT (SEQ ID NO: 479)	

[0274] In some embodiments, the cleavable peptide comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 96-153, 236-242, 264, 270-302, 306-317, 342-347, 356-415, 420-491, 494-501, 504-535, and 538-555. In some embodiments, the cleavable peptide comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 270-302, 306-317, 342-347, 356-415, 420-491, 494-501, 504-535, and 538-555. In some embodiments, the cleavable peptide comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 281, 293, 297, 399-415, 420-491, 494-501, 504-535, and 538-555. In some embodiments, the cleavable peptide comprises the amino acid sequence of SEQ ID NO: 96. In some embodiments, the cleavable peptide comprises the amino acid sequence of SEQ ID NO: 264. In some embodiments, the cleavable peptide comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 96-153, 264, 270-302, 306-317, 342-347, 356-415, 420-491, 494-501, 504-535, and 538-555, and an amino acid sequence selected from the group consisting of SEQ ID NOs: 236-242. In some embodiments, the cleavable peptide comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 96-131, and 264, and an amino acid sequence selected from the group consisting of SEQ ID NOs: 236-242. In some embodiments, the cleavable peptide comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 96-131, and an amino acid sequence selected from the group consisting of SEQ ID NOs: 236-242. In embodiments in which the cleavable peptide comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 96-153, 264, 270-302, 306-317, 342-347,

356-415, 420-491, 494-501, 504-535, and 538-555, and an amino acid sequence selected from the group consisting of SEQ ID NOs: 236-242, the two amino acid sequences may be linked in any order. For example, in embodiments in which the cleavable peptide comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 96-153, 236-242, 264, 270-302, 306-317, 342-347, 356-415, 420-491, 494-501, 504-535, and 538-555, and an amino acid sequence selected from the group consisting of SEQ ID NOs: 236-242, the amino acid sequence selected from the group consisting of SEQ ID NOs: 96-153, 236-242, 264, 270-302, 306-317, 342-347, 356-415, 420-491, 494-501, 504-535, and 538-555 comprises an N-terminus and a C-terminus, and the amino acid sequence selected from the group consisting of SEQ ID NOs: 236-242 is linked to the N-terminus or the C-terminus of the amino acid sequence selected from the group consisting of SEQ ID NOs: 96-153, 264, 270-302, 306-317, 342-347, 356-415, 420-491, 494-501, 504-535, and 538-555. In some embodiments in which the cleavable peptide comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 96-131, and 264, and an amino acid sequence selected from the group consisting of SEQ ID NOs: 236-242, the amino acid sequence selected from the group consisting of SEQ ID NOs: 96-131, and 264, comprises an N-terminus and a C-terminus, and the amino acid sequence selected from the group consisting of SEQ ID NOs: 236-242 is linked to the N-terminus or the C-terminus of the amino acid sequence selected from the group consisting of SEQ ID NOs: 96-131, and 264.

[0275] In some embodiments, one or more additional amino acids are incorporated by addition into to the amino acid sequence of the cleavable peptide. In some embodiments, the one or more amino acids that are incorporated by addition into the amino acid sequence of the cleavable peptide are selected from the group consisting of hydrophilic amino acids (e.g., lysine, arginine, histidine, aspartic acid, glutamic acid, serine, threonine, asparagine, or glutamine), hydrophobic amino acids (e.g., alanine, valine, isoleucine, leucine, methionine, phenylalanine, tyrosine, tryptophan, cysteine, glycine, or proline), polar amino acids (e.g., serine, threonine, cysteine, asparagine, glutamine, or tyrosine), nonpolar amino acids (e.g., glycine, alanine, valine, proline, leucine, isoleucine, methionine, tryptophan, or phenylalanine), amino acids with aliphatic side chains (e.g., glycine, alanine, valine, leucine, or isoleucine), amino acids with hydroxyl-containing side chains (e.g., serine or threonine), amino acids with sulfur-containing side chains (e.g., cysteine or methionine), charged amino acids (e.g., arginine, lysine, aspartic acid, or glutamic acid), uncharged amino acids (e.g., serine, threonine, asparagine, or glutamine), aromatic amino acids (e.g., tyrosine, tryptophan, or phenylalanine), cyclic amino acids (e.g., proline), acidic amino acids (e.g., aspartic acid, asparagine, glutamic acid, or glutamine), basic amino acids (e.g., histidine, lysine, or arginine), and bulky amino acids (e.g., phenylalanine, tyrosine, or tryptophan). In some embodiments, a glycine (G) is incorporated by addition to the N-terminus and/or C-terminus of the amino acid sequence of the cleavable peptide. In some embodiments, a glycine (G) and a proline (P) are incorporated by addition to the N-terminus and/or C-terminus of the amino acid sequence of the cleavable peptide, such

as by incorporating the amino acid sequence GP or PG to the N-terminus and/or C-terminus of the amino acid sequence of the cleavable peptide.

[0276] The cleavable peptide comprises an amino-terminus and a carboxy-terminus. In some embodiments, the cleavable peptide is linked to an N-terminal spacer domain and/or a C-terminal spacer domain. In some embodiments, an N-terminal spacer domain is linked to the amino-terminus of the cleavable peptide. In some embodiments, a C-terminal spacer domain is linked to the carboxy-terminus of the cleavable peptide. In some embodiments, an N-terminal spacer domain is linked to the amino-terminus of the cleavable peptide, and a C-terminal spacer domain is linked to the carboxy-terminus of the cleavable peptide. In some embodiments, an N-terminal spacer domain is linked to the amino-terminus of the cleavable peptide, and a C-terminal spacer domain is linked to the carboxy-terminus of the cleavable peptide.

[0277] In some embodiments, the amino-terminus of the cleavable peptide is linked to a component other than the N-terminal spacer domain. In some embodiments, the carboxy-terminus of the cleavable peptide is linked to a component other than the C-terminal spacer domain. In some embodiments, a masking moiety is linked to the amino-terminus or the carboxy-terminus of the cleavable peptide. In some embodiments, a cytokine or functional fragment thereof is linked to the amino-terminus or the carboxy-terminus of the cleavable peptide. In some embodiments, a half-life extension domain is linked to the amino-terminus or the carboxy-terminus of the cleavable peptide. In some embodiments, a first half-life extension domain is linked to the amino-terminus or the carboxy-terminus of the cleavable peptide. In some embodiments, a second half-life extension domain is linked to the amino-terminus or the carboxy-terminus of the cleavable peptide.

2. Spacer Domains

[0278] In some embodiments, the linker comprises a spacer domain. As used herein, a "spacer domain" may, in some embodiments, refer to an N-terminal spacer domain and/or a C-terminal spacer domain. In some embodiments, the linker comprises an N-terminal spacer domain and/or a C-terminal spacer domain. In some embodiments, the linker comprises an N-terminal spacer domain. In some embodiments, the linker comprises a C-terminal spacer domain. In some embodiments, the linker comprises an N-terminal spacer domain and a C-terminal spacer domain. In some embodiments, the linker comprises an N-terminal spacer domain and a cleavable peptide. In some embodiments, the linker comprises a cleavable peptide and a C-terminal spacer domain. In some embodiments, the linker comprises an N-terminal spacer domain, a cleavable peptide, and a C-terminal spacer domain.

[0279] In some embodiments, such as some embodiments having more than one N-terminal spacer domain, an N-terminal spacer domain may be referred to as a first N-terminal spacer domain, a second N-terminal spacer domain, or a third N-terminal spacer domain, each of which is considered "an N-terminal spacer domain" and may be any of the N-terminal spacer domains described herein. Likewise,

in some embodiments, such as some embodiments having more than one C-terminal spacer domain, a C-terminal spacer domain may be referred to as a first C-terminal spacer domain, a second C-terminal spacer domain, or a third C-terminal spacer domain, each of which is considered "a C-terminal spacer domain" and may be any of the C-terminal spacer domains described herein. For example, reference to "an N-terminal spacer domain" or "the N-terminal spacer domain" can refer to the N-terminal spacer domain in a masked cytokine comprising a single N-terminal spacer domain, or it can refer to the first N-terminal spacer domain in a masked cytokine comprising a first N-terminal spacer domain and a second N-terminal spacer domain, or it can refer to the second N-terminal spacer domain in a masked cytokine comprising a first N-terminal spacer domain and a second N-terminal spacer domain, or it can refer to the first N-terminal spacer domain and the second N-terminal spacer domain in a masked cytokine comprising a first N-terminal spacer domain and a second N-terminal spacer domain, or it can refer to the first N-terminal spacer domain, the second N-terminal spacer domain, and/or the third N-terminal spacer domain in a masked cytokine comprising a first N-terminal spacer domain, a second N-terminal spacer domain, and a third N-terminal spacer domain.

[0280] The N-terminal spacer domain and the C-terminal spacer domain each comprise an amino-terminus and a carboxy-terminus. In some embodiments, a masking moiety is linked to the amino-terminus or the carboxy-terminus of the N-terminal spacer domain. In some embodiments, a cytokine or functional fragment thereof is linked to the amino-terminus or the carboxy-terminus of the N-terminal spacer domain. In some embodiments, a half-life extension domain is linked to the amino-terminus or the carboxy-terminus of the N-terminal spacer domain. In some embodiments, a first half-life extension domain is linked to the amino-terminus or the carboxy-terminus of the N-terminal spacer domain. In some embodiments, a second half-life extension domain is linked to the amino-terminus or the carboxy-terminus of the N-terminal spacer domain.

[0281] In some embodiments, a masking moiety is linked to the amino-terminus or the carboxy-terminus of the C-terminal spacer domain. In some embodiments, a cytokine or functional fragment thereof is linked to the amino-terminus or the carboxy-terminus of the C-terminal spacer domain. In some embodiments, a half-life extension domain is linked to the amino-terminus or the carboxy-terminus of the C-terminal spacer domain. In some embodiments, a first half-life extension domain is linked to the amino-terminus or the carboxy-terminus of the C-terminal spacer domain. In some embodiments, a second half-life extension domain is linked to the amino-terminus or the carboxy-terminus of the C-terminal spacer domain.

[0282] In some embodiments, a masking moiety is linked to the amino-terminus of the N-terminal spacer domain, and a half-life extension domain is linked to the carboxy-terminus of the N-terminal spacer domain. In some embodiments, a cytokine or functional fragment thereof is linked to the amino-terminus of the N-terminal spacer domain, and a half-life extension domain is linked to the carboxy-terminus of the N-terminal spacer domain. In some embodiments, a masking moiety is linked to the

carboxy-terminus of the N-terminal spacer domain and, a half-life extension domain is linked to the amino-terminus of the N-terminal spacer domain. In some embodiments, a cytokine or functional fragment thereof is linked to the carboxy-terminus of the N-terminal spacer domain, and a half-life extension domain is linked to the amino-terminus of the N-terminal spacer domain.

[0283] In some embodiments, a masking moiety is linked to the amino-terminus of the C-terminal spacer domain, and a half-life extension domain is linked to the carboxy-terminus of the C-terminal spacer domain. In some embodiments, a cytokine or functional fragment thereof is linked to the amino-terminus of the C-terminal spacer domain, and a half-life extension domain is linked to the carboxy-terminus of the C-terminal spacer domain. In some embodiments, a masking moiety is linked to the carboxy-terminus of the C-terminal spacer domain and, a half-life extension domain is linked to the amino-terminus of the C-terminal spacer domain. In some embodiments, a cytokine or functional fragment thereof is linked to the carboxy-terminus of the C-terminal spacer domain, and a half-life extension domain is linked to the amino-terminus of the C-terminal spacer domain.

[0284] In some embodiments comprising a first masking moiety and a second masking moiety, the first masking moiety or the second masking moiety is linked to the amino-terminus of the N-terminal spacer domain, and a cytokine or functional fragment thereof is linked to the carboxy-terminus of the N-terminal spacer domain. In some embodiments comprising a first masking moiety and a second masking moiety, the first masking moiety or the second masking moiety is linked to the carboxy-terminus of the N-terminal spacer domain, and a cytokine or functional fragment thereof is linked to the amino-terminus of the N-terminal spacer domain.

[0285] In some embodiments comprising a first masking moiety and a second masking moiety, the first masking moiety or the second masking moiety is linked to the amino-terminus of the C-terminal spacer domain, and a cytokine or functional fragment thereof is linked to the carboxy-terminus of the C-terminal spacer domain. In some embodiments comprising a first masking moiety and a second masking moiety, the first masking moiety or the second masking moiety is linked to the carboxy-terminus of the C-terminal spacer domain, and a cytokine or functional fragment thereof is linked to the amino-terminus of the C-terminal spacer domain.

[0286] In some embodiments comprising a first masking moiety and a second masking moiety, the first masking moiety is linked to the amino-terminus of the C-terminal spacer domain, and the second masking moiety is linked to the carboxy-terminus of the C-terminal spacer domain. In some embodiments comprising a first masking moiety and a second masking moiety, the first masking moiety is linked to the carboxy-terminus of the C-terminal spacer domain, and the second masking moiety is linked to the amino-terminus of the C-terminal spacer domain.

[0287] In some embodiments comprising a first masking moiety and a second masking moiety, the half-life extension domain is linked to the amino-terminus of the N-terminal spacer domain, and either the first masking moiety or the second masking moiety is linked to the carboxy-terminus of the N-

terminal spacer domain. In some embodiments comprising a first masking moiety and a second masking moiety, the half-life extension domain is linked to the carboxy-terminus of the N-terminal spacer domain, and either the first masking moiety or the second masking moiety is linked to the amino-terminus of the N-terminal spacer domain.

[0288] In some embodiments comprising a first masking moiety and a second masking moiety, the first masking moiety is linked to the amino-terminus of the N-terminal spacer domain, and the second masking moiety is linked to the carboxy-terminus of the N-terminal spacer domain. In some embodiments comprising a first masking moiety and a second masking moiety, the first masking moiety is linked to the carboxy-terminus of the N-terminal spacer domain, and the second masking moiety is linked to the amino-terminus of the N-terminal spacer domain.

[0289] In some embodiments comprising a first masking moiety and a second masking moiety, the half-life extension domain is linked to the amino-terminus of the C-terminal spacer domain, and either the first masking moiety or the second masking moiety is linked to the carboxy-terminus of the C-terminal spacer domain. In some embodiments comprising a first masking moiety and a second masking moiety, the half-life extension domain is linked to the carboxy-terminus of the C-terminal spacer domain, and either the first masking moiety or the second masking moiety is linked to the amino-terminus of the C-terminal spacer domain.

[0290] In some embodiments comprising a first half-life extension domain and a second half-life extension domain, a masking moiety is linked to the amino-terminus of the N-terminal spacer domain, and either the first half-life extension domain or the second half-life extension domain is linked to the carboxy-terminus of the N-terminal spacer domain. In some embodiments comprising a first half-life extension domain and a second half-life extension domain, a masking moiety is linked to the carboxy-terminus of the N-terminal spacer domain, and either the first half-life extension domain or the second half-life extension domain is linked to the amino-terminus of the N-terminal spacer domain. In some embodiments comprising a first half-life extension domain and a second half-life extension domain, a cytokine or functional fragment thereof is linked to the amino-terminus of the N-terminal spacer domain, and either the first half-life extension domain or the second half-life extension domain is linked to the carboxy-terminus of the N-terminal spacer domain. In some embodiments comprising a first half-life extension domain and a second half-life extension domain, a cytokine or functional fragment thereof is linked to the carboxy-terminus of the N-terminal spacer domain, and either the first half-life extension domain or the second half-life extension domain is linked to the amino-terminus of the N-terminal spacer domain.

[0291] In some embodiments comprising a first half-life extension domain and a second half-life extension domain, a masking moiety is linked to the amino-terminus of the C-terminal spacer domain, and either the first half-life extension domain or the second half-life extension domain is linked to the carboxy-terminus of the C-terminal spacer domain. In some embodiments comprising a first half-life

extension domain and a second half-life extension domain, a masking moiety is linked to the carboxy-terminus of the C-terminal spacer domain, and either the first half-life extension domain or the second half-life extension domain is linked to the amino-terminus of the C-terminal spacer domain. In some embodiments comprising a first half-life extension domain and a second half-life extension domain, a cytokine or functional fragment thereof is linked to the amino-terminus of the C-terminal spacer domain, and either the first half-life extension domain or the second half-life extension domain is linked to the carboxy-terminus of the C-terminal spacer domain. In some embodiments comprising a first half-life extension domain and a second half-life extension domain, a cytokine or functional fragment thereof is linked to the carboxy-terminus of the C-terminal spacer domain, and either the first half-life extension domain or the second half-life extension domain is linked to the amino-terminus of the C-terminal spacer domain.

[0292] In some embodiments comprising a first half-life extension domain, a second half-life extension domain, a first masking moiety, and a second masking moiety, the first masking moiety is linked to the amino-terminus of the N-terminal spacer domain, and the first half-life extension domain is linked to the carboxy-terminus of the N-terminal spacer domain. In some embodiments comprising a first half-life extension domain, a second half-life extension domain, a first masking moiety, and a second masking moiety, the first masking moiety is linked to the carboxy-terminus of the N-terminal spacer domain, and the first half-life extension domain is linked to the amino-terminus of the N-terminal spacer domain. In some embodiments comprising a first half-life extension domain, a second half-life extension domain, a first masking moiety, and a second masking moiety, the first masking moiety is linked to the amino-terminus of the C-terminal spacer domain, and the first half-life extension domain is linked to the carboxy-terminus of the C-terminal spacer domain. In some embodiments comprising a first half-life extension domain, a second half-life extension domain, a first masking moiety, and a second masking moiety, the first masking moiety is linked to the carboxy-terminus of the C-terminal spacer domain, and the first half-life extension domain is linked to the amino-terminus of the C-terminal spacer domain.

[0293] In some embodiments comprising a first half-life extension domain, a second half-life extension domain, a first masking moiety, and a second masking moiety, the second masking moiety is linked to the amino-terminus of the N-terminal spacer domain, and the cytokine or functional fragment thereof is linked to the carboxy-terminus of the N-terminal spacer domain. In some embodiments comprising a first half-life extension domain, a second half-life extension domain, a first masking moiety, and a second masking moiety, the second masking moiety is linked to the carboxy-terminus of the N-terminal spacer domain, and the cytokine or functional fragment thereof is linked to the amino-terminus of the N-terminal spacer domain. In some embodiments comprising a first half-life extension domain, a second half-life extension domain, a first masking moiety, and a second masking moiety, the second masking moiety is linked to the amino-terminus of the C-terminal spacer domain, and the cytokine or functional fragment thereof is linked to the carboxy-terminus of the C-terminal spacer

domain. In some embodiments comprising a first half-life extension domain, a second half-life extension domain, a first masking moiety, and a second masking moiety, the second masking moiety is linked to the carboxy-terminus of the C-terminal spacer domain, and the cytokine or functional fragment thereof is linked to the amino-terminus of the C-terminal spacer domain.

[0294] In some embodiments comprising a first half-life extension domain, a second half-life extension domain, a first masking moiety, and a second masking moiety, the second half-life extension domain is linked to the amino-terminus of the N-terminal spacer domain, and either the cytokine or functional fragment thereof or the second masking moiety is linked to the carboxy-terminus of the N-terminal spacer domain. In some embodiments comprising a first half-life extension domain, a second half-life extension domain, a first masking moiety, and a second masking moiety, the second half-life extension domain is linked to the carboxy-terminus of the N-terminal spacer domain, and either the cytokine or functional fragment thereof or the second masking moiety is linked to the amino-terminus of the N-terminal spacer domain. In some embodiments comprising a first half-life extension domain, a second half-life extension domain, a first masking moiety, and a second masking moiety, the second half-life extension domain is linked to the amino-terminus of the C-terminal spacer domain, and either the cytokine or functional fragment thereof or the second masking moiety is linked to the carboxy-terminus of the C-terminal spacer domain. In some embodiments comprising a first half-life extension domain, a second half-life extension domain, a first masking moiety, and a second masking moiety, the second half-life extension domain is linked to the carboxy-terminus of the C-terminal spacer domain, and either the cytokine or functional fragment thereof or the second masking moiety is linked to the amino-terminus of the C-terminal spacer domain.

[0295] In some embodiments comprising a first half-life extension domain and a second half-life extension domain, the first half-life extension domain is linked to the second half-life extension domain via a linker. In some embodiments, the linker linking the first half-life extension domain and the second half-life extension domain comprises an N-terminal spacer domain and/or a C-terminal spacer domain. In some embodiments, the linker linking the first half-life extension domain and the second half-life extension domain comprises a cleavable peptide and an N-terminal spacer domain and/or a C-terminal spacer domain. In some embodiments comprising a first half-life extension domain and a second half-life extension domain that are linked together via a linker, the linker comprises an amino-terminus and a carboxy terminus, and the first half-life extension domain is linked to the amino-terminus of the linker and the second half-life extension domain is linked to the carboxy-terminus of the linker. In some embodiments comprising a first half-life extension domain and a second half-life extension domain that are linked together via a linker, the linker comprises an amino-terminus and a carboxy terminus, and the first half-life extension domain is linked to the carboxy-terminus of the linker and the second half-life extension domain is linked to the amino-terminus of the linker.

[0296] In some embodiments, the N-terminal spacer domain comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 20-95, 235, 268, 269, 303-305, 323-338, 340, 341, 727, 794, and 799. In some embodiments, the C-terminal spacer domain comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 20-95, 235, 268, 269, 303-305, 323-338, 340, 341, 727, 794, and 799. In some embodiments, the N-terminal spacer domain comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 20-95, 235, 268, 269, 303-305, 323-338, 340, 341, 727, 794, and 799, and the C-terminal spacer domain comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 20-95, 235, 268, 269, 303-305, 323-338, 340, 341, 727, 794, and 799.

[0297] In some embodiments, the N-terminal spacer domain comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 20-95, 235, 268, and 269. In some embodiments, the C-terminal spacer domain comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 20-95, 235, 268, and 269. In some embodiments, the N-terminal spacer domain comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 20-95,235, 268, and 269, and the C-terminal spacer domain comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 20-95, 235, 268, and 269. In some embodiments, the linker comprises an N-terminal spacer domain comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 20-95, 235, 268, and 269, and an C-terminal spacer domain comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 20-95, 235, 268, and 269. In some embodiments, the linker comprises an N-terminal spacer domain comprising the amino acid sequence of SEQ ID NO: 268, and an C-terminal spacer domain comprising the amino acid sequence of SEQ ID NO: 269. In some embodiments, the linker comprises an N-terminal spacer domain comprising the amino acid sequence of SEQ ID NO: 268, a cleavable peptide comprising the amino acid sequence of SEQ ID NO: 264, and an C-terminal spacer domain comprising the amino acid sequence of SEQ ID NO: 269. In some embodiments, the linker comprises an N-terminal spacer domain comprising the amino acid sequence of SEQ ID NO: 269, and an C-terminal spacer domain comprising the amino acid sequence of SEQ ID NO: 268. In some embodiments, the linker comprises an N-terminal spacer domain comprising the amino acid sequence of SEQ ID NO: 269, a cleavable peptide comprising the amino acid sequence of SEQ ID NO: 264, and an C-terminal spacer domain comprising the amino acid sequence of SEQ ID NO: 268.

[0298] In some embodiments, the N-terminal spacer domain comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 20-95, 235, 268, and 269. In some embodiments, the N-terminal spacer domain comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of any one of SEQ ID NOs: 20-95, 235, 268, 269, 303-305, 323-338, 340, 341, 727, 794, and 799. In some embodiments, the N-terminal spacer domain comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%,

98%, or 99% sequence identity to the amino acid sequence of any one of SEQ ID NOs: 20-95, 235, 268, and 269. In some embodiments, the C-terminal spacer domain comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of any one of SEQ ID NOs: 20-95, 235, 268, 269, 303-305, 323-338, 340, 341, 727, 794, and 799. In some embodiments, the C-terminal spacer domain comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 20-95, 235, 268, and 269. In some embodiments, the C-terminal spacer domain comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of any one of SEQ ID NOs: 20-95, 235, 268, and 269. In some embodiments, the N-terminal spacer domain comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 20-95, 235, 268, and 269, and the C-terminal spacer domain comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 20-95, 235, 268, and 269. In some embodiments, the N-terminal spacer domain comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of any one of SEQ ID NOs: 20-95, 235, 268, and 269, and the C-terminal spacer domain comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of any one of SEQ ID NOs: 20-95, 235, 268, and 269. In some embodiments, the N-terminal spacer domain comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 268, and the C-terminal spacer domain comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 269. In some embodiments, the N-terminal spacer domain comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 268, the cleavable peptide comprises the amino acid sequence of SEQ ID NO: 264, and the C-terminal spacer domain comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 269. Exemplary spacer domains (e.g., N-terminal spacer domains and/or C-terminal spacer domains) are shown in Table 2.

Table 2. Exemplary spacer domains

PA (SEQ ID NO: 20)	SPGGSS (SEQ ID NO: 74)
GGGGSGGGGSGGGGS (SEQ ID NO: 21)	GGPGSSP (SEQ ID NO: 75)
PSGPSAGGAA (SEQ ID NO: 22)	SGPPGGPSS (SEQ ID NO: 76)

GGPPASAGS (SEQ ID NO: 23)	GPGPGSPPGGSS (SEQ ID NO: 77)
GSPPAGGAP (SEQ ID NO: 24)	SGPP (SEQ ID NO: 78)
GPGSGSGGAA (SEQ ID NO: 25)	PGSPSSS (SEQ ID NO: 79)
GGGGSGGGGS (SEQ ID NO: 26)	PSPGGPS (SEQ ID NO: 80)
GGGGSGGGGSGGGGSGGGGS (SEQ ID NO: 27)	GGPPS (SEQ ID NO: 81)
PGSGS (SEQ ID NO: 28)	PSPPSS (SEQ ID NO: 82)
GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG (SEQ ID NO: 29)	SGGPGP (SEQ ID NO: 83)
GGGGSGGGGSGGGGSGGGGSGGGGS (SEQ ID NO: 30)	GPSPGS (SEQ ID NO: 84)
GGGGSGGGGSGGGGSGGGGSGGGGSGGGGS (SEQ ID NO: 31)	GSPGPSP (SEQ ID NO: 85)
GGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGS (SEQ ID NO: 32)	PSSGGSS (SEQ ID NO: 86)
GGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGS (SEQ ID NO: 33)	SGSSGP (SEQ ID NO: 87)
GGSSPP (SEQ ID NO: 34)	GGSSSPP (SEQ ID NO: 88)
SGP (SEQ ID NO: 35)	GSPGSP (SEQ ID NO: 89)
GSP (SEQ ID NO: 36)	PPPS (SEQ ID NO: 90)
GSPP (SEQ ID NO: 37)	APPPS (SEQ ID NO: 91)
GSPS (SEQ ID NO: 38)	AAPPPS (SEQ ID NO: 92)
GPPSGSSP (SEQ ID NO: 39)	SAPPPS (SEQ ID NO: 93)
GSSGGPPGG (SEQ ID NO: 40)	SSGP (SEQ ID NO: 94)
SGSPSGSGGG (SEQ ID NO: 41)	SSPGP (SEQ ID NO: 95)
GPPGPPGSSG (SEQ ID NO: 42)	SGGSGGGGSGGGSGGGGSLQ (SEQ ID NO: 235)
SGGG (SEQ ID NO: 43)	GSGP (SEQ ID NO: 268)
GSSSGPPGPPS (SEQ ID NO: 44)	GPAP (SEQ ID NO: 269)
GGS (SEQ ID NO: 45)	SGS (SEQ ID NO: 727)
GGGSSGGS (SEQ ID NO: 46)	SG (SEQ ID NO: 794)
GGSGG (SEQ ID NO: 47)	GSG (SEQ ID NO: 799)
GGGS (SEQ ID NO: 48)	PGPGP (SEQ ID NO: 323)
GS (SEQ ID NO: 48)	SGGCGGHQYERRGGC (SEQ ID NO: 324)
GSGGGSSGGS (SEQ ID NO: 50)	SGGCSGHQYERREGC (SEQ ID NO: 325)
GSSGGS (SEQ ID NO: 51)	SGGCGGHYFERHGGC (SEQ ID NO: 326)
GGGSSGGSG (SEQ ID NO: 52)	SGGCSGHYFERHEGC (SEQ ID NO: 327)
GGSAGGS (SEQ ID NO: 53)	SGGCSFHQYERHEGC (SEQ ID NO: 328)
GHS (SEQ ID NO: 54)	PSGSS (SEQ ID NO: 329)
GPS (SEQ ID NO: 55)	GSPG (SEQ ID NO: 330)
GAS (SEQ ID NO: 56)	GGSPGG (SEQ ID NO: 331)
SGG (SEQ ID NO: 57)	GGPGGP (SEQ ID NO: 332)
SGGSGG (SEQ ID NO: 58)	GGSG (SEQ ID NO: 333)
SSG (SEQ ID NO: 59)	GSPPGG (SEQ ID NO: 334)
GGGSGG (SEQ ID NO: 60)	GPGSPG (SEQ ID NO: 335)
GG (SEQ ID NO: 61)	GSSPPG (SEQ ID NO: 336)
GGG (SEQ ID NO: 62)	GGP (SEQ ID NO: 337)
SHGG (SEQ ID NO: 63)	SGPGSGS (SEQ ID NO: 338)

HGGG (SEQ ID NO: 64)	SGPGSGS (SEQ ID NO: 340)
SGAA (SEQ ID NO: 65)	SGSGGSP (SEQ ID NO: 341)
SGPA (SEQ ID NO: 66)	GGGSSP (SEQ ID NO: 303)
GGSGGS (SEQ ID NO: 67)	SGGP (SEQ ID NO: 304)
GGSGGP (SEQ ID NO: 68)	SGPSGSPG (SEQ ID NO: 305)
GGSGGG (SEQ ID NO: 69)	
GSGGPGPS (SEQ ID NO: 70)	
SGPPGSS (SEQ ID NO: 71)	
SSGGSGP (SEQ ID NO: 72)	
SSPSPSGG (SEQ ID NO: 73)	

[0299] In some embodiments, the N-terminal spacer domain comprises an amino acid sequence produced by modifying the amino acid sequence of any of the N-terminal spacer domains described herein. In some embodiments, the N-terminal spacer domain comprises an amino acid sequence produced by modifying the amino acid sequence of any one of SEQ ID NOs: 20-95, 235, 268, 269, 303-305, 323-338, 340, 341, 727, 794, and 799. In some embodiments, the C-terminal spacer domain comprises an amino acid sequence produced by modifying the amino acid sequence of any of the C-terminal spacer domains described herein. In some embodiments, the C-terminal spacer domain comprises an amino acid sequence produced by modifying the amino acid sequence of any one of SEQ ID NOs: 20-95, 235, 268, 269, 303-305, 323-338, 340, 341, 727, 794, and 799. In some embodiments, the N-terminal spacer domain comprises an amino acid sequence produced by modifying the amino acid sequence of any one of SEQ ID NOs: 20-95, 235, 268, 269, 303-305, 323-338, 340, 341, 727, 794, and 799, and the C-terminal spacer domain comprises an amino acid sequence produced by modifying the amino acid sequence of any one of SEQ ID NOs: 20-95, 235, 268, 269, 303-305, 323-338, 340, 341, 727, 794, and 799. In some embodiments, the N-terminal spacer domain and/or the C-terminal spacer domain comprises the amino acid sequence of SEQ ID NO: 28.

[0300] In some embodiments, the N-terminal spacer domain and/or the C-terminal spacer domain consists of one or more amino acids. In some embodiments, the one or more amino acids of the N-terminal spacer domain and/or the C-terminal spacer domain are selected from the group consisting of hydrophilic amino acids (e.g., lysine, arginine, histidine, aspartic acid, glutamic acid, serine, threonine, asparagine, or glutamine), hydrophobic amino acids (e.g., alanine, valine, isoleucine, leucine, methionine, phenylalanine, tyrosine, tryptophan, cysteine, glycine, or proline), polar amino acids (e.g., serine, threonine, cysteine, asparagine, glutamine, or tyrosine), nonpolar amino acids (e.g., glycine, alanine, valine, proline, leucine, isoleucine, methionine, tryptophan, or phenylalanine), amino acids with aliphatic side chains (e.g., glycine, alanine, valine, leucine, or isoleucine), amino acids with hydroxyl-containing side chains (e.g., serine or threonine), amino acids with sulfur-containing side chains (e.g., cysteine or methionine), charged amino acids (e.g., arginine, lysine, aspartic acid, or glutamic acid), uncharged amino acids (e.g., serine, threonine, asparagine, or glutamine), aromatic amino acids (e.g., tyrosine, tryptophan, or phenylalanine), cyclic amino acids (e.g., proline), acidic amino acids (e.g.,

aspartic acid, asparagine, glutamic acid, or glutamine), basic amino acids (e.g., histidine, lysine, or arginine), and bulky amino acids (e.g., phenylalanine, tyrosine, or tryptophan). In some embodiments, the N-terminal spacer domain and/or the C-terminal spacer domain consists of a glycine (G). In some embodiments, the N-terminal spacer domain and/or the C-terminal spacer domain consists of a glycine (G) and a proline (P), and has the amino acid sequence of GP or PG.

[0301] It is understood that a modification to a "spacer domain," as described in some embodiments, can refer to a modification to any one or more of the spacer domains described herein (e.g., any N-terminal spacer domain and/or any C-terminal spacer domain described herein). For example, a modification to a spacer domain can refer to (a) a modification to any N-terminal spacer domain described herein, (b) a modification to any C-terminal spacer domain described herein, or (c) a modification to any N-terminal spacer domain and to any C-terminal spacer domain described herein. As such, any of the linkers described herein that include an N-terminal spacer domain include embodiments where the N-terminal spacer domain is modified in accordance with the modifications described herein, any of the linkers described herein that include a C-terminal spacer domain include embodiments where the C-terminal spacer domain is modified in accordance with the modifications described herein, and any of the linkers described herein that include an N-terminal spacer domain and a C-terminal spacer domain include embodiments where the N-terminal spacer domain and/or the C-terminal spacer domain is/are modified in accordance with the modifications described herein.

[0302] The modification to the sequence of the N-terminal spacer domain and/or the C-terminal spacer domain can be any modification to the amino acid sequence of the spacer domain, including the incorporation of any additional amino acid into the sequence, the substitution of any amino acid for a different amino acid, and/or the removal of any amino acid from the sequence.

[0303] In some embodiments, one or more additional amino acids are incorporated by addition into to the amino acid sequence of the N-terminal spacer domain and/or the C-terminal spacer domain. In some embodiments, the one or more amino acids that are incorporated by addition into the amino acid sequence of the N-terminal spacer domain and/or the C-terminal spacer domain are selected from the group consisting of hydrophilic amino acids (e.g., lysine, arginine, histidine, aspartic acid, glutamic acid, serine, threonine, asparagine, or glutamine), hydrophobic amino acids (e.g., alanine, valine, isoleucine, leucine, methionine, phenylalanine, tyrosine, tryptophan, cysteine, glycine, or proline), polar amino acids (e.g., serine, threonine, cysteine, asparagine, glutamine, or tyrosine), nonpolar amino acids (e.g., glycine, alanine, valine, proline, leucine, isoleucine, methionine, tryptophan, or phenylalanine), amino acids with aliphatic side chains (e.g., glycine, alanine, valine, leucine, or isoleucine), amino acids with hydroxyl-containing side chains (e.g., serine or threonine), amino acids with sulfur-containing side chains (e.g., cysteine or methionine), charged amino acids (e.g., arginine, lysine, aspartic acid, or glutamic acid), uncharged amino acids (e.g., serine, threonine, asparagine, or glutamine), aromatic amino acids (e.g., tyrosine, tryptophan, or phenylalanine), cyclic amino acids (e.g., proline), acidic amino acids (e.g.,

aspartic acid, asparagine, glutamic acid, or glutamine), basic amino acids (e.g., histidine, lysine, or arginine), and bulky amino acids (e.g., phenylalanine, tyrosine, or tryptophan).

[0304] In some embodiments, one or more amino acids are substituted into the amino acid sequence of the N-terminal spacer domain and/or the C-terminal spacer domain. In some embodiments, the one or more amino acids that are substituted into the amino acid sequence of the spacer domain are selected from the group consisting of hydrophilic amino acids (e.g., lysine, arginine, histidine, aspartic acid, glutamic acid, serine, threonine, asparagine, or glutamine), hydrophobic amino acids (e.g., alanine, valine, isoleucine, leucine, methionine, phenylalanine, tyrosine, tryptophan, cysteine, glycine, or proline), polar amino acids (e.g., serine, threonine, cysteine, asparagine, glutamine, or tyrosine), nonpolar amino acids (e.g., glycine, alanine, valine, proline, leucine, isoleucine, methionine, tryptophan, or phenylalanine), amino acids with aliphatic side chains (e.g., glycine, alanine, valine, leucine, or isoleucine), amino acids with hydroxyl-containing side chains (e.g., serine or threonine), amino acids with sulfur-containing side chains (e.g., cysteine or methionine), charged amino acids (e.g., arginine, lysine, aspartic acid, or glutamic acid), uncharged amino acids (e.g., serine, threonine, asparagine, or glutamine), aromatic amino acids (e.g., tyrosine, tryptophan, or phenylalanine), cyclic amino acids (e.g., proline), acidic amino acids (e.g., aspartic acid, asparagine, glutamic acid, or glutamine), basic amino acids (e.g., histidine, lysine, or arginine), and bulky amino acids (e.g., phenylalanine, tyrosine, or tryptophan).

[0305] In some embodiments, the modification to the amino acid sequence of the N-terminal spacer domain and/or the C-terminal spacer domain comprises the substitution of at least one hydrophilic amino acid for a hydrophobic amino acid, the substitution of at least one hydrophobic amino acid for a hydrophilic amino acid, the substitution of at least one polar amino acid for a nonpolar amino acid, the substitution of at least one nonpolar amino acid for a polar amino acid, the substitution of at least one charged amino acid for an uncharged amino acid, the substitution of at least one uncharged amino acid for a charged amino acid, the substitution of at least one acidic amino acid for a basic amino acid, the substitution of at least one basic amino acid for an acidic amino acid, the substitution of at least one non-bulky amino acid for a bulky amino acid, the substitution of at least one bulky amino acid for a non-bulky amino acid, the substitution of at least one amino acid with a hydroxyl-containing side chain or a sulfur-containing side chain for an aliphatic amino acid, the substitution of at least one amino acid with a hydroxyl-containing side chain or a sulfur-containing side chain for an aromatic amino acid, or the substitution of at least one aromatic amino acid for an amino acid with a hydroxyl-containing side chain or a sulfur-containing side chain.

[0306] In some embodiments, the one or more amino acids that are removed from the amino acid sequence of the N-terminal spacer domain and/or the C-terminal spacer domain are selected from the group consisting of hydrophilic amino acids (e.g., lysine, arginine, histidine, aspartic acid, glutamic acid, serine, threonine, asparagine, or glutamine), hydrophobic amino acids (e.g., alanine, valine, isoleucine,

leucine, methionine, phenylalanine, tyrosine, tryptophan, cysteine, glycine, or proline), polar amino acids (e.g., serine, threonine, cysteine, asparagine, glutamine, or tyrosine), nonpolar amino acids (e.g., glycine, alanine, valine, proline, leucine, isoleucine, methionine, tryptophan, or phenylalanine), amino acids with aliphatic side chains (e.g., glycine, alanine, valine, leucine, or isoleucine), amino acids with hydroxyl-containing side chains (e.g., serine or threonine), amino acids with sulfur-containing side chains (e.g., cysteine or methionine), charged amino acids (e.g., arginine, lysine, aspartic acid, or glutamic acid), uncharged amino acids (e.g., serine, threonine, asparagine, or glutamine), aromatic amino acids (e.g., tyrosine, tryptophan, or phenylalanine), cyclic amino acids (e.g., proline), acidic amino acids (e.g., aspartic acid, asparagine, glutamic acid, or glutamine), basic amino acids (e.g., histidine, lysine, or arginine), and bulky amino acids (e.g., phenylalanine, tyrosine, or tryptophan).

[0307] Any of the modifications to the spacer domains described herein (e.g., any N-terminal spacer domain and/or any C-terminal spacer domain) can be modifications made to the amino acid sequence of any of the N-terminal spacer domains and/or C-terminal spacer domains described herein, including any one of SEQ ID NOs: 20-95, 235, 268, 269, 303-305, 323-338, 340, 341, 727, 794, and 799. Any of the modifications to the spacer domains described herein can be modifications made for any purpose. For instance, modifications to the N-terminal spacer domain and/or the C-terminal spacer domain of a linker that includes a cleavable peptide can be made for the purpose of altering the conformation of the linker such that the efficiency of the cleavage of the cleavable peptide is altered. Modifications to the N-terminal spacer domain and/or the C-terminal spacer domain of a linker that includes a cleavable peptide can also be made for the purpose of altering the structure of a linker that includes a cleavable peptide such that cleavage efficiency of the cleavable peptide is altered under certain pH conditions.

D. Half-life Extension Domains

[0308] A long half-life in vivo is important for therapeutic proteins. Unfortunately, cytokines that are administered to a subject generally have a short half-life since they are normally cleared rapidly from the subject by mechanisms including clearance by the kidney and endocytic degradation. Thus, in some embodiments of the masked cytokine provided herein, a half-life extension domain is linked to the masked cytokine for the purpose of extending the half-life of the cytokine in vivo.

[0309] In some embodiments, the masked cytokine provided herein comprises a half-life extension domain selected from the group consisting of antibodies and fragments thereof, albumin, albumin-binding proteins, IgG-binding proteins, and polyamino acid sequences. It is contemplated that other mechanisms for extending the half-life of the masked cytokine available in the art may also be employed. The half-life extension domain comprises an amino-terminus and a carboxy-terminus.

[0310] In some embodiments, the masked cytokine comprises a half-life extension domain. In some embodiments, the masked cytokine comprises a single half-life extension domain. In some embodiments, the masked cytokine comprises more than one half-life extension domain, each of which

can be any of the half-life extension domains described herein. In some embodiments, the masked cytokine comprises a first half-life extension domain and a second half-life extension domain. It is understood that reference to "a half-life extension domain" or "the half-life extension domain" can refer to the half-life extension domain in a masked cytokine comprising a single half-life extension domain, or it can refer to the first half-life extension domain in a masked cytokine comprising a first half-life extension domain and a second half-life extension domain, or it can refer to the second half-life extension domain in a masked cytokine comprising a first half-life extension domain and a second half-life extension domain, or it can refer to the first half-life extension domain and the second half-life extension domain in a masked cytokine comprising a first half-life extension domain and a second half-life extension domain.

[0311] In some embodiments comprising a first half-life extension domain and a second half-life extension domain, the first half-life extension domain is linked to the second half-life extension domain. In some embodiments comprising a first half-life extension domain and a second half-life extension domain, the first half-life extension domain is linked to the second half-life extension domain via a linker. The first half-life extension domain and the second half-life extension domain that are linked can, in some embodiments, each be any half-life extension domain described herein. For instance, in some embodiments, the first half-life extension domain and/or the second half-life extension domain of the linked first and second half-life extension domains is an Fc domain or fragment thereof. In some embodiments, the first half-life extension domain and/or the second half-life extension domain of the linked first and second half-life extension domains is an antibody, or a fragment, variant, or derivative thereof.

1. Antibodies and Fragments Thereof

[0312] By linking a masked cytokine to an antibody or fragment thereof that is capable of FcRn-mediated recycling, clearance of the masked cytokine from a subject can be reduced or otherwise delayed, thereby prolonging the half-life of the administered masked cytokine.

[0313] In some embodiments of the masked cytokine, the half-life extension domain comprises an antibody or fragment thereof. In some embodiments, the masked cytokine comprises more than one antibody or fragment thereof, each of which can be any of the antibodies or fragments thereof described herein. In some embodiments, the masked cytokine comprises a first half-life extension domain and a second half-life extension domain, each of which comprises an antibody or fragment thereof. It is understood that reference to "an antibody or fragment thereof" or "the antibody or fragment thereof" can refer to the antibody or fragment thereof of the half-life extension domain in a masked cytokine comprising a single half-life extension domain, or it can refer to the antibody or fragment thereof of the first half-life extension domain in a masked cytokine comprising a first half-life extension domain and a second half-life extension domain, or it can refer to the antibody or fragment thereof of the second half-

life extension domain in a masked cytokine comprising a first half-life extension domain and a second half-life extension domain, or it can refer to the antibody or fragment thereof of the first half-life extension domain and the antibody or fragment thereof of the second half-life extension domain in a masked cytokine comprising a first half-life extension domain and a second half-life extension domain.

[0314] The antibody or fragment thereof can be any antibody or fragment thereof. In some embodiments, the antibody or fragment thereof is any antibody or fragment thereof that is capable of FcRn-mediated recycling, such as any heavy chain polypeptide or portion thereof (e.g., Fc domain or fragment thereof) that is capable of FcRn-mediated recycling. However, in some embodiments of a masked cytokine comprising a first half-life extension domain and a second half-life extension domain, either the first half-life extension domain or the second half-life extension domain may comprise an antibody or fragment thereof that does not bind to the FcRn receptor, such as a light chain polypeptide. For example, in some embodiments of the masked cytokine, a first half-life extension domain comprises an antibody or fragment thereof that comprises a light chain polypeptide or portion thereof that does not directly interact with the FcRn receptor, but the masked cytokine nonetheless has an extended half-life due to comprising a second half-life extension domain that is capable of interacting with the FcRn receptor, such as by comprising a heavy chain polypeptide. It is recognized in the art that FcRn-mediated recycling requires binding of the FcRn receptor to the Fc region of the antibody or fragment thereof. For instance, studies have shown that residues I253, S254, H435, and Y436 (numbering according to the Kabat EU index numbering system) are important for the interaction between the human Fc region and the human FcRn complex. *See, e.g.*, Firan, M., et al., Int. Immunol. 13 (2001) 993-1002; Shields, R.L., et al, J. Biol. Chem. 276 (2001) 6591-6604). Various mutants of residues 248-259, 301-317, 376-382, and 424-437 (numbering according to the Kabat EU index numbering system) have also been examined and reported. Yeung, Y.A., et al. (J. Immunol. 182 (2009) 7667-7671.

[0315] In some embodiments, the antibody or fragment thereof comprises either a heavy chain polypeptide or a light chain polypeptide. In some embodiments, the antibody or fragment thereof comprises a portion of either a heavy chain polypeptide or a light chain polypeptide. In some embodiments, the antibody or fragment thereof comprises an Fc domain or fragment thereof. In some embodiments, the antibody or fragment thereof comprises a CH2 and CH3 domain or a fragment thereof. In some embodiments, the antibody or fragment thereof comprises the constant domain of the heavy chain polypeptide. In some embodiments, the antibody or fragment thereof comprises the constant domain of the light chain polypeptide. In some embodiments, the antibody or fragment thereof comprises a heavy chain polypeptide or fragment thereof (e.g., an Fc domain or fragment thereof). In some embodiments, the antibody or fragment thereof comprises a light chain polypeptide.

[0316] In some embodiments, the heavy chain polypeptide comprises the amino acid sequence of SEQ ID NO: 158. In some embodiments, the light chain polypeptide comprises the amino acid sequence of SEQ ID NO: 157. In some embodiments, the heavy chain polypeptide comprises an amino acid

sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 158. In some embodiments, the heavy chain polypeptide comprises the amino acid sequence of SEQ ID NO: 168. In some embodiments, the heavy chain polypeptide comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 168. In some embodiments, the heavy chain polypeptide comprises the amino acid sequence of SEQ ID NO: 169. In some embodiments, the heavy chain polypeptide comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 169.

[0317] In some embodiments, the light chain polypeptide comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 157. In some embodiments, the light chain polypeptide comprises the amino acid sequence of SEQ ID NO: 170. In some embodiments, the light chain polypeptide comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 170.

[0318] In some embodiments, the antibody of fragment thereof comprises an Fc domain or fragment thereof. In some embodiments, the antibody of fragment thereof is an Fc domain or fragment thereof.

[0319] In some embodiments, the Fc domain or fragment thereof comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 616, 619, 622, 625, 721,772-774, 793, and 796. In some embodiments, the Fc domain or fragment thereof comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NOs: 616, 619, 622, 625, 721,772-774, 793, and 796. In some embodiments, the Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 154. In some embodiments, the Fc domain or fragment thereof comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 154. In some embodiments, the Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 155. In some embodiments, the Fc domain or fragment thereof comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 155. In some embodiments, the Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 156. In some embodiments, the Fc domain or fragment thereof comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 156. In some

embodiments, the Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 265. In some embodiments, the Fc domain or fragment thereof comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 265. In some embodiments, the Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 155. In some embodiments, the Fc domain or fragment thereof comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 155. In some embodiments, the Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 772, or comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 772. In some embodiments, the Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 773, or comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 773. In some embodiments, the Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 774, or comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 774.

[0320] In some embodiments comprising a first half-life extension domain and a second half-life extension domain, the first half-life extension domain comprises an Fc domain or fragment thereof comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 154-156, 265, 616, 619, 622, 625, 721,772-774, 793, and 796, and the second half-life extension domain comprises an Fc domain or fragment thereof comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 154-156, 265, 616, 619, 622, 625, 721,772-774, 793, and 796. In some embodiments comprising a first half-life extension domain and a second half-life extension domain, the first half-life extension domain comprises an Fc domain or fragment thereof comprising an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NOs: 154-156, 265, 616, 619, 622, 625, 721,772-774, 793, and 796, and the second half-life extension domain comprises an Fc domain or fragment thereof comprising an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NOs: 154-156, 265, 616, 619, 622, 625, 721,772-774, 793, and 796. In some embodiments comprising a first half-life extension domain and a second half-life extension domain, the first half-life extension domain comprises the amino acid sequence of any of the first half-life extension domains listed in Tables 4-11,

and the second half-life extension domain comprises the amino acid sequence of any of the first half-life extension domains listed in Tables 4-11.

[0321] In some embodiments comprising a first half-life extension domain and a second half-life extension domain, the first half-life extension domain comprises an Fc domain or fragment thereof comprising the amino acid sequence of SEQ ID NO: 155, and the second half-life extension domain comprises an Fc domain or fragment thereof comprising the amino acid sequence of SEQ ID NO: 156. In some embodiments comprising a first half-life extension domain and a second half-life extension domain, the first half-life extension domain comprises an Fc domain or fragment thereof comprising the amino acid sequence of SEQ ID NO: 156, and the second half-life extension domain comprises an Fc domain or fragment thereof comprising the amino acid sequence of SEQ ID NO: 155. In some embodiments comprising a first half-life extension domain and a second half-life extension domain, the first half-life extension domain comprises an Fc domain or fragment thereof comprising an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 155, and the second half-life extension domain comprises an Fc domain or fragment thereof comprising an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 156. In some embodiments comprising a first half-life extension domain and a second half-life extension domain, the first half-life extension domain comprises an Fc domain or fragment thereof comprising an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 156, and the second half-life extension domain comprises an Fc domain or fragment thereof comprising an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 155.

[0322] In some embodiments comprising a first half-life extension domain and a second half-life extension domain, the first half-life extension domain comprises an Fc domain or fragment thereof comprising the amino acid sequence of SEQ ID NO: 155, and the second half-life extension domain comprises an Fc domain or fragment thereof comprising the amino acid sequence of SEQ ID NO: 616. In some embodiments comprising a first half-life extension domain and a second half-life extension domain, the first half-life extension domain comprises an Fc domain or fragment thereof comprising the amino acid sequence of SEQ ID NO: 616, and the second half-life extension domain comprises an Fc domain or fragment thereof comprising the amino acid sequence of SEQ ID NO: 155. In some embodiments comprising a first half-life extension domain and a second half-life extension domain, the first half-life extension domain comprises an Fc domain or fragment thereof comprising an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 155, and the

second half-life extension domain comprises an Fc domain or fragment thereof comprising an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 616. In some embodiments comprising a first half-life extension domain and a second half-life extension domain, the first half-life extension domain comprises an Fc domain or fragment thereof comprising an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 616, and the second half-life extension domain comprises an Fc domain or fragment thereof comprising an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 155.

[0323] In some embodiments comprising a first half-life extension domain and a second half-life extension domain, the first half-life extension domain comprises an Fc domain or fragment thereof comprising the amino acid sequence of SEQ ID NO: 156, and the second half-life extension domain comprises an Fc domain or fragment thereof comprising the amino acid sequence of SEQ ID NO: 265. In some embodiments comprising a first half-life extension domain and a second half-life extension domain, the first half-life extension domain comprises an Fc domain or fragment thereof comprising the amino acid sequence of SEQ ID NO: 265, and the second half-life extension domain comprises an Fc domain or fragment thereof comprising the amino acid sequence of SEQ ID NO: 156. In some embodiments comprising a first half-life extension domain and a second half-life extension domain, the first half-life extension domain comprises an Fc domain or fragment thereof comprising an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 265, and the second half-life extension domain comprises an Fc domain or fragment thereof comprising an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 156. In some embodiments comprising a first half-life extension domain and a second half-life extension domain, the first half-life extension domain comprises an Fc domain or fragment thereof comprising an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 156, and the second half-life extension domain comprises an Fc domain or fragment thereof comprising an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 265.

[0324] In some embodiments comprising a first half-life extension domain and a second half-life extension domain, the first half-life extension domain comprises an Fc domain or fragment thereof comprising the amino acid sequence of SEQ ID NO: 156, and the second half-life extension domain comprises an Fc domain or fragment thereof comprising the amino acid sequence of SEQ ID NO: 155.

In some embodiments comprising a first half-life extension domain and a second half-life extension domain, the first half-life extension domain comprises an Fc domain or fragment thereof comprising the amino acid sequence of SEQ ID NO: 155, and the second half-life extension domain comprises an Fc domain or fragment thereof comprising the amino acid sequence of SEQ ID NO: 156. In some embodiments comprising a first half-life extension domain and a second half-life extension domain, the first half-life extension domain comprises an Fc domain or fragment thereof comprising an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 155, and the second half-life extension domain comprises an Fc domain or fragment thereof comprising an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 156. In some embodiments comprising a first half-life extension domain and a second half-life extension domain, the first half-life extension domain comprises an Fc domain or fragment thereof comprising an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 156, and the second half-life extension domain comprises an Fc domain or fragment thereof comprising an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 155.

[0325] In some embodiments comprising a first half-life extension domain and a second half-life extension domain, the first half-life extension domain comprises an Fc domain or fragment thereof comprising the amino acid sequence of SEQ ID NO: 721, and the second half-life extension domain comprises an Fc domain or fragment thereof comprising the amino acid sequence of SEQ ID NO: 619. In some embodiments comprising a first half-life extension domain and a second half-life extension domain, the first half-life extension domain comprises an Fc domain or fragment thereof comprising the amino acid sequence of SEQ ID NO: 619, and the second half-life extension domain comprises an Fc domain or fragment thereof comprising the amino acid sequence of SEQ ID NO: 721. In some embodiments comprising a first half-life extension domain and a second half-life extension domain, the first half-life extension domain comprises an Fc domain or fragment thereof comprising an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 619, and the second half-life extension domain comprises an Fc domain or fragment thereof comprising an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 721. In some embodiments comprising a first half-life extension domain and a second half-life extension domain, the first half-life extension domain comprises an Fc domain or fragment thereof comprising an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%,

96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 721, and the second half-life extension domain comprises an Fc domain or fragment thereof comprising an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 619.

[0326] In some embodiments comprising a first half-life extension domain and a second half-life extension domain, the first half-life extension domain comprises an Fc domain or fragment thereof comprising the amino acid sequence of SEQ ID NO: 721, and the second half-life extension domain comprises an Fc domain or fragment thereof comprising the amino acid sequence of SEQ ID NO: 772. In some embodiments comprising a first half-life extension domain and a second half-life extension domain, the first half-life extension domain comprises an Fc domain or fragment thereof comprising the amino acid sequence of SEQ ID NO: 772, and the second half-life extension domain comprises an Fc domain or fragment thereof comprising the amino acid sequence of SEQ ID NO: 721. In some embodiments comprising a first half-life extension domain and a second half-life extension domain, the first half-life extension domain comprises an Fc domain or fragment thereof comprising an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 772, and the second half-life extension domain comprises an Fc domain or fragment thereof comprising an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 721. In some embodiments comprising a first half-life extension domain and a second half-life extension domain, the first half-life extension domain comprises an Fc domain or fragment thereof comprising an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 721, and the second half-life extension domain comprises an Fc domain or fragment thereof comprising an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 772.

[0327] In some embodiments comprising a first half-life extension domain and a second half-life extension domain, the first half-life extension domain comprises an Fc domain or fragment thereof comprising the amino acid sequence of SEQ ID NO: 793, and the second half-life extension domain comprises an Fc domain or fragment thereof comprising the amino acid sequence of SEQ ID NO: 622. In some embodiments comprising a first half-life extension domain and a second half-life extension domain, the first half-life extension domain comprises an Fc domain or fragment thereof comprising the amino acid sequence of SEQ ID NO: 622, and the second half-life extension domain comprises an Fc domain or fragment thereof comprising the amino acid sequence of SEQ ID NO: 793. In some embodiments comprising a first half-life extension domain and a second half-life extension domain, the first half-life extension domain comprises an Fc domain or fragment thereof comprising an amino acid

sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 622, and the second half-life extension domain comprises an Fc domain or fragment thereof comprising an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 793. In some embodiments comprising a first half-life extension domain and a second half-life extension domain, the first half-life extension domain comprises an Fc domain or fragment thereof comprising an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 793, and the second half-life extension domain comprises an Fc domain or fragment thereof comprising an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 622.

[0328] In some embodiments comprising a first half-life extension domain and a second half-life extension domain, the first half-life extension domain comprises an Fc domain or fragment thereof comprising the amino acid sequence of SEQ ID NO: 793, and the second half-life extension domain comprises an Fc domain or fragment thereof comprising the amino acid sequence of SEQ ID NO: 773. In some embodiments comprising a first half-life extension domain and a second half-life extension domain, the first half-life extension domain comprises an Fc domain or fragment thereof comprising the amino acid sequence of SEQ ID NO: 773, and the second half-life extension domain comprises an Fc domain or fragment thereof comprising the amino acid sequence of SEQ ID NO: 793. In some embodiments comprising a first half-life extension domain and a second half-life extension domain, the first half-life extension domain comprises an Fc domain or fragment thereof comprising an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 773, and the second half-life extension domain comprises an Fc domain or fragment thereof comprising an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 793. In some embodiments comprising a first half-life extension domain and a second half-life extension domain, the first half-life extension domain comprises an Fc domain or fragment thereof comprising an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 793, and the second half-life extension domain comprises an Fc domain or fragment thereof comprising an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 773.

[0329] In some embodiments comprising a first half-life extension domain and a second half-life extension domain, the first half-life extension domain comprises an Fc domain or fragment thereof

comprising the amino acid sequence of SEQ ID NO: 796, and the second half-life extension domain comprises an Fc domain or fragment thereof comprising the amino acid sequence of SEQ ID NO: 625. In some embodiments comprising a first half-life extension domain and a second half-life extension domain, the first half-life extension domain comprises an Fc domain or fragment thereof comprising the amino acid sequence of SEQ ID NO: 625, and the second half-life extension domain comprises an Fc domain or fragment thereof comprising the amino acid sequence of SEQ ID NO: 796. In some embodiments comprising a first half-life extension domain and a second half-life extension domain, the first half-life extension domain comprises an Fc domain or fragment thereof comprising an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 625, and the second half-life extension domain comprises an Fc domain or fragment thereof comprising an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 796. In some embodiments comprising a first half-life extension domain and a second half-life extension domain, the first half-life extension domain comprises an Fc domain or fragment thereof comprising an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 796, and the second half-life extension domain comprises an Fc domain or fragment thereof comprising an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 625.

[0330] In some embodiments comprising a first half-life extension domain and a second half-life extension domain, the first half-life extension domain comprises an Fc domain or fragment thereof comprising the amino acid sequence of SEQ ID NO: 796, and the second half-life extension domain comprises an Fc domain or fragment thereof comprising the amino acid sequence of SEQ ID NO: 774. In some embodiments comprising a first half-life extension domain and a second half-life extension domain, the first half-life extension domain comprises an Fc domain or fragment thereof comprising the amino acid sequence of SEQ ID NO: 774, and the second half-life extension domain comprises an Fc domain or fragment thereof comprising the amino acid sequence of SEQ ID NO: 796. In some embodiments comprising a first half-life extension domain and a second half-life extension domain, the first half-life extension domain comprises an Fc domain or fragment thereof comprising an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 774, and the second half-life extension domain comprises an Fc domain or fragment thereof comprising an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 796. In some embodiments comprising a first half-life extension domain and a second half-life extension domain, the

first half-life extension domain comprises an Fc domain or fragment thereof comprising an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 796, and the second half-life extension domain comprises an Fc domain or fragment thereof comprising an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 774.

[0331] In some embodiments comprising a first half-life extension domain and a second half-life extension domain, the first half-life extension domain comprises an Fc domain or fragment thereof comprising the amino acid sequence of SEQ ID NO: 793, and the second half-life extension domain comprises an Fc domain or fragment thereof comprising the amino acid sequence of SEQ ID NO: 773. In some embodiments comprising a first half-life extension domain and a second half-life extension domain, the first half-life extension domain comprises an Fc domain or fragment thereof comprising the amino acid sequence of SEQ ID NO: 774 and the second half-life extension domain comprises an Fc domain or fragment thereof comprising the amino acid sequence of SEQ ID NO: 793. In some embodiments comprising a first half-life extension domain and a second half-life extension domain, the first half-life extension domain comprises an Fc domain or fragment thereof comprising an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 773, and the second half-life extension domain comprises an Fc domain or fragment thereof comprising an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 793. In some embodiments comprising a first half-life extension domain and a second half-life extension domain, the first half-life extension domain comprises an Fc domain or fragment thereof comprising an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 793, and the second half-life extension domain comprises an Fc domain or fragment thereof comprising an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 773.

[0332] In some embodiments comprising a first half-life extension domain and a second half-life extension domain, the first half-life extension domain comprises an Fc domain or fragment thereof comprising the amino acid sequence of SEQ ID NO: 796, and the second half-life extension domain comprises an Fc domain or fragment thereof comprising the amino acid sequence of SEQ ID NO: 774. In some embodiments comprising a first half-life extension domain and a second half-life extension domain, the first half-life extension domain comprises an Fc domain or fragment thereof comprising the amino acid sequence of SEQ ID NO: 774, and the second half-life extension domain comprises an Fc domain or fragment thereof comprising the amino acid sequence of SEQ ID NO: 796. In some

embodiments comprising a first half-life extension domain and a second half-life extension domain, the first half-life extension domain comprises an Fc domain or fragment thereof comprising an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 774, and the second half-life extension domain comprises an Fc domain or fragment thereof comprising an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 796. In some embodiments comprising a first half-life extension domain and a second half-life extension domain, the first half-life extension domain comprises an Fc domain or fragment thereof comprising an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 796, and the second half-life extension domain comprises an Fc domain or fragment thereof comprising an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 774.

[0333] In some embodiments comprising a first half-life extension domain and a second half-life extension domain, the first half-life extension domain comprises an Fc domain or fragment thereof comprising the amino acid sequence of SEQ ID NO: 156, and the second half-life extension domain comprises an Fc domain or fragment thereof comprising the amino acid sequence of SEQ ID NO: 155. In some embodiments comprising a first half-life extension domain and a second half-life extension domain, the first half-life extension domain comprises an Fc domain or fragment thereof comprising the amino acid sequence of SEQ ID NO: 155, and the second half-life extension domain comprises an Fc domain or fragment thereof comprising the amino acid sequence of SEQ ID NO: 156 In some embodiments comprising a first half-life extension domain and a second half-life extension domain, the first half-life extension domain comprises an Fc domain or fragment thereof comprising an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 155, and the second half-life extension domain comprises an Fc domain or fragment thereof comprising an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 156. In some embodiments comprising a first half-life extension domain and a second half-life extension domain, the first half-life extension domain comprises an Fc domain or fragment thereof comprising an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 156, and the second half-life extension domain comprises an Fc domain or fragment thereof comprising an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 155.

[0334] In some embodiments comprising a first half-life extension domain and a second half-life extension domain, the first half-life extension domain comprises an Fc domain or fragment thereof comprising the amino acid sequence of SEQ ID NO: 772, and the second half-life extension domain comprises an Fc domain or fragment thereof comprising the amino acid sequence of SEQ ID NO: 721. In some embodiments comprising a first half-life extension domain and a second half-life extension domain, the first half-life extension domain comprises an Fc domain or fragment thereof comprising the amino acid sequence of SEQ ID NO: 721, and the second half-life extension domain comprises an Fc domain or fragment thereof comprising the amino acid sequence of SEQ ID NO: 772. In some embodiments comprising a first half-life extension domain and a second half-life extension domain, the first half-life extension domain comprises an Fc domain or fragment thereof comprising an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 721, and the second half-life extension domain comprises an Fc domain or fragment thereof comprising an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 772. In some embodiments comprising a first half-life extension domain and a second half-life extension domain, the first half-life extension domain comprises an Fc domain or fragment thereof comprising an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 772, and the second half-life extension domain comprises an Fc domain or fragment thereof comprising an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 721.

[0335] In some embodiments comprising a first half-life extension domain and a second half-life extension domain, the first half-life extension domain comprises an Fc domain or fragment thereof comprising the amino acid sequence of SEQ ID NO: 156, and the second half-life extension domain comprises an Fc domain or fragment thereof comprising the amino acid sequence of SEQ ID NO: 156. In some embodiments comprising a first half-life extension domain and a second half-life extension domain, the first half-life extension domain comprises an Fc domain or fragment thereof comprising the amino acid sequence of SEQ ID NO: 156, and the second half-life extension domain comprises an Fc domain or fragment thereof comprising the amino acid sequence of SEQ ID NO: 156. In some embodiments comprising a first half-life extension domain and a second half-life extension domain, the first half-life extension domain comprises an Fc domain or fragment thereof comprising an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 156, and the second half-life extension domain comprises an Fc domain or fragment thereof comprising an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%,

96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 156. In some embodiments comprising a first half-life extension domain and a second half-life extension domain, the first half-life extension domain comprises an Fc domain or fragment thereof comprising an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 156, and the second half-life extension domain comprises an Fc domain or fragment thereof comprising an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 156.

[0336] In some embodiments comprising a first half-life extension domain and a second half-life extension domain, the first half-life extension domain comprises an Fc domain or fragment thereof comprising the amino acid sequence of SEQ ID NO: 157, and the second half-life extension domain comprises an Fc domain or fragment thereof comprising the amino acid sequence of SEQ ID NO: 158. In some embodiments comprising a first half-life extension domain and a second half-life extension domain, the first half-life extension domain comprises an Fc domain or fragment thereof comprising the amino acid sequence of SEQ ID NO: 158, and the second half-life extension domain comprises an Fc domain or fragment thereof comprising the amino acid sequence of SEQ ID NO: 157. In some embodiments comprising a first half-life extension domain and a second half-life extension domain, the first half-life extension domain comprises an Fc domain or fragment thereof comprising an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 157, and the second half-life extension domain comprises an Fc domain or fragment thereof comprising an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 158. In some embodiments comprising a first half-life extension domain and a second half-life extension domain, the first half-life extension domain comprises an Fc domain or fragment thereof comprising an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 158, and the second half-life extension domain comprises an Fc domain or fragment thereof comprising an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 157.

[0337] In some embodiments, the Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 168. In some embodiments, the Fc domain or fragment thereof comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 168. In some embodiments, the Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 169. In some embodiments, the Fc domain or fragment thereof comprises an amino acid sequence

having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 169.

[0338] In some embodiments, a half-life extension domain comprises an amino acid sequence produced by introducing one or more modifications to the amino acid sequence of the half-life extension domain, such as by introducing one or more amino acid substitutions, additions, or deletions to the amino acid sequence of any one of SEQ ID NOs: 154-158, 168-170, 265, 616, 619, 622, 625, 721,772-774, 793, and 796, or to any one of the amino acid sequences of the half-life extension domain described herein. The one or more modifications can be any modifications or alterations described herein, including, in some embodiments, any modifications or alterations disclosed herein that promote heterodimerization of polypeptide chains and/or suppresses homodimerization of polypeptide chains, alter effector function, or enhance effector function.

[0339] In some embodiments, the half-life extension domain comprises a heavy chain polypeptide that comprises one or more amino acid substitutions altering effector function. In some embodiments, the half-life extension domain is an IgG1 heavy chain polypeptide and comprises the amino substitution(s): N297A, N297G, or N297Q; L234A and L235A; C220S, C226S, C229S, and P238S; C226S, C229S, E233P, L234V, and L235A; L234F, L235E, and P331S; S267E and L328F; D265A; and/or L234A, L235A, and P329G, numbered according to the Kabat EU numbering system. In some embodiments, the half-life extension domain is an IgG1 heavy chain polypeptide and comprises one or more amino acid substitutions selected from the group consisting of N297A, N297G, N297Q, L234A, L235A, C220S, C226S, C229S, P238S, E233P, L234V, L234F, L235E, P331S, S267E, L328F, D265A, and P329G, numbered according to the Kabat EU numbering system. In some embodiments, the half-life extension domain is an IgG2 heavy chain polypeptide and comprises the amino substitution(s): V234A and G237A; H268Q, V309L, A330S, and A331S; or V234A, G237A, P238S, H268A, V309L, and A330S, numbered according to the Kabat EU numbering system. In some embodiments, the half-life extension domain is an IgG2 heavy chain polypeptide and comprises one or more amino acid substitutions selected from the group consisting of V234A, G237A, H268Q, V309L, A330S, A331S, P238S, H268A, and V309L, numbered according to the Kabat EU numbering system. In some embodiments, the half-life extension domain is an IgG4 heavy chain polypeptide and comprises the amino substitution(s): L235A, G237A, and E318A; S228P, L234A, and L235A; H268Q, V309L, A330S, and P331S; and/or S228P and L235A, numbered according to the Kabat EU numbering system. In some embodiments, the half-life extension domain is an IgG2 heavy chain polypeptide and comprises one or more amino acid substitutions selected from the group consisting of L235A, G237A, E318A, S228P, L234A, H268Q, V309L, A330S, and P331S, numbered according to the Kabat EU numbering system.

[0340] In some embodiments, the half-life extension domain comprises a heavy chain polypeptide that comprises one or more amino acid substitutions enhancing effector function. In some embodiments, the half-life extension domain is an IgG1 heavy chain polypeptide and comprises the amino acid

substitution(s): S298A, E333A, and K334A; S239D and I332E; S239D, A330L, and I332E; P247I and A339D or A339Q; D280H and K290S; D280H, K290S, and either S298D or S298V; F243L, R292P, and Y300L; F243L, R292P, Y300L, and P396L; F243L, R292P, Y300L, V305I, and P396L; G236A, S239D, and I332E; K326A and E333A; K326W and E333S; K290E, S298G, and T299A; K290E, S298G, T299A, and K326E; K290N, S298G, and T299A; K290N, S298G, T299A, and K326E; K334V; L235S, S239D, and K334V; K334V and Q331M, S239D, F243V, E294L, or S298T; E233L, Q311M, and K334V; L234I, Q311M, and K334V; K334V and S298T, A330M, or A330F; K334V, Q311M, and either A330M or A330F; K334V, S298T, and either A330M or A330F; K334V, S239D, and either A330M or S298T; L234Y, Y296W, and K290Y, F243V, or E294L; Y296W and either L234Y or K290Y; S239D, A330S, and I332E, V264I; F243L and V264I; L328M; I332E; L328M and I332E; V264I and I332E; S239E and I332E; S239Q and I332E; S239E; A330Y; I332D; L328I and I332E; L328Q and I332E; V264T; V240I; V266I; S239D; S239D and I332D; S239D and I332N; S239D and I332Q; S239E and I332D; S239E and I332N; S239E and I332Q; S239N and I332D; S239N and I332E; S239Q and I332D; A330Y and I332E; V264I, A330Y, and I332E; A330L and I332E; V264I, A330L, and I332E; L234E, L234Y, or L234I; L235D, L235S, L235Y, or L235I; S239T; V240M; V264Y; A330I; N325T; I332E and L328D, L328V, L328T, or L328I; V264I, I332E, and either S239E or S239Q; S239E, V264I, A330Y, and I332E; A330Y, I332E, and either S239D or S239N; A330L, I332E, and either S239D or S239N; V264I, S298A, and I332E; S298A, I332E, and either S239D or S239N; S239D, V264I, and I332E; S239D, V264I, S298A, and I332E; S239D, V264I, A330L, and I332E; S239D, I332E, and A330I; P230A; P230A, E233D, and I332E; E272Y; K274T, K274E, K274R, K274L, or K274Y; F275W; N276L; Y278T; V302I; E318R; S324D, S324I or S324V; K326I or K326T; T335D, T335R, or T335Y; V240I and V266I; S239D, A330Y, I332E, and L234I; S239D, A330Y, I332E, and L235D; S239D, A330Y, I332E, and V240I; S239D, A330Y, I332E, and V264T; and/or S239D, A330Y, I332E, and either K326E or K326T, numbered according to the Kabat EU numbering system. In some embodiments, the half-life extension domain is an IgG1 heavy chain polypeptide and comprises one or more amino acid substitution(s) selected from the group consisting of: P230A, E233D, L234E, L234Y, L234I, L235D, L235S, L235Y, L235I, S239D, S239E, S239N, S239Q, S239T, V240I, V240M, F243L, V264I, V264T, V264Y, V266I, E272Y, K274T, K274E, K274R, K274L, K274Y, F275W, N276L, Y278T, V302I, E318R, S324D, S324I, S324V, N325T, K326I, K326T, L328M, L328I, L328Q, L328D, L328V, L328T, A330Y, A330L, A330I, I332D, I332E, I332N, I332Q, T335D, T335R, and T335Y.

[0341] In some embodiments, the half-life extension domain comprises an Fc domain or fragment thereof that comprises one or more amino acid substitutions altering effector function. In some embodiments, the half-life extension domain is an IgG1 Fc domain or fragment thereof and comprises the amino substitution(s): N297A, N297G, or N297Q; L234A and L235A; C220S, C226S, C229S, and P238S; C226S, C229S, E233P, L234V, and L235A; L234F, L235E, and P331S; S267E and L328F; D265A; and/or L234A, L235A, and P329G, numbered according to the Kabat EU numbering system. In

some embodiments, the half-life extension domain is an IgG1 Fc domain or fragment thereof and comprises one or more amino acid substitutions selected from the group consisting of N297A, N297G, N297Q, L234A, L235A, C220S, C226S, C229S, P238S, E233P, L234V, L234F, L235E, P331S, S267E, L328F, D265A, and P329G, numbered according to the Kabat EU numbering system. In some embodiments, the half-life extension domain is an IgG2 Fc domain or fragment thereof and comprises the amino substitution(s): V234A and G237A; H268Q, V309L, A330S, and A331S; and/or V234A, G237A, P238S, H268A, V309L, and A330S, numbered according to the Kabat EU numbering system. In some embodiments, the half-life extension domain is an IgG2 Fc domain or fragment thereof and comprises one or more amino acid substitutions selected from the group consisting of V234A, G237A, H268Q, V309L, A330S, A331S, P238S, H268A, and V309L, numbered according to the Kabat EU numbering system. In some embodiments, the half-life extension domain is an IgG4 Fc domain or fragment thereof and comprises the amino substitution(s): L235A, G237A, and E318A; S228P, L234A, and L235A; H268Q, V309L, A330S, and P331S; and/or S228P and L235A, numbered according to the Kabat EU numbering system. In some embodiments, the half-life extension domain is an IgG2 Fc domain or fragment thereof and comprises one or more amino acid substitutions selected from the group consisting of L235A, G237A, E318A, S228P, L234A, H268Q, V309L, A330S, and P331S, numbered according to the Kabat EU numbering system.

[0342] In some embodiments, the half-life extension domain comprises Fc domain or fragment thereof that comprises one or more amino acid substitutions enhancing effector function. In some embodiments, the half-life extension domain is an IgG1 Fc domain or fragment thereof and comprises the amino acid substitution(s): S298A, E333A, and K334A; S239D and I332E; S239D, A330L, and I332E; P247I and A339D or A339Q; D280H and K290S; D280H, K290S, and either S298D or S298V; F243L, R292P, and Y300L; F243L, R292P, Y300L, and P396L; F243L, R292P, Y300L, V305I, and P396L; G236A, S239D, and I332E; K326A and E333A; K326W and E333S; K290E, S298G, and T299A; K290E, S298G, T299A, and K326E; K290N, S298G, and T299A; K290N, S298G, T299A, and K326E; K334V; L235S, S239D, and K334V; K334V and Q331M, S239D, F243V, E294L, or S298T; E233L, Q311M, and K334V; L234I, Q311M, and K334V; K334V and S298T, A330M, or A330F; K334V, Q311M, and either A330M or A330F; K334V, S298T, and either A330M or A330F; K334V, S239D, and either A330M or S298T; L234Y, Y296W, and K290Y, F243V, or E294L; Y296W and either L234Y or K290Y; S239D, A330S, and I332E, V264I; F243L and V264I; L328M; I332E; L328M and I332E; V264I and I332E; S239E and I332E; S239Q and I332E; S239E; A330Y; I332D; L328I and I332E; L328Q and I332E; V264T; V240I; V266I; S239D; S239D and I332D; S239D and I332N; S239D and I332Q; S239E and I332D; S239E and I332N; S239E and I332Q; S239N and I332D; S239N and I332E; S239Q and I332D; A330Y and I332E; V264I, A330Y, and I332E; A330L and I332E; V264I, A330L, and I332E; L234E, L234Y, or L234I; L235D, L235S, L235Y, or L235I; S239T; V240M; V264Y; A330I; N325T; I332E and L328D, L328V, L328T, or L328I; V264I, I332E, and either S239E or S239Q; S239E,

V264I, A330Y, and I332E; A330Y, I332E, and either S239D or S239N; A330L, I332E, and either S239D or S239N; V264I, S298A, and I332E; S298A, I332E, and either S239D or S239N; S239D, V264I, and I332E; S239D, V264I, S298A, and I332E; S239D, V264I, A330L, and I332E; S239D, I332E, and A330I; P230A; P230A, E233D, and I332E; E272Y; K274T, K274E, K274R, K274L, or K274Y; F275W; N276L; Y278T; V302I; E318R; S324D, S324I or S324V; K326I or K326T; T335D, T335R, or T335Y; V240I and V266I; S239D, A330Y, I332E, and L234I; S239D, A330Y, I332E, and L235D; S239D, A330Y, I332E, and V240I; S239D, A330Y, I332E, and V264T; and/or S239D, A330Y, I332E, and either K326E or K326T, numbered according to the Kabat EU numbering system. In some embodiments, the half-life extension domain is an IgG1 Fc domain or fragment thereof and comprises one or more amino acid substitution(s) selected from the group consisting of: P230A, E233D, L234E, L234Y, L234I, L235D, L235S, L235Y, L235I, S239D, S239E, S239N, S239Q, S239T, V240I, V240M, F243L, V264I, V264T, V264Y, V266I, E272Y, K274T, K274E, K274R, K274L, K274Y, F275W, N276L, Y278T, V302I, E318R, S324D, S324I, S324V, N325T, K326I, K326T, L328M, L328I, L328Q, L328D, L328V, L328T, A330Y, A330L, A330I, I332D, I332E, I332N, I332Q, T335D, T335R, and T335Y.

[0343] In some embodiments, the half-life extension domain comprises one or more amino acid substitution(s) that enhance binding of the half-life extension domain to FcRn. In some embodiments, the one or more amino acid substitution(s) increase binding affinity of an Fc-containing polypeptide (e.g., a heavy chain polypeptide or an Fc domain or fragment thereof) to FcRn at acidic pH. In some embodiments, the half-life extension domain comprises one or more amino acid substitution(s) selected from the group consisting of M428L; T250Q and M428L; M252Y, S254T, and T256E; P257I and N434H; D376V and N434H; P257I and Q3111; N434A; N434W; M428L and N434S; V259I and V308F; M252Y, S254T, and T256E; V259I, V308F and M428L; T307Q and N434A; T307Q and N434S; T307Q, E380A, and N434A; V308P and N434A; N434H; and V308P.

[0344] In some embodiments, the masked cytokine is a dimer is that is formed by the half-life extension domain of one copy of the masked cytokine forming a disulfide bond with the corresponding half-life extension domain of a second copy of the masked cytokine.

2. Albumin

[0345] Albumin (also referred to herein as human serum albumin (HSA)) is a natural carrier protein that has an extended serum half-life of approximately three weeks due to its size and its susceptibility to FcRn-mediated recycling, which prevents intracellular degradation. Thus, linking a masked cytokine to albumin can greatly extend the half-life of the masked cytokine. This approach has been taken to extend the plasma half-life of therapeutically beneficial proteins. *See, e.g.*, WO 2001/079271A1 and WO 2003/59934A2, the contents of which are herein incorporated by reference. HSA in its mature form is a polypeptide of 585 amino acids as shown in SEQ ID NO: 171.

[0346] In some embodiments, the masked cytokine comprises a half-life extension domain that comprises an albumin polypeptide or a fragment or variant thereof (hereinafter referred to as "albumin" or "albumin polypeptide"). As used herein, the terms "albumin" and "albumin polypeptide" includes fragments of albumin as well as variants of albumin. The albumin polypeptide comprises an amino-terminus and a carboxy-terminus. The albumin polypeptide can be any albumin polypeptide, including any fragment or variant thereof, such as any albumin polypeptide described in WO 2001/079271A1; WO 2003/59934A2; US20160152686A1; WO 2012/059486; WO 2011/124718; US20070048282, the contents of which are herein incorporated by reference. In some embodiments, the albumin polypeptide is HSA.

[0347] In some embodiments of the masked cytokine, the half-life extension domain comprises an albumin polypeptide. In some embodiments, the masked cytokine comprises more than one albumin polypeptide, each of which can be any of the albumin polypeptides described herein. In some embodiments, the masked cytokine comprises a first half-life extension domain and a second half-life extension domain, each of which comprises an albumin polypeptide. It is understood that reference to "an albumin polypeptide" or "the albumin polypeptide" can refer to the albumin polypeptide of the half-life extension domain in a masked cytokine comprising a single half-life extension domain, or it can refer to the albumin polypeptide of the first half-life extension domain in a masked cytokine comprising a first half-life extension domain and a second half-life extension domain, or it can refer to the albumin polypeptide of the second half-life extension domain in a masked cytokine comprising a first half-life extension domain and a second half-life extension domain, or it can refer to the albumin polypeptide of the first half-life extension domain and the albumin polypeptide of the second half-life extension domain in a masked cytokine comprising a first half-life extension domain and a second half-life extension domain.

[0348] In some embodiments, the albumin polypeptide is linked to a masking moiety. In some embodiments, a masking moiety is linked to the amino-terminus or the carboxy-terminus of the albumin polypeptide. In some embodiments, the albumin polypeptide is linked to a masking moiety via a linker. In some embodiments, a linker is linked to the amino-terminus or the carboxy-terminus of the albumin polypeptide. In some embodiments, an N-terminal spacer domain or a C-terminal spacer domain of the linker is linked to the amino-terminus or the carboxy-terminus of the albumin polypeptide. In some embodiments, a cleavable peptide of the linker is linked to the amino-terminus or the carboxy-terminus of the albumin polypeptide. In some embodiments, the albumin polypeptide is linked to a cytokine or functional fragment thereof. In some embodiments, a cytokine or functional fragment thereof is linked to the amino-terminus or the carboxy-terminus of the albumin polypeptide. In some embodiments, the albumin polypeptide is linked to a cytokine or functional fragment thereof via a linker. In some embodiments, a linker is linked to the amino-terminus or the carboxy-terminus of the albumin polypeptide.

[0349] In some embodiments, the albumin polypeptide comprises the amino acid sequence of SEQ ID NO: 171. In some embodiments, the albumin polypeptide comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 171.

[0350] In some embodiments, the albumin polypeptide is a variant of albumin consisting of a fragment of HSA (optionally with one or more amino acid modifications). In some embodiments, the fragment of HSA is a fragment of wildtype HSA. In some embodiments, the albumin polypeptide comprises HSA domain 1 (amino acid residues 1-194 of SEQ ID NO: 171), HSA domain 2 (amino acid residues 195-387 of SEQ ID NO: 171), HSA domain 3 (amino acid residues 388-585), HSA domains 1 and 2, HSA domains 2 and 3, HSA domains 1 and 3, or two copies of HSA domain 3. In some embodiments, the albumin polypeptide consists of HSA domain 1 (amino acid residues 1-194 of SEQ ID NO: 171), HSA domain 2 (amino acid residues 195-387 of SEQ ID NO: 171), HSA domain 3 (amino acid residues 388-585), HSA domains 1 and 2, HSA domains 2 and 3, HSA domains 1 and 3, or two copies of HSA domain 3.

[0351] In some embodiments, the albumin polypeptide comprises amino acid residues 1-194 of SEQ ID NO: 171. In some embodiments, the albumin polypeptide comprises amino acid residues 195-387 of SEQ ID NO: 171. In some embodiments, the albumin polypeptide comprises amino acid residues 388-585 of SEQ ID NO: 171. In some embodiments, the albumin polypeptide comprises amino acid residues 1-387 of SEQ ID NO: 171. In some embodiments, the albumin polypeptide comprises amino acid residues 195-585 of SEQ ID NO: 171. In some embodiments, the albumin polypeptide comprises amino acid residues 1-105 of SEQ ID NO: 171. In some embodiments, the albumin polypeptide comprises amino acid residues 120-194 of SEQ ID NO: 171. In some embodiments, the albumin polypeptide comprises amino acid residues 195-291 of SEQ ID NO: 171. In some embodiments, the albumin polypeptide comprises amino acid residues 316-387 of SEQ ID NO: 171. In some embodiments, the albumin polypeptide comprises amino acid residues 388-491 of SEQ ID NO: 171. In some embodiments, the albumin polypeptide comprises amino acid residues 512-585 of SEQ ID NO: 171. In some embodiments, the albumin polypeptide comprises amino acid residues 1-194 and 388-585 of SEQ ID NO: 171. In some embodiments, the albumin polypeptide comprises two copies of amino acid residues 388-585 of SEQ ID NO: 171.

[0352] In some embodiments, the albumin polypeptide comprises an amino acid sequence produced by one or more amino acid modifications to the amino acid sequence of any of the embodiments of the albumin polypeptide described herein. In some embodiments, the albumin polypeptide comprises an amino acid sequence comprising one or more amino acid modifications that increase the half-life of the albumin polypeptide in serum. Exemplary amino acid modifications that increase the half-life of the albumin polypeptide in serum include amino acid substitutions made to E492, N503, D550, and/or K573 of HSA. In some embodiments, the albumin polypeptide comprises one or more amino acid

modifications that increase the affinity of the albumin polypeptide for the FcRn receptor. Exemplary amino acid modifications that increase the affinity of the albumin polypeptide for the FcRn receptor include V418M, T420A, E505G, and V547A. In some embodiments, the albumin polypeptide comprises an amino acid sequence produced by one or more amino acid modifications to the amino acid sequence of SEQ ID NO: 171. In some embodiments, the albumin polypeptide comprises an amino acid sequence produced by one or more amino acid modifications to the amino acid sequence of SEQ ID NO: 171. In some embodiments, the one or more amino acid modifications to the amino acid sequence of any of the albumin polypeptides described herein is/are selected from the group consisting of Q417A, H440Q, H464Q, A490D, E492G/T/P/H, V493P/L, D494N/Q/A/E/P, E495Q/A, T496A, P499A, K500E/G/D/A/S/C/P/H/F/N/W/T/M/Y/V/Q/L/I/R, E501A/P/Q, N503K/D/H, A504E, E505K/D, T506F/S, H510Q, H535Q, K536A, P537A, K538A/H, T540S, K541A/D/G/N/E, E542P/D, D550N, K573Y/W/P/H/F/V/I/T/N/S/G/M/C/A/E/Q/R/L/D, K574N, Q580K, L575F, A577T/E, A578R/S, S579C/T, Q580K, A581D, A582T, and G584A. In some embodiments, the one or more amino acid modifications to the amino acid sequence of any of the albumin polypeptides described herein is/are selected from the group consisting of V418M, T420A, E505G, and V547A.

3. Binding Proteins

[0353] Additional strategies for extending the half-life of masked cytokines in serum include linking the masked cytokine to certain binding proteins, such as albumin-binding proteins or IgG-binding proteins. The binding proteins can be any protein that binds to a serum protein having a prolonged half-life, such as albumin or IgG. Albumin and IgG are polypeptides that are known to have long half-lives in serum. Since albumin-binding proteins bind to, or otherwise associate with, albumin in serum, masked cytokines that are linked to an albumin-binding protein can exhibit an extended half-life in serum. Likewise, since IgG-binding proteins bind, or otherwise associate with, IgG in serum, masked cytokines that are linked to an IgG-binding protein can exhibit an extended half-life in serum.

[0354] Albumin-binding proteins and methods by which they are linked to proteins of interest are described, for example, in WO 1991/01743, WO 2001/45746, WO 2002/076489, WO 2004/041865, or US20070269422A1, the contents of which are herein incorporated by reference.

[0355] In some embodiments, the half-life extension domain comprises an albumin-binding protein. The albumin-binding protein can be any of the albumin-binding proteins described, for instance, in WO1991/01743, WO2001/45746, WO2002/076489, WO2004/041865, US20070269422A1; US20160152686A1; Dennis et al. (2002), JBC 277(38): 35035-35043.

[0356] In some embodiments of the masked cytokine, the half-life extension domain comprises an albumin-binding protein. In some embodiments, the masked cytokine comprises more than one albumin-binding protein, each of which can be any of the albumin-binding proteins described herein. In some embodiments, the masked cytokine comprises a first half-life extension domain and a second half-life

extension domain, each of which comprises an albumin-binding protein. It is understood that reference to "an albumin-binding protein" or "the albumin-binding protein" can refer to the albumin-binding protein of the half-life extension domain in a masked cytokine comprising a single half-life extension domain, or it can refer to the albumin-binding protein of the first half-life extension domain in a masked cytokine comprising a first half-life extension domain and a second half-life extension domain, or it can refer to the albumin-binding protein of the second half-life extension domain in a masked cytokine comprising a first half-life extension domain and a second half-life extension domain, or it can refer to the albumin-binding protein of the first half-life extension domain and the albumin-binding protein of the second half-life extension domain in a masked cytokine comprising a first half-life extension domain and a second half-life extension domain.

[0357] In some embodiments, the albumin-binding protein comprises an albumin-binding domain (ABD) of Streptococcal protein G (SPG). *See, e.g.*, Nygren et al. J. Mol. Recogn. (1988) 1(2): 69-74. In some embodiments, the albumin-binding protein comprises an ABD of SPG strain G148. In some embodiments, the albumin-binding protein comprises the C-terminal albumin-binding domain 3 (ABD3) of SPG strain G148. *See, e.g.*, Nilvebrant and Hober (2013), Comput. Struct. Biotechol. J., 6: e201303009. In some embodiments, the albumin-binding protein comprises the amino acid sequence of SEQ ID NO: 172. In some embodiments, the albumin-binding protein comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 172.

[0358] In some embodiments, the albumin-binding protein comprises a natural or synthetic peptide. In some embodiments, the albumin-binding protein comprises the amino acid sequence of SEQ ID NO: 173 or 174. In some embodiments, the albumin-binding protein comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO: 173 or 174.

[0359] In some embodiments, an albumin-binding domain comprises an amino acid sequence produced by introducing one or more modifications to the amino acid sequence of the albumin-binding domain, such as by introducing one or more amino acid substitutions, additions, or deletions to the amino acid sequence of any one of SEQ ID NOs: 172-174.

[0360] In some embodiments, the albumin-binding protein is a single-domain antibody or fragment thereof, such as a Nanobody, that binds to or otherwise associates with albumin. *See, e.g.*, WO 2004041865A2 and US20070269422A1, the contents of which are herein incorporated by reference. In some embodiments, the single-domain antibody or fragment thereof comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 252-259. In some embodiments, the single-domain antibody or fragment thereof comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NOs: 252-259.

[0361] In some embodiments, the albumin-binding protein is linked to a masking moiety. In some embodiments, a masking moiety is linked to the amino-terminus or the carboxy-terminus of the albumin-binding protein. In some embodiments, the albumin-binding protein is linked to a masking moiety via a linker. In some embodiments, a linker is linked to the amino-terminus or the carboxy-terminus of the albumin-binding protein. In some embodiments, an N-terminal spacer domain or a C-terminal spacer domain of the linker is linked to the amino-terminus or the carboxy-terminus of the albumin-binding domain. In some embodiments, a cleavable peptide of the linker is linked to the amino-terminus or the carboxy-terminus of the albumin-binding domain. In some embodiments, the albumin-binding protein is linked to a cytokine or functional fragment thereof. In some embodiments, a cytokine or functional fragment thereof is linked to the amino-terminus or the carboxy-terminus of the albumin-binding protein. In some embodiments, the albumin-binding protein is linked to a cytokine or functional fragment thereof via a linker. In some embodiments, a linker is linked to the amino-terminus or the carboxy-terminus of the albumin-binding protein.

[0362] Another example of a binding protein is an IgG-binding protein. IgG-binding proteins have been reported. For an overview of IgG-binding proteins, including specific IgG-binding proteins and their applications, *see, e.g.*, Choe et al. (2016) Materials 9(12): 994, the contents of which are herein incorporated by reference.

[0363] In some embodiments of the masked cytokine, the half-life extension domain comprises an IgG-binding protein. In some embodiments, the masked cytokine comprises more than one IgG-binding protein, each of which can be any of the IgG-binding proteins described herein. In some embodiments, the masked cytokine comprises a first half-life extension domain and a second half-life extension domain, each of which comprises an IgG-binding protein. It is understood that reference to "an IgG-binding protein" or "the IgG-binding protein" can refer to the IgG-binding protein of the half-life extension domain in a masked cytokine comprising a single half-life extension domain, or it can refer to the IgG-binding protein of the first half-life extension domain in a masked cytokine comprising a first half-life extension domain and a second half-life extension domain, or it can refer to the IgG-binding protein of the second half-life extension domain in a masked cytokine comprising a first half-life extension domain and a second half-life extension domain, or it can refer to the IgG-binding protein of the first half-life extension domain and the IgG-binding protein of the second half-life extension domain in a masked cytokine comprising a first half-life extension domain and a second half-life extension domain.

[0364] In some embodiments, the half-life extension domain comprises an IgG-binding protein. The IgG-binding protein can be any IgG-binding protein. The IgG-binding protein can be any IgG-binding protein described, *e.g.*, in Choe et al. (2016) Materials 9(12): 994; US20140046037A1. For instance, a variety of bacterial proteins have been shown to bind to mammalian IgGs, including Protein A, G, L, and Z, and fusion proteins of Protein LG and LA. *See, e.g.*, Choe et al. (2016) Materials 9(12):

994. In some embodiments, the IgG-binding protein is a Staphylococcal protein A (SpA) protein from the bacterium *Staphylococcus aureus*, or fragment or variant thereof. In some embodiments, the IgG-binding domain is an IgG-binding domain of SpA, or a fragment or variant thereof. In some embodiments, the IgG-binding domain is one or more of the SpA IgG-binding domain E, D, A, B, C, and Z, or fragments or variants thereof.

[0365] In some embodiments, the IgG-binding domain comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 175-186. In some embodiments, the IgG-binding protein comprises an amino acid sequence having about or at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of any one of SEQ ID NOs: 175-186.

[0366] In some embodiments, an IgG-binding domain comprises an amino acid sequence produced by introducing one or more modifications to the amino acid sequence of the IgG-binding domain, such as by introducing one or more amino acid substitutions, additions, or deletions to the amino acid sequence of any one of SEQ ID NOs: 175-186.

[0367] In some embodiments, the IgG-binding protein is linked to a masking moiety. In some embodiments, a masking moiety is linked to the amino-terminus or the carboxy-terminus of the IgG-binding protein. In some embodiments, the IgG -binding protein is linked to a masking moiety via a linker. In some embodiments, a linker is linked to the amino-terminus or the carboxy-terminus of the IgG -binding protein. In some embodiments, an N-terminal spacer domain or a C-terminal spacer domain of the linker is linked to the amino-terminus or the carboxy-terminus of the IgG-binding domain. In some embodiments, a cleavable peptide of the linker is linked to the amino-terminus or the carboxy-terminus of the IgG-binding domain. In some embodiments, the IgG-binding protein is linked to a cytokine or functional fragment thereof. In some embodiments, a cytokine or functional fragment thereof is linked to the amino-terminus or the carboxy-terminus of the IgG-binding protein. In some embodiments, the IgG-binding protein is linked to a cytokine or functional fragment thereof via a linker. In some embodiments, a linker is linked to the amino-terminus or the carboxy-terminus of the IgG-binding protein.

4. Antibody Derivatives

[0368] The masked cytokines described herein may alternatively be linked to various antibody derivatives including, but not limited to, an scFv, an scFc, a dual-variable domain (DVD), and antibody derivatives based on the CrossMab approach. *See, e.g.*, Klein et al. (2012), MAbs, 4(6): 653-663; US20070071675A1. The antibody derivatives include antibody derivatives engineered as bispecific antibodies or fragments thereof. As such, in some embodiments, a half-life extension domain can comprise any antibody derivative, variant, or fusion product thereof including, but not limited to an scFv,

an scFc, a dual-variable domain (DVD), antibody derivatives based on the CrossMab approach, and bispecific antibodies or fragments thereof.

5. Polyamino acid sequences

[0369] An additional strategy for extending the half-life of masked cytokines in serum is by linking the masked cytokine to a polyamino acid sequence. As such, in some embodiments, the half-life extension domain comprises a polyamino acid sequence. The polyamino acid sequence can be any polyamino acid sequence capable of extending the half-life of the masked cytokine in serum when it is linked to the masked cytokine. Examples of polyamino acid sequences include PAS polypeptides and XTEN polypeptides.

[0370] In some embodiments, the polyamino acid sequence is a polypeptide chain comprising the small amino acid residues proline, alanine, and, optionally, serine (PAS polypeptide). PAS sequences are hydrophilic and uncharged polymers that have biophysical properties similar to polyethylene glycol (PEG), which is commonly linked to therapeutic proteins as a strategy for extending the therapeutic protein's half-life in vivo. *See, e.g.*, Schlapschy et al. (2013) Protein Eng. Des. Sel., 26(8): 489-501; WO2008155134A1; WO2011144756A1; WO2016130451A1, the contents of which are herein incorporated by reference. Attachment of a PAS polypeptide to a therapeutic protein has been observed to increase stability in vivo and/or in vitro compared to the therapeutic protein in its native state without the PAS polypeptide attached. In some embodiments, the PAS polypeptide assumes a random coil conformation. In some embodiments, the PAS polypeptide forms a random coil conformation domain.

[0371] In some embodiments, the half-life extension domain comprises a PAS polypeptide that comprises the amino acid residues proline and alanine. In some embodiments, the half-life extension domain comprises a PAS polypeptide that comprises the amino acid residues proline, alanine, and serine. In some embodiments, the PAS polypeptide comprises at least 25 amino acid residues, at least 50 amino acid residues, at least 100 amino acid residues, at least 150 amino acid residues, at least 200 amino acid residues, at least 250 amino acid residues, at least 300 amino acid residues, at least 400 amino acid residues, at least 500 amino acid residues, at least 600 amino acid residues, at least 700 amino acid residues, at least 800 amino acid residues, at least 900 amino acid residues, at least 1000 amino acid residues, at least 1100 amino acid residues, at least 1200 amino acid residues, at least 1300 amino acid residues, at least 1500 amino acid residues, at least 2000 amino acid residues, at least 2500 amino acid residues, or at least 3000 amino acid residues. In some embodiments, the PAS polypeptide comprises at least 25 amino acid residues, at least 50 amino acid residues, at least 100 amino acid residues, at least 150 amino acid residues, at least 200 amino acid residues, at least 250 amino acid residues, at least 300 amino acid residues, at least 400 amino acid residues, at least 500 amino acid residues, at least 600 amino acid residues, at least 700 amino acid residues, at least 800 amino acid residues, at least 900 amino acid residues, at least 1000 amino acid residues, at least 1100 amino acid residues, at least 1200 amino acid

residues, at least 1300 amino acid residues, at least 1500 amino acid residues, at least 2000 amino acid residues, at least 2500 amino acid residues, or at least 3000 amino acid residues, wherein each amino acid residue is either a proline or an alanine. In some embodiments, the PAS polypeptide comprises at least 25 amino acid residues, at least 50 amino acid residues, at least 100 amino acid residues, at least 150 amino acid residues, at least 200 amino acid residues, at least 250 amino acid residues, at least 300 amino acid residues, at least 400 amino acid residues, at least 500 amino acid residues, at least 600 amino acid residues, at least 700 amino acid residues, at least 800 amino acid residues, at least 900 amino acid residues, at least 1000 amino acid residues, at least 1100 amino acid residues, at least 1200 amino acid residues, at least 1300 amino acid residues, at least 1500 amino acid residues, at least 2000 amino acid residues, at least 2500 amino acid residues, or at least 3000 amino acid residues, wherein each amino acid residue is an amino acid selected from the group consisting of a proline, an alanine, and a serine.

[0372] In some embodiments, the polyamino acid sequence is an extended recombinant polypeptide (XTEN polypeptide). XTEN polypeptides are polypeptides with non-naturally occurring, substantially non-repetitive sequences having a low degree or no secondary or tertiary structure under physiologic conditions. XTEN polypeptides typically have from about 36 to about 3000 amino acid residues, of which the majority or the entirety are small hydrophilic amino acids (e.g., arginine, lysine, threonine, alanine, asparagine, glutamine, aspartate, glutamate, serine, and glycine). The physiochemical properties, as well as the unstructured characteristic, of XTEN polypeptides is result, in part, from the overall amino acid composition that is disproportionately limited to 4-6 types of hydrophilic amino acids, the linking of the amino acids in a non-repetitive design, and the length of the XTEN polypeptide. The attachment of an XTEN polypeptide to a therapeutic protein has been observed to improve solubility and stability, and to enhance the half-life of the therapeutic protein. *See, e.g.*, Podust et al. (2016) J. Controlled Release, 240: 52-66; WO2013130683A2, the contents of which are herein incorporated by reference.

[0373] In some embodiments, the half-life extension domain comprises an XTEN polypeptide that comprises an amino acid sequence that is made up of four, five, or six types of amino acid residues selected from the group consisting of glycine (G), alanine (A), serine (S), threonine (T), glutamate (E) and proline (P).

[0374] In some embodiments, the XTEN polypeptide comprises an amino acid sequence of about 25 to about 500 amino acid residues, about 200 to about 1000 amino acid residues, about 500 to about 1500 amino acid residues, about 1000 to about 2000 amino acid residues, or about 1500 to about 3000 amino acid residues. In some embodiments, at least about 70%, 75%, 80%, or 85% of the amino acid sequence consists of non-overlapping sequence motifs. In some embodiments, each of the motifs has 5 to 100 amino acid residues, 5 to 50 amino acids residues, or 9 to 36 amino acid residues, and wherein at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% of each of the motifs consists of four, five, or six types of amino acid

residues selected from the group consisting of glycine (G), alanine (A), serine (S), threonine (T), glutamate (E) and proline (P), In some embodiments, the content of any one amino acid type in the full-length XTEN polypeptide does not exceed about 40%, about 35%, about 30%, about 25%, about 15%, about 10%, or about 8%.

[0375] In some embodiments, the XTEN polypeptide comprises an amino acid sequence of about 25 to about 500 amino acid residues, about 200 to about 1000 amino acid residues, about 500 to about 1500 amino acid residues, about 1000 to about 2000 amino acid residues, or about 1500 to about 3000 amino acid residues, wherein at least about 80% of the amino acid sequence consists of non-overlapping sequence motifs where each of the motifs has 9 to 36 amino acid residues and wherein at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% of each of the motifs consists of four, five, or six types of amino acid residues selected from the group consisting of glycine (G), alanine (A), serine (S), threonine (T), glutamate (E) and proline (P), and wherein the content of any one amino acid type in the full-length XTEN polypeptide does not exceed about 40%, about 35%, about 30%, about 25%, about 15%, about 10%, or about 8%.

6. PEGylation and Glycosylation

[0376] Additional strategies for extending the half-life of the masked cytokines provided herein include PEGylation and the engineering of additional glycosylation sites. Each of these strategies is discussed in further detail below.

[0377] "PEGylation" refers to a process of covalent or non-covalent attachment or amalgamation of polyethylene glycol (PEG) polymer chains to molecules and macrostructures, such as a drug, therapeutic protein, polypeptide, antibody, antibody fragment, antibody derivative, or to any of the masked cytokines or components thereof provided herein (e.g., the half-life extension domain of a masked cytokine and/or the cytokine or functional fragment thereof of the masked cytokine). The benefits of PEGylation include, for example, (1) markedly improved circulating half-lives in vivo due to either evasion of renal clearance as a result of the polymer increasing the apparent size of the molecule to above the glomerular filtration limit, and/or through evasion of cellular clearance mechanisms, (2) reduced antigenicity and immunogenicity of the molecule to which PEG is attached, (3) improved pharmacokinetics, (4) improved solubility, (5) improved formulation and dosing options, (6) improved bioavailability via reduced losses at subcutaneous injection sites, (7) improved thermal and mechanical stability of the PEGylated molecule.

[0378] Methods for the pegylation of various molecules and macrostructures are well known in the art. *See, e.g.*, US20140256636A1; Fee and Damodaran (2010) European Pharmaceutical Review, 15(1): 18-26; Chapman et al. (1999) Nature Biotechnol., 17: 780-783; Yang et al. (2003), Protein Eng., 16(10): 761-770; Chapman, Adv. Drug. Deliv. Rev. (2002), 54(4): 531-545, the contents of which are herein incorporated by reference.

[0379] In some embodiments, the masked cytokine of any of the embodiments herein is PEGylated. For instance, in some embodiments, this is accomplished by functionalizing PEG with group-specific reagents so that the conjugation of PEG to the protein (e.g., a half-life extension domain, or a cytokine or functional fragment thereof) can be targeted to specific side chain groups of the protein, such as amino, carboxyl, sulfhydryl, or guanidine groups. In some embodiments, cysteine (C) residues are introduced by amino acid substitution into the protein (e.g., a half-life extension domain, or a cytokine or functional fragment thereof) in a site-specific manner. The thiol groups of the newly introduced cysteine residues can then be targeted for PEGylation using malemide chemistry-based PEG reagents. The replacement of serine (S) or threonine (T) with cysteine has an advantage in that the net charge of the modified protein is not altered as a result of the PEGylation. As such, in some embodiments, a component of the masked cytokine, such as any of the cytokines or functional fragments thereof and/or any of the half-life extension domains, can be modified, or further modified, by introducing cysteine residues for PEGylation.

[0380] "Glycosylation" refers to the addition of saccharides or glycosyl groups to a polypeptide. Glycosylation of polypeptides is typically either N-linked or O-linked. N-linked refers to the attachment of a carbohydrate moiety to the side chain of an asparagine residue. The tripeptide sequences asparagine-X-serine (N-X-S) and asparagine-X-threonine (N-X-T), where X is any amino acid except proline (P), are the recognition sequences for enzymatic attachment of the carbohydrate moiety to the asparagine side chain. Thus, the presence of either of these tripeptide sequences in a polypeptide creates a potential glycosylation site. O-linked glycosylation refers to the attachment of one of the sugars (e.g., N-aceylgalactosamine, galactose, or xylose) to a hydroxyamino acid, most commonly serine or threonine, although 5-hydroxyproline or 5-hydroxylysine may also be used.

[0381] Naturally-occurring glycosylation has been shown to increase the molecular stability of proteins. *See, e.g.*, Sola et al. (2007), Cell. Mol. Life Sci., 64(16): 2133-2152. It has also been shown that the engineering of additional glycosylation sites can stabilize a variety of protein therapeutics against most major physiochemical instabilities. *See, e.g.*, Sola and Griebenow (2009), J. Pharm. Sci., 98(4): 1223-1245. Among the pharmaceutically relevant protein instabilities that have been shown to be improved by glycosylation are, for example, oxidation; cross-linking; pH-, chemical-, thermal-, and freezing-induced denaturation/unfolding; precipitation; kinetic activation; and aggregation. *Id.*

[0382] Addition of glycosylation sites to the masked cytokine is conveniently accomplished by altering the amino acid sequence such that one or more of the above-described tripeptide sequences (for N-linked glycosylation sites) is created in the amino acid sequence of the masked cytokine (e.g., in the amino acid sequence of the half-life extension domain and/or the cytokine or functional fragment thereof). The alteration may also be made by the addition to, or substitution of, one or more serine or threonine residues in the amino acid sequence of the masked cytokine (e.g., in the amino acid sequence

of the half-life extension domain and/or the cytokine or functional fragment thereof) (for O-linked glycosylation sites).

[0383] In some embodiments, the masked cytokine of any of the embodiments herein is modified, or is further modified, by altering the amino acid sequence of the masked cytokine (e.g., the amino acid sequence of the half-life extension domain and/or the cytokine or functional fragment thereof) such that one or more additional N-X-S and/or N-X-T tripeptide sequence(s) is/are introduced into the amino acid sequence of the masked cytokine or component thereof (for the addition of one or more N-linked glycosylation sites). In some embodiments, the masked cytokine of any of the embodiments herein is modified, or is further modified, by altering the amino acid sequence of the masked cytokine or component thereof (e.g., the amino acid sequence of the half-life extension domain and/or the cytokine or functional fragment thereof) such that one or more additional serine or threonine residues is/are introduced into the amino acid sequence of the masked cytokine or component thereof (for the addition of one or more O-linked glycosylation sites). In some embodiments, the alteration of the amino acid sequence for the addition of one or more N-linked glycosylation sites and/or for the addition of one or more O-linked glycosylation sites is accomplished by the addition of one or more amino acids to the amino acid sequence of the masked cytokine or component thereof. In some embodiments, the alteration of the amino acid sequence for the addition of one or more N-linked glycosylation sites and/or for the addition of one or more O-linked glycosylation sites is accomplished by the substitution of one or more amino acids in the amino acid sequence of the masked cytokine or component thereof. In some embodiments, the alteration of the amino acid sequence for the addition of one or more N-linked glycosylation sites and/or for the addition of one or more O-linked glycosylation sites is accomplished by the addition of one or more amino acids to the amino acid sequence and by the substitution of one or more amino acids in the amino acid sequence of the masked cytokine or component thereof.

7. Heterodimerization Modifications

[0384] The half-life extension domains described herein may include one or more modifications that promote heterodimerization of two different half-life extension domains. In some embodiments comprising a first half-life extension domain and a second half-life extension domain, it is desirable to promote heterodimerization of the first and second half-life extension domains such that production of the masked cytokine in its correct heterodimeric form is produced efficiently. As such, one or more amino acid modifications can be made to the first half-life extension domain and one or more amino acid modifications can be made to the second half-life extension domain using any strategy available in the art, including any strategy as described in Klein et al. (2012), MAbs, 4(6): 653-663. Exemplary strategies and modifications are described in detail below.

a. Knobs-into-Holes Approach

[0385] One strategy for promoting heterodimerization of two different half-life extension domains is an approach termed the "knobs-into-holes."

[0386] In some embodiments, the masked cytokine comprises a first half-life extension domain and a second half-life extension domain, each of which comprises a CH3 domain. In some embodiments, the half-life extension domain comprising a CH3 domain is a heavy chain polypeptide or a fragment thereof (e.g., an Fc domain or fragment thereof). The CH3 domains of the two half-life extension domains can be altered by the "knobs-into-holes" technology, which is described in detail with several examples in, *e.g.*, WO 1996/027011; Ridgway, J.B. et al., Protein Eng. (1996) 9(7): 617-621; Merchant, A.M., et al., Nat. Biotechnol. (1998) 16(7): 677-681. *See also* Klein et al. (2012), MAbs, 4(6): 653-663. Using the knob-into-holes method, the interaction surfaces of the two CH3 domains are altered to increase the heterodimerization of the two half-life extension domains containing the two altered CH3 domains. This occurs by introducing a bulky residue into the CH3 domain of one of the half-life extension domains, which acts as the "knob." Then, in order to accommodate the bulky residue, a "hole" is formed in the other half-life extension domain that can accommodate the knob. Either of the altered CH3 domains can be the "knob" while the other can be the "hole." The introduction of a disulfide bridge further stabilizes the heterodimers (Merchant, A.M., et al., Nat. Biotechnol. (1998) 16(7); Atwell, S., et al., J. Mol. Biol. (1997) 270(1): 26-35) as well as increases yield.

[0387] It has been reported that heterodimerization yields above 97% can be achieved by introducing the S354C and T366W mutations in a heavy chain to create the "knob" and by introducing the Y349C, T366S, L368A, and Y407V mutations in a heavy chain to create the "hole" (numbering of the residues according to the Kabat EU numbering system). Carter et al. (2001), J. Immunol. Methods, 248: 7-15; Klein et al. (2012), MAbs, 4(6): 653-663.

[0388] In some embodiments comprising a first half-life extension domain and a second half-life extension domain, the first half-life extension domain comprises a heavy chain polypeptide or portion thereof (e.g., an Fc domain or fragment thereof) that comprises one or more amino acid mutations that create a "knob," and the second half-life extension domain comprises a heavy chain polypeptide or portion thereof (e.g., an Fc domain or fragment thereof) that comprises one or more amino acid mutations that create a "hole." In some embodiments comprising a first half-life extension domain and a second half-life extension domain, the first half-life extension domain comprises a heavy chain polypeptide or portion thereof (e.g., an Fc domain or fragment thereof) that comprises one or more amino acid mutations that create a "hole," and the second half-life extension domain comprises a heavy chain polypeptide or portion thereof (e.g., an Fc domain or fragment thereof) that comprises one or more amino acid mutations that create a "knob." Methods for introducing a hole or knob in a heavy chain polypeptide or portion thereof (e.g., an Fc domain or fragment thereof) is known in the art, e.g., in WO 1996/027011; Ridgway, J.B. et al., Protein Eng. (1996) 9(7): 617-621; Merchant, A.M., et al., Nat. Biotechnol. (1998) 16(7): 677-681; Klein et al. (2012), MAbs, 4(6): 653-663.

[0389] In some embodiments comprising a first half-life extension domain and a second half-life extension domain, the first half-life extension domain comprises a heavy chain polypeptide or portion thereof (e.g., an Fc domain or fragment thereof) that comprises the amino acid mutations S354C and T366W (numbered according to the Kabat EU numbering system), and the second half-life extension domain comprises a heavy chain polypeptide or portion thereof (e.g., an Fc domain or fragment thereof) that comprises the amino acid mutations Y349C, T366S, L368A, and Y407V (numbered according to the Kabat EU numbering system). In some embodiments comprising a first half-life extension domain and a second half-life extension domain, the first half-life extension domain comprises a heavy chain polypeptide or portion thereof (e.g., an Fc domain or fragment thereof) that comprises the amino acid mutations Y349C, T366S, L368A, and Y407V (numbered according to the Kabat EU numbering system), and the second half-life extension domain comprises a heavy chain polypeptide or portion thereof (e.g., an Fc domain or fragment thereof) that comprises the amino acid mutations S354C and T366W (numbered according to the Kabat EU numbering system). In some embodiments comprising a first half-life extension domain and a second half-life extension domain, the first half-life extension domain comprises an Fc domain or fragment thereof comprising the amino acid sequence of SEQ ID NO: 155, and the second half-life extension domain comprises an Fc domain or fragment thereof comprising the amino acid sequence of SEQ ID NO: 156. In some embodiments comprising a first half-life extension domain and a second half-life extension domain, the first half-life extension domain comprises an Fc domain or fragment thereof comprising the amino acid sequence of SEQ ID NO: 156, and the second half-life extension domain comprises an Fc domain or fragment thereof comprising the amino acid sequence of SEQ ID NO: 155. In some embodiments comprising a first half-life extension domain and a second half-life extension domain, the first half-life extension domain comprises an Fc domain or fragment thereof comprising the amino acid sequence of SEQ ID NO: 265, and the second half-life extension domain comprises an Fc domain or fragment thereof comprising the amino acid sequence of SEQ ID NO: 156. In some embodiments comprising a first half-life extension domain and a second half-life extension domain, the first half-life extension domain comprises an Fc domain or fragment thereof comprising the amino acid sequence of SEQ ID NO: 156, and the second half-life extension domain comprises an Fc domain or fragment thereof comprising the amino acid sequence of SEQ ID NO: 265. In some embodiments comprising a first half-life extension domain and a second half-life extension domain, the first half-life extension domain comprises an Fc domain or fragment thereof comprising the amino acid sequence of SEQ ID NO: 155, and the second half-life extension domain comprises an Fc domain or fragment thereof comprising the amino acid sequence of SEQ ID NO: 156. In some embodiments comprising a first half-life extension domain and a second half-life extension domain, the first half-life extension domain comprises an Fc domain or fragment thereof comprising the amino acid sequence of SEQ ID NO: 156, and the second half-life extension domain comprises an Fc domain or fragment thereof comprising the amino acid sequence of SEQ ID NO: 155.

[0390] Additional examples of substitutions that can be made to form knobs and holes include those described in US20140302037A1, the contents of which are herein incorporated by reference. For example, in some embodiments, any of the following amino acid substitutions can be made to a first half-life extension domain ("first domain") and a paired second half-life extension domain ("second domain") that each contain an Fc domain: (a) Y407T in the first domain and T366Y in the second domain; (b) Y407A in the first domain and T366W in the second domain; (c) F405A in the first domain and T394W in the second domain; (d) F405W in the first domain and T394S in the second domain; (e) Y407T in the first domain and T366Y in the second domain; (f) T366Y and F405A in the first domain and T394W and Y407T in the second domain; (g) T366W and F405W in the first domain and T394S and Y407A in the second domain; (h) F405W and Y407A in the first domain and T366W and T394S in the second domain; or (i) T366W in the first domain and T366S, L368A, and Y407V in the second domain, numbered according to the Kabat EU numbering system.

[0391] In some embodiments, any of the following amino acid substitutions can be made to a first half-life extension domain ("first domain") and a paired second half-life extension domain ("second domain") that each contain an Fc domain: (a) Y407T in the second domain and T366Y in the first domain; (b) Y407A in the second domain and T366W in the first domain; (c) F405A in the second domain and T394W in the first domain; (d) F405W in the second domain and T394S in the first domain; (e) Y407T in the second domain and T366Y in the first domain; (f) T366Y and F405A in the second domain and T394W and Y407T in the first domain; (g) T366W and F405W in the second domain and T394S and Y407A in the first domain; (h) F405W and Y407A in the second domain and T366W and T394S in the first domain; or (i) T366W in the second domain and T366S, L368A, and Y407V in the first domain, numbered according to the Kabat EU numbering system.

[0392] In embodiments comprising a first half-life extension domain and a second half-life extension domain that each comprise an Fc domain, any of the heterodimerizing alterations described herein can be used in the Fc domains to promote heterodimerization of any of the masked cytokines described herein. For instance, any of the heterodimerization alterations described herein, including combinations thereof, can be used to alter an amino acid sequence selected from the group consisting of SEQ ID NOs: 154-156, 158, 168, 169, 265, 616, 619, 622, 625, 721,772-774, 793, and 796.

b. Ionic/Electrostatic Interactions

[0393] Another strategy for promoting heterodimerization of two different half-life extension domains is by stabilizing ionic interactions that favor heterodimerization through altering charged residues.

[0394] In some embodiments, the masked cytokine comprises a first half-life extension domain and a second half-life extension domain, each of which comprises a CH3 domain. In some embodiments, the half-life extension domain comprising a CH3 domain is a heavy chain polypeptide or a fragment thereof

(e.g., an Fc domain or fragment thereof). It has been observed that altering the charge polarities between two different Fc domains can result in ionic interactions such that heterodimerization is favored while homodimerization is suppressed. *See, e.g.*, WO 2006/106905A1; Gunasekaran et al. (2010) 285(25): 19637-19646. For example, it was observed that negatively charged E356 pairs of an Fc domain pairs with positively charged K439 of another Fc domain, negatively charged E357, E357, and D399 of a first Fc domain pairs with positively charged K439, K370, and K409, respectively, of a second Fc domain. *See* WO 2006/106905A1; Gunasekaran et al. (2010) 285(25): 19637-19646. As such, by introducing at least two of the mutations of E356K, E357K, and D399K in a first Fc domain, and the mutations K370E, K409D, and K439E into a second Fc domain, efficient heterodimerization can be achieved while suppressing homodimer formation. *Id.* Efficient heterodimerization has been achieved by introducing K392D and K409D mutations in a first Fc chain, and by introducing D399K and E356K mutations in a second Fc chain. Gunasekaran et al. (2010) 285(25): 19637-19646.

[0395] Additional examples of substitutions that can be made to charged pairs of amino acids include those described in US20140302037A1, the contents of which are herein incorporated by reference. For instance, in some embodiments, any of the following amino acid substitutions can be made to a first half-life extension domain ("first domain") and a paired second half-life extension domain ("second domain") that each contain an Fc domain: (a) K409E in the first domain and D399K in the second domain; (b) K409E in the first domain and D399R in the second domain; (c) K409D in the first domain and D399K in the second domain; (d) K409D in the first domain and D399R in the second domain; (e) K392E in the first domain and D399R in the second domain; (f) K392E in the first domain and D399K in the second domain; (g) K392D in the first domain and D399R in the second domain; (h) K392D in the first domain and D399K in the second domain; (i) K409D and K360D in the first domain and D399K and E356K in the second domain; (j) K409D and K370D in the first domain and D399K and E357K in the second domain; (k) K409D and K392D in the first domain and D399K, E356K, and E357K in the second domain; (l) K409D and K392D in the first domain and D399K in the second domain; (m) K409D and K392D in the first domain and D399K and E356K in the second domain; (n) K409D and K392D in the first domain and D399K and E357K in the second domain; (o) K409D and K370D in the first domain and D399K and D357K in the second domain; (p) D399K in the first domain and K409D and K360D in the second domain; and/or (q) K409D and K439D in the first domain and D399K and E356K in the second domain, numbered according to the Kabat EU numbering system.

[0396] In some embodiments, any of the following amino acid substitutions can be made to a first half-life extension domain ("first domain") and a paired second half-life extension domain ("second domain") that each contain an Fc domain: (a) K409E in the second domain and D399K in the first domain; (b) K409E in the second domain and D399R in the first domain; (c) K409D in the second domain and D399K in the first domain; (d) K409D in the second domain and D399R in the first domain; (e) K392E in the second domain and D399R in the first domain; (f) K392E in the second domain and

D399K in the first domain; (g) K392D in the second domain and D399R in the first domain; (h) K392D in the second domain and D399K in the first domain; (i) K409D and K360D in the second domain and D399K and E356K in the first domain; (j) K409D and K370D in the second domain and D399K and E357K in the first domain; (k) K409D and K392D in the second domain and D399K, E356K, and E357K in the first domain; (l) K409D and K392D in the second domain and D399K in the first domain; (m) K409D and K392D in the second domain and D399K and E356K in the first domain; (n) K409D and K392D in the second domain and D399K and E357K in the first domain; (o) K409D and K370D in the second domain and D399K and D357K in the first domain; (p) D399K in the second domain and K409D and K360D in the first domain; and/or (q) K409D and K439D in the second domain and D399K and E356K in the first domain, numbered according to the Kabat EU numbering system.

[0397] In some embodiments, any of the following amino acid substitutions can be made to a first half-life extension domain ("first domain") and a paired second half-life extension domain ("second domain") that each contain an Fc domain: (a) K409D or K409E in the first domain and D399K or D399R in the second domain; (b) K392D or K392E in the first domain and D399K or D399R in the second domain; (c) K439D or K439E in the first domain and E356K or E356R in the second domain; and/or (d) K370D or K370E in the first domain and E357K or E357R in the second domain, numbered according to the Kabat EU numbering system.

[0398] In some embodiments, any of the following amino acid substitutions can be made to a first half-life extension domain ("first domain") and a paired second half-life extension domain ("second domain") that each contain an Fc domain: (a) K409D or K409E in the second domain and D399K or D399R in the first domain; (b) K392D or K392E in the second domain and D399K or D399R in the first domain; (c) K439D or K439E in the second domain and E356K or E356R in the first domain; and/or (d) K370D or K370E in the second domain and E357K or E357R in the first domain, numbered according to the Kabat EU numbering system.

[0399] In some embodiments comprising a first half-life extension domain and a second half-life extension domain that each comprise an Fc domain, one or more of the following substitutions may be further included in both the first half-life extension domain and the second half-life extension domain to stabilize the heterodimers: R355D, R355E, K360D, and K360R.

[0400] In some embodiments comprising a first half-life extension domain and a second half-life extension domain, the first half-life extension domain comprises a heavy chain polypeptide or portion thereof (e.g., an Fc domain or fragment thereof) that comprises one or more mutations that promote stabilizing ionic interactions with the second half-life extension domain while suppressing homodimerization, and the second half-life extension domain comprises one or more mutations that promote stabilizing ionic interactions with the first half-life extension domain while suppressing homodimerization.

[0401] In some embodiments comprising a first half-life extension domain and a second half-life extension domain, the first half-life extension domain comprises a heavy chain polypeptide or portion thereof (e.g., an Fc domain or fragment thereof) that comprises the amino acid mutations K392D and K409D (numbered according to the Kabat EU numbering system), and the second half-life extension domain comprises a heavy chain polypeptide or portion thereof (e.g., an Fc domain or fragment thereof) that comprises the amino acid mutations D399K and E356K (numbered according to the Kabat EU numbering system).

[0402] In embodiments comprising a first half-life extension domain and a second half-life extension domain that each comprise an Fc domain, any of the heterodimerizing alterations described herein can be used in the Fc domains to promote heterodimerization of any of the masked cytokines described herein. For instance, any of the heterodimerization alterations described herein, including combinations thereof, can be used to alter an amino acid sequence selected from the group consisting of SEQ ID NOs: 154-156, 158, 168, 169, 265, 616, 619, 622, 625, 721,772-774, 793, and 796.

c. Structural and Sequenced-Based Approaches

[0403] Another strategy for promoting heterodimerization of two different half-life extension domains is by using structure- and sequence-based approaches to identify alterations that could promote heterodimerization and/or suppress homodimerization.

[0404] Among the ways of identifying alterations that promote heterodimerization is by performing structural calculations to determine the energies of paired variant combinations for residues that interact across the CH3-CH3 dimer interface, as was the approach taken in Moore et al. (2011) 3(6): 546-557, the contents of which are herein incorporated by reference. Moore et al. identified the pairs that were predicted to have lower energy in the heterodimer form relative to the homodimer form as a starting point for further analysis. It was observed that a heterodimerization yield of 89% could be achieved by introducing S364H and F405A mutations in a first Fc domain and by introducing Y349T and T394F mutations in a second Fc domain. *Id.*

[0405] In some embodiments comprising a first half-life extension domain and a second half-life extension domain that each comprise an Fc domain, the first half-life extension domain comprises amino acid mutations of S364H and F405A, and the second half-life extension domain comprises amino acid mutations of Y349T and T394F, numbered according to the Kabat EU numbering system. In some embodiments comprising a first half-life extension domain and a second half-life extension domain that each comprise an Fc domain, the second half-life extension domain comprises amino acid mutations of S364H and F405A, and the first half-life extension domain comprises amino acid mutations of Y349T and T394F, numbered according to the Kabat EU numbering system.

[0406] In embodiments comprising a first half-life extension domain and a second half-life extension domain that each comprise an Fc domain, any of the heterodimerizing alterations described

herein can be used in the Fc domains to promote heterodimerization of any of the masked cytokines described herein. For instance, any of the heterodimerization alterations described herein, including combinations thereof, can be used to alter an amino acid sequence selected from the group consisting of SEQ ID NOs: 154-156, 158, 168, 169, 265, 616, 619, 622, 625, 721,772-774, 793, and 796.

E. Binding Assays

[0407] The strength, or affinity of immunological binding interactions, such as between a cytokine or functional fragment thereof and a binding partner (e.g., a target protein, such as a cytokine receptor) for which the cytokine or functional fragment thereof is specific, can be expressed in terms of the dissociation constant (Kd) of the interaction, wherein a smaller Kd represents a greater affinity. For example, the binding of the IL-2 cytokine to the IL-2R cytokine receptor (e.g., the IL-2R or a component thereof, such as IL-2Rα, IL-2Rβ, IL-2Rγ, or combinations thereof), can be expressed in terms of the Kd. In some embodiments, the immunological binding interactions are between a masked cytokine (in the presence or absence of a protease) and a target protein, such as a cytokine receptor. In the context of IL-2 cytokine binding, the target protein could be the IL-2R (comprising the IL-2Rα, IL-2Rβ, and IL-2Rγ chains), the IL-2Rα chain, the IL-2Rβ chain, or the IL-2Rα/β dimeric complex. Immunological binding properties of proteins can be quantified using methods well known in the art. For example, one method comprises measuring the rates of cytokine receptor (e.g., IL-2R)/cytokine (e.g., IL-2) complex formation and dissociation, wherein those rates depend on the concentrations of the complex partners, the affinity of the interaction, and geometric parameters that equally influence the rate in both directions. Both the "on rate constant" (Kon) and the "off rate constant" (Koff) can be determined by calculation of the concentrations and the actual rates of association and dissociation. The ratio of Koff/Kon enables the cancelation of all parameters not related to affinity, and is equal to the dissociation constant Kd. See Davies et al., Annual Rev Biochem. 59:439-473, (1990).

[0408] In some aspects, a masked cytokine described herein binds to a target protein with about the same or higher affinity upon cleavage with a protease as compared to the parental cytokine that comprises a masking moiety but does not comprise a cleavable peptide. The target protein can be any cytokine receptor. In some embodiments, the target protein is IL-2R (comprising the IL-2Rα, IL-2Rβ, and IL-2Rγ chains). In some embodiments, the target protein is IL-2Rα. In some embodiments, the target protein is IL-2Rβ. In some embodiments, the target protein is the IL-2Rα/β dimeric complex. In some embodiments, the target protein is IL-15R (comprising the IL-15Rα, IL-2Rβ, and IL-2Rγ chains), or is a component thereof, such as IL-15Rα, IL-2Rβ, or IL-2Rγ, or a combination thereof.

[0409] In some embodiments, a masked cytokine provided herein that does not comprise a cleavable peptide in the linker has a dissociation constant (Kd) of ≤ 1μM, ≤ 150 nM, ≤ 100 nM, ≤ 50 nM, ≤ 10 nM, ≤ 1 nM, ≤ 0.1 nM, ≤ 0.01 nM, or ≤ 0.001 nM (e.g. 10-8 M or less, e.g. from 10-8 M to 10-13 M, e.g., from 10-9 M to 10-13 M) with the target protein. In some embodiments, a masked cytokine provided

herein that comprises a cleavable peptide in the linker has a dissociation constant (Kd) of ≤ 1μM, ≤ 150 nM, ≤ 100 nM, ≤ 50 nM, ≤ 10 nM, ≤ 1 nM, ≤ 0.1 nM, ≤ 0.01 nM, or ≤ 0.001 nM (e.g. 10-8 M or less, e.g. from 10-8 M to 10-13 M, e.g., from 10-9 M to 10-13 M) with the target protein prior to cleavable with a protease. In some embodiments, a masked cytokine provided herein that comprises a cleavable peptide in the linker has a dissociation constant (Kd) of ≤ 1μM, ≤ 150 nM, ≤ 100 nM, ≤ 50 nM, ≤ 10 nM, ≤ 1 nM, ≤ 0.1 nM, ≤ 0.01 nM, or ≤ 0.001 nM (e.g. 10-8 M or less, e.g. from 10-8 M to 10-13 M, e.g., from 10-9 M to 10-13 M) with the target protein upon cleavage with a protease. In some embodiments, the cytokine or functional fragment thereof of a masked cytokine provided herein has a dissociation constant (Kd) of ≥ 500μM, ≥ 250μM, ≥ 200μM, ≥ 150μM, ≥ 100μM, ≥ 50μM, ≥ 10μM, ≥ 1μM, ≥ 500 nM, ≥ 250 nM, ≥ 150 nM, ≥ 100 nM, ≥ 50 nM, ≥ 10 nM, ≥ 1 nM, ≥ 0.1 nM, ≥ 0.01 nM, or ≥ 0.001 nM with the masking moiety of the masked cytokine. In some embodiments, the cytokine or functional fragment thereof of a masked cytokine provided herein has a dissociation constant (Kd) that is between about 200μM and about 50 nM, such as about or at least about 175μM, about or at least about 150μM, about or at least about 125μM, about or at least about 100μM, about or at least about 75μM, about or at least about 50μM, about or at least about 25μM, about or at least about 5μM, about or at least about 1μM, about or at least about 750 nM, about or at least about 500 nM, about or at least about 250 nM, about or at least about 150 nM, about or at least about 100 nM, about or at least about 75 nM, or about or at least about 50 nM. Assays for assessing binding affinity are well known in the art.

[0410] In some aspects, masked cytokines that exhibit a desired occlusion ratio are provided. The term "occlusion ratio" as used herein refers a ratio of (a) a maximum detected level of a parameter under a first set of conditions to (b) a minimum detected value of that parameter under a second set of conditions. For example, in the context of a masked IL-2 polypeptide, the occlusion ratio refers to the ratio of (a) a maximum detected level of target protein (e.g., IL-2R protein) binding to the masked IL-2 polypeptide in the presence of at least one protease capable of cleaving the cleavable peptide of the masked IL-2 polypeptide to (b) a minimum detected level of target protein (e.g., IL-2R protein) binding to the masked IL-2 polypeptide in the absence of the protease. Thus, the occlusion ratio for a masked cytokine can be calculated by dividing the EC50 of the masked cytokine pre-cleavage by the EC50 of the masked cytokine post-cleavage. The occlusion ratio of a masked cytokine can also be calculated as the ratio of the dissociation constant of the masked cytokine before cleavage with a protease to the dissociation constant of the masked cytokine after cleavage with a protease. In some embodiments, a greater occlusion ratio for the masked cytokine indicates that target protein bound by the masked cytokine occurs to a greater extent (e.g., predominantly occurs) in the presence of a protease capable of cleaving the cleavable peptide of the masked cytokine than in the absence of a protease.

[0411] In some embodiments, masked cytokines with an optimal occlusion ratio are provided herein. In some embodiments, an optimal occlusion ratio of a masked cytokine indicates the masked cytokine has desirable properties useful for the methods or compositions contemplated herein. In some

embodiments, a masked cytokine provided herein exhibits an optimal occlusion ratio of about 2 to about 10,000, e.g., about 80 to about 100. In a further embodiment of any of the masked cytokine provided herein, the occlusion ratio is about 2 to about 7,500, about 2 to about 5,000, about 2 to about 2,500, about 2 to about 2,000, about 2 to about 1,000, about 2 to about 900, about 2 to about 800, about 2 to about 700, about 2 to about 600, about 2 to about 500, about 2 to about 400, about 2 to about 300, about 2 to about 200, about 2 to about 100, about 2 to about 50, about 2 to about 25, about 2 to about 15, about 2 to about 10, about 5 to about 10, about 5 to about 15, about 5 to about 20, about 10 to about 100, about 20 to about 100, about 30 to about 100, about 40 to about 100, about 50 to about 100, about 60 to about 100, about 70 to about 100, about 80 to about 100, or about 100 to about 1,000. In some embodiments, a masked cytokine provided herein exhibits an optimal occlusion ratio of about 2 to about 1,000. Binding of a masked IL-2 polypeptide to a target protein before cleavage and/or after cleavage with a protease can be determined using techniques well known in the art such as by ELISA.

[0412] In some embodiments, a masking moiety described herein binds to a cytokine or functional fragment thereof as described herein with lower affinity than the affinity between the cytokine or functional fragment thereof and a target protein (e.g., cytokine receptor). In certain embodiments, a masking moiety provided herein binds to a cytokine or functional fragment thereof as described herein with a dissociation constant (Kd) of $\geq$ 500μM, $\geq$ 250μM, $\geq$ 200μM, $\geq$ 150μM, $\geq$ 100μM, $\geq$ 50μM, $\geq$ 10μM, $\geq$ 1μM, $\geq$ 500 nM, $\geq$ 250 nM, $\geq$ 150 nM, $\geq$ 100 nM, $\geq$ 50 nM, $\geq$ 10 nM, $\geq$ 1 nM, $\geq$ 0.1 nM, $\geq$ 0.01 nM, or $\geq$ 0.001 nM.

II. Masked Cytokine Production

[0413] The masked cytokines described herein are prepared using techniques available in the art, exemplary methods of which are described.

A. Antibody Production

[0414] Some embodiments of the masked cytokine comprise an antibody or fragment thereof. The following sections provide further detail on the production of antibodies and antibody fragments, variants, and derivatives thereof, that may be used in some embodiments of the masked cytokine provided herein. In some embodiments, the masked cytokine is in the form of a dimer produced by two copies of a masked cytokine that are associated through disulfide bonds.

1. Antibody Fragments

[0415] The present invention encompasses, in some embodiments, antibody fragments. The antibody fragments can be any antibody fragments, such as an Fc domain, a portion of the heavy chain, a portion of the light chain, an Fab, an Fv, or an scFv, among other fragments. Antibody fragments may be

generated by traditional means, such as enzymatic digestion, or by recombinant techniques. In certain circumstances, there are advantages of linking antibody fragments, rather than whole antibodies, to the masked cytokines described herein. For a review of certain antibody fragments, see Hudson et al. (2003) Nat. Med. 9:129-134.

[0416] Various techniques have been developed for the production of antibody fragments. Traditionally, these fragments were derived via proteolytic digestion of intact antibodies (see, e.g., Morimoto et al., Journal of Biochemical and Biophysical Methods 24:107-117 (1992); and Brennan et al., Science, 229:81 (1985)). However, these fragments can now be produced directly by recombinant host cells. Fab, Fv and ScFv antibody fragments can all be expressed in and secreted from E. coli and other cell types, such as HEK293 and CHO cells, thus allowing the facile production of large amounts of these fragments. Alternatively, Fab′-SH fragments can be directly recovered from culture media and chemically coupled to form F(ab′)2 fragments (Carter et al., Bio/Technology 10: 163-167 (1992)). According to another approach, F(ab′)2 fragments can be isolated directly from recombinant host cell culture. Fab and F(ab′)2 fragments with increased in vivo half-life comprising FcRN / salvage receptor binding epitope residues are described in U.S. Pat. No. 5,869,046. Other techniques for the production of antibody fragments for use in the masked cytokines will be apparent to the skilled practitioner. In certain embodiments, a masked cytokine comprises a single chain Fv fragment (scFv). *See* WO 93/16185; U.S. Pat. Nos. 5,571,894; and 5,587,458. scFv fusion proteins may be constructed to yield fusion of an effector protein at either the amino or the carboxy terminus of an scFv. *See* Antibody Engineering, ed. Borrebaeck, supra. Also, in some embodiments, bi-scFv comprising two scFvs linked via a polypeptide linker can be used with the masked cytokines.

[0417] The present invention includes, in some embodiments, a linear antibody (e.g., as described in U.S. Pat. No. 5,641,870) or a single chain immunoglobulin comprising heavy and light chain sequences of the antibody linked via an appropriate linker. Such linear antibodies or immunoglobulins may be monospecific or bispecific. Such a single chain immunoglobulin can be dimerized to thereby maintain a structure and activities similar to those of the antibody, which is originally a tetramer. Also, in some embodiments, the antibody or fragment thereof may be an antibody that has a single heavy chain variable region and has no light chain sequence. Such an antibody is called a single domain antibody (sdAb) or a nanobody. These antibodies are also encompassed in the meaning of the functional fragment of the antibody according to the present invention. Antibody fragments can be linked to the masked cytokines described herein according to the guidance provided herein.

2. Humanized Antibodies

[0418] The invention encompasses, in some embodiments, humanized antibodies or antibody fragments thereof. In some embodiments, the humanized antibodies can be any antibodies, including any antibody fragment. Various methods for humanizing non-human antibodies are known in the art. For

example, a humanized antibody can have one or more amino acid residues introduced into it from a source which is non-human. These non-human amino acid residues are often referred to as "import" residues, which are typically taken from an "import" variable domain. Humanization can be essentially performed following the method of Winter (Jones et al. (1986) Nature 321:522-525; Riechmann et al. (1988) Nature 332:323-327; Verhoeyen et al. (1988) Science 239:1534-1536), by substituting hypervariable region sequences for the corresponding sequences of a human antibody. Accordingly, such "humanized" antibodies are chimeric antibodies (U.S. Pat. No. 4,816,567) wherein substantially less than an intact human variable domain has been substituted by the corresponding sequence from a non-human species. In practice, humanized antibodies are typically human antibodies in which some hypervariable region residues and possibly some FR residues are substituted by residues from analogous sites in rodent antibodies. Humanized antibodies can be linked to the masked cytokines described herein according to the guidance provided herein.

3. Human Antibodies

[0419] Human antibodies of some embodiments of the invention can be constructed by combining Fv clone variable domain sequence(s) selected from human-derived phage display libraries with known human constant domain sequences(s). Alternatively, human monoclonal antibodies of some embodiments of the invention can be made by the hybridoma method, e.g., by using mouse, rat, bovine (e.g., cow), or rabbit cells, for example, to produce the human monoclonal antibodies. In some embodiments, the human antibodies and human monoclonal antibodies can be antibodies that bind to any antigen. In some embodiments, human monoclonal antibodies of the invention can be made by immunizing a non-human animal that comprises human immunoglobulin loci with the target antigen, and isolating the antibody from the immunized animal or from cells derived from the immunized animal. Examples of suitable non-human animals include a transgenic or transchromosomic animal, such as HuMAb Mouse® (Medarex, Inc.), KM Mouse®, "TC mice," and Xenomouse™. *See, e.g.*, Lonberg, et al. (1994) Nature 368: 856-859; Fishwild, D. et al. (1996) Nature Biotechnology 14: 845-851; WO2002/43478; U.S. Pat. Nos. 5,939,598; 6,075,181; 6,114,598; 6,150,584; 6,162,963; and Tomizuka et al. (2000) Proc. Natl. Acad. Sci. USA 97:722-727.

[0420] Human myeloma and murine-human heteromyeloma cell lines for the production of human monoclonal antibodies have been described, for example, by Kozbor J. Immunol., 133: 3001 (1984); Brodeur et al., Monoclonal Antibody Production Techniques and Applications, pp. 51-63 (Marcel Dekker, Inc., New York, 1987); and Boerner et al., J. Immunol., 147: 86 (1991). Human antibodies can be linked to the masked cytokines described herein according to the guidance provided herein.

4. Bispecific Antibodies

[0421] Bispecific antibodies are monoclonal antibodies that have binding specificities for at least two different antigens. In certain embodiments, bispecific antibodies are human or humanized antibodies. In some embodiments, one of the binding specificities is for a first antigen and the other binding specificity is for a second antigen, which may be either two different epitopes on the same target protein, or two different epitopes on two different target proteins. Bispecific antibodies may also be used to localize cytotoxic agents to cells which express the first antigen and/or the second antigen. Bispecific antibodies may also be used to recruit cells, such as T cells or natural killer cells, to kill certain cells, e.g., cancer cells. Bispecific antibodies can be prepared as full-length antibodies or antibody fragments (e.g. F(ab′)2 bispecific antibodies). Bispecific antibodies can be linked to the masked cytokines described herein according to the guidance provided herein.

[0422] Methods for making bispecific antibodies are known in the art. *See* Milstein and Cuello, Nature, 305: 537 (1983), WO 93/08829 published May 13, 1993, Traunecker et al., EMBO J., 10: 3655 (1991); Kontermann and Brinkmann, Drug Discovery Today, 20(7):838-847. For further details of generating bispecific antibodies see, for example, Suresh et al., Methods in Enzymology, 121:210 (1986). Bispecific antibodies include cross-linked or "heteroconjugate" antibodies. For example, one of the antibodies in the heteroconjugate can be coupled to avidin, the other to biotin. Heteroconjugate antibodies may be made using any convenient cross-linking method. Suitable cross-linking agents are well known in the art, and are disclosed in U.S. Pat. No. 4,676,980, along with a number of cross-linking techniques.

5. Single-Domain Antibodies

[0423] In some embodiments, a single-domain antibody is linked to the masked cytokine in accordance with the guidance provided herein. The single-domain antibody can be any antibody. A single-domain antibody is a single polypeptide chain comprising all or a portion of the heavy chain variable domain or all or a portion of the light chain variable domain of an antibody. In certain embodiments, a single-domain antibody is a human single-domain antibody (Domantis, Inc., Waltham, Mass.; see, e.g., U.S. Pat. No. 6,248,516 B1). In some embodiments, a single-domain antibody consists of all or a portion of the heavy chain variable domain of an antibody. In some embodiment, the single domain antibody is a camelid-derived antibody obtained by immunization of a camelid with the target antigen. In some embodiments, the single domain antibody is a shark-derived antibody obtained by immunization of a shark with the target antigen. In some embodiments, the single domain antibody is a Nanobody (*see, e.g.*, WO 2004041865A2 and US20070269422A1).

6. Antibody Variants

[0424] In some embodiments, amino acid sequence modification(s) of the antibodies or fragments thereof described herein are contemplated. For example, it may be desirable to improve the FcRn-

binding affinity and/or pH-dependent FcRn-binding affinity of the antibody. It may also be desirable to promote heterodimerization of antibody heavy chains by introducing certain amino acid modifications. Methods for promoting heterodimerization of antibody chains, including certain modifications that can be made to facilitate heterodimerization, is described by Klein et al. (2012), MAbs, 4(6): 653-663.

[0425] Amino acid sequence variants of the antibody may be prepared by introducing appropriate changes into the nucleotide sequence encoding the antibody, or by peptide synthesis. Such modifications include, for example, deletions from, and/or insertions into and/or substitutions of, residues within the amino acid sequences of the antibody. Any combination of deletion, insertion, and substitution can be made to arrive at the final construct, provided that the final construct possesses the desired characteristics. The amino acid alterations may be introduced in the subject antibody amino acid sequence at the time that sequence is made.

[0426] A useful method for identification of certain residues or regions of the antibody that are preferred locations for mutagenesis is called "alanine scanning mutagenesis" as described by Cunningham and Wells (1989) Science, 244:1081-1085. Here, a residue or group of target residues are identified (e.g., charged residues such as arg, asp, his, lys, and glu) and replaced by a neutral or negatively charged amino acid (e.g., alanine or polyalanine) to affect the interaction of the amino acids with antigen. Those amino acid locations demonstrating functional sensitivity to the substitutions then are refined by introducing further or other variants at, or for, the sites of substitution. Thus, while the site for introducing an amino acid sequence variation is predetermined, the nature of the mutation per se need not be predetermined. For example, to analyze the performance of a mutation at a given site, ala scanning or random mutagenesis is conducted at the target codon or region and the expressed immunoglobulins are screened for the desired activity.

[0427] Amino acid sequence insertions include amino- and/or carboxyl-terminal fusions ranging in length from one residue to polypeptides containing a hundred or more residues, as well as intrasequence insertions of single or multiple amino acid residues. Examples of terminal insertions include an antibody with an N-terminal methionyl residue. Other insertional variants of the antibody molecule include the fusion to the N- or C-terminus of the antibody to an enzyme or a polypeptide which increases the serum half-life of the antibody.

[0428] In some embodiments, the masked cytokine is modified to eliminate, reduce, or otherwise hinder protease cleavage near the hinge region. The "hinge region" of an IgG is generally defined as including E216 and terminating at P230 of human IgG1 according to the EU index as in Kabat, but, functionally, the flexible portion of the chain may be considered to include additional residues termed the upper and lower hinge regions, such as from E216 to G237 (Roux et al., 1998 J Immunol 161:4083) and the lower hinge has been referred to as residues 233 to 239 of the Fc region where FcγR binding was generally attributed. Modifications to any of the masked cytokines described herein, can be performed,

for example, according to the methods described in US 20150139984A1, which is incorporated herein by reference, as well as by incorporating any of the modifications described therein.

[0429] In some embodiments, FcRn mutations that improve pharmacokinetics include, but are not limited to, M428L, T250Q/M428L, M252Y/S254T/T256E, P257I/N434H, D376V/N434H, P257I/Q3111, N434A, N434W, M428L/N434S, V259I/V308F, M252Y/S254T/T256E, V259I/V308F/M428L, T307Q/N434A, T307Q/N434S, T307Q/E380A/N434A, V308P/N434A, N434H, V308P. In some embodiments, such mutations enhance antibody binding to FcRn at low pH but do not change the antibody affinity at neutral pH.

[0430] In certain embodiments, an antibody or fragment thereof is altered to increase or decrease the extent to which the antibody is glycosylated. Glycosylation of polypeptides is typically either N-linked or O-linked. N-linked refers to the attachment of a carbohydrate moiety to the side chain of an asparagine residue. The tripeptide sequences asparagine-X-serine and asparagine-X-threonine, where X is any amino acid except proline, are the recognition sequences for enzymatic attachment of the carbohydrate moiety to the asparagine side chain. Thus, the presence of either of these tripeptide sequences in a polypeptide creates a potential glycosylation site. O-linked glycosylation refers to the attachment of one of the sugars N-aceylgalactosamine, galactose, or xylose to a hydroxyamino acid, most commonly serine or threonine, although 5-hydroxyproline or 5-hydroxylysine may also be used.

[0431] Addition or deletion of glycosylation sites to the masked cytokine is conveniently accomplished by altering the amino acid sequence such that one or more of the above-described tripeptide sequences (for N-linked glycosylation sites) is created or removed. The alteration may also be made by the addition, deletion, or substitution of one or more serine or threonine residues to the sequence of the original antibody (for O-linked glycosylation sites).

[0432] Where the antibody or fragment thereof comprises an Fc region, the carbohydrate attached thereto may be altered. For example, antibodies with a mature carbohydrate structure that lacks fucose attached to an Fc region of the antibody are described in US Pat Appl No US 2003/0157108 (Presta, L.). See also US 2004/0093621 (Kyowa Hakko Kogyo Co., Ltd). Antibodies with a bisecting N-acetylglucosamine (GlcNAc) in the carbohydrate attached to an Fc region of the antibody are referenced in WO 2003/011878, Jean-Mairet et al. and U.S. Pat. No. 6,602,684, Umana et al. Antibodies with at least one galactose residue in the oligosaccharide attached to an Fc region of the antibody are reported in WO 1997/30087, Patel et al. See, also, WO 1998/58964 (Raju, S.) and WO 1999/22764 (Raju, S.) concerning antibodies with altered carbohydrate attached to the Fc region thereof. See also US 2005/0123546 (Umana et al.) on antigen-binding molecules with modified glycosylation.

[0433] In certain embodiments, a glycosylation variant comprises an Fc region, wherein a carbohydrate structure attached to the Fc region lacks fucose or has reduced fucose. Such variants have improved ADCC function. Optionally, the Fc region further comprises one or more amino acid substitutions therein which further improve ADCC, for example, substitutions at positions 298, 333,

and/or 334 of the Fc region (Eu numbering of residues). Examples of publications related to "defucosylated" or "fucose-deficient" antibodies include: US 2003/0157108; WO 2000/61739; WO 2001/29246; US 2003/0115614; US 2002/0164328; US 2004/0093621; US 2004/0132140; US 2004/0110704; US 2004/0110282; US 2004/0109865; WO 2003/085119; WO 2003/084570; WO 2005/035586; WO 2005/035778; WO2005/053742; Okazaki et al. J. Mol. Biol. 336:1239-1249 (2004); Yamane-Ohnuki et al. Biotech. Bioeng. 87: 614 (2004). Examples of cell lines producing defucosylated antibodies include Lec13 CHO cells deficient in protein fucosylation (Ripka et al. Arch. Biochem. Biophys. 249:533-545 (1986); US Pat Appl No US 2003/0157108 A1, Presta, L; and WO 2004/056312 A1, Adams et al., especially at Example 11), and knockout cell lines, such as alpha-1,6-fucosyltransferase gene, FUT8, knockout CHO cells (Yamane-Ohnuki et al. Biotech. Bioeng. 87: 614 (2004)), and cells overexpressing β1,4-N-acetylglycosminyltransferase III (GnT-III) and Golgi μ-mannosidase II (ManII).

[0434] In any of the embodiments herein, the masked cytokine can be engineered to improve antibody-dependent cell-mediated cytotoxicity (ADCC) activity. In some embodiments, the masked cytokine may be produced in a cell line having a alpha1,6-fucosyltransferase (Fut8) knockout. In some embodiments, the host cells have been modified to have reduced intrinsic alpha1,6-fucosylation activity. Examples of methods for modifying the fucosylation pathways in mammalian host cells can be found in, e.g., Yamane-Ohnuki and Satoh, MAbs, 1(3): 230-236 (2009), the contents of which are incorporated herein by reference. Examples of methods and compositions for partially or completely inactivating the expression of the FUT8 gene can be found in, e.g., US Pub. No. 20160194665A1; WO2006133148A2, the contents of which are incorporated herein by reference. In some embodiments, the masked cytokine is produced in the Lec13 variant of CHO cells (see, e.g., Shields et al., J. Biol. Chem., 277(30):26733-40 (2002)) or the YB2/0 cell line having reduced FUT8 activity (see, e.g., Shinkawa et al., J. Biol. Chem., 278(5): 3466-73 (2003)). In some embodiments, small interfering RNA (siRNA) against genes relevant to alpha1,6-fucosylation can be introduced (see, e.g., Mori et al., Biotechnol. Bioeng. 88(7): 901-908 (2004); Imai-Nishiya et al., BMC Biotechnol. 7: 84 (2007); Omasa et al., J. Biosci. Bioeng., 106(2): 168-173 (2008)). In some further embodiments, the masked cytokine may be produced in a cell line overexpressing β1,4-N-acetylglycosminyltransferase III (GnT-III). In further embodiments, the cell line additionally overexpresses Golgi μ-mannosidase II (ManII). In some of the embodiments herein, the masked cytokine may comprise at least one amino acid substitution in the Fc region that improves ADCC activity.

[0435] In some embodiments, the masked cytokine is altered to improve its serum half-life. To increase the serum half-life of the cytokine, one may incorporate a FcRN /salvage receptor binding epitope into a linked antibody (especially an antibody fragment) as described in U.S. Pat. No. 5,739,277, for example. As used herein, the term "salvage receptor binding epitope" refers to an epitope of the Fc region of an IgG molecule (e.g., IgG1, IgG2, IgG3, or IgG4) that is responsible for increasing the in vivo

serum half-life of the IgG molecule (US 2003/0190311, U.S. Pat. No. 6,821,505; U.S. Pat. No. 6,165,745; U.S. Pat. No. 5,624,821; U.S. Pat. No. 5,648,260; U.S. Pat. No. 6,165,745; U.S. Pat. No. 5,834,597).

[0436] Another type of variant is an amino acid substitution variant. These variants have at least one amino acid residue in the antibody molecule replaced by a different residue. Sites of interest for substitutional mutagenesis include the hypervariable regions, but FR alterations are also contemplated. Conservative substitutions are shown in Table 3 under the heading of "preferred substitutions." If such substitutions result in a desirable change in biological activity, then more substantial changes, denominated "exemplary substitutions" in Table 3, or as further described below in reference to amino acid classes, may be introduced and the products screened.

Table 3

Original Residue	Exemplary Substitutions	Preferred Substitutions
Ala (A)	Val; Leu; Ile	Val
Arg (R)	Lys; Gln; Asn	Lys
Asn (N)	Gln; His; Asp, Lys; Arg	Gln
Asp (D)	Glu; Asn	Glu
Cys (C)	Ser; Ala	Ser
Gln (Q)	Asn; Glu	Asn
Glu (E)	Asp; Gln	Asp
Gly (G)	Ala	Ala
His (H)	Asn; Gln; Lys; Arg	Arg
Ile (I)	Leu; Val; Met; Ala; Phe; Norleucine	Leu
Leu (L)	Norleucine; Ile; Val; Met; Ala; Phe	Ile
Lys (K)	Arg; Gln; Asn	Arg
Met (M)	Leu; Phe; Ile	Leu
Phe (F)	Trp; Leu; Val; Ile; Ala; Tyr	Tyr
Pro (P)	Ala	Ala
Ser (S)	Thr	Thr
Thr (T)	Val; Ser	Ser
Trp (W)	Tyr; Phe	Tyr
Tyr (Y)	Trp; Phe; Thr; Ser	Phe
Val (V)	Ile; Leu; Met; Phe; Ala; Norleucine	Leu

[0437] Substantial modifications in the biological properties of the antibody are accomplished by selecting substitutions that differ significantly in their effect on maintaining (a) the structure of the polypeptide backbone in the area of the substitution, for example, as a sheet or helical conformation, (b) the charge or hydrophobicity of the molecule at the target site, or c) the bulk of the side chain. Amino acids may be grouped according to similarities in the properties of their side chains (in A. L. Lehninger, in Biochemistry, second ed., pp. 73-75, Worth Publishers, New York (1975)):

(1) non-polar: Ala (A), Val (V), Leu (L), Ile (I), Pro (P), Phe (F), Trp (W), Met (M)

(2) uncharged polar: Gly (G), Ser (S), Thr (T), Cys (C), Tyr (Y), Asn (N), Gln (Q)

(3) acidic: Asp (D), Glu (E)

(4) basic: Lys (K), Arg (R), His (H)

[0438] Alternatively, naturally occurring residues may be divided into groups based on common side-chain properties:

(1) hydrophobic: Norleucine, Met, Ala, Val, Leu, Ile;

(2) neutral hydrophilic: Cys, Ser, Thr, Asn, Gln;

(3) acidic: Asp, Glu;

(4) basic: His, Lys, Arg;

(5) residues that influence chain orientation: Gly, Pro;

(6) aromatic: Trp, Tyr, Phe.

[0439] Non-conservative substitutions will entail exchanging a member of one of these classes for another class. Such substituted residues also may be introduced into the conservative substitution sites or, into the remaining (non-conserved) sites.

[0440] Another type of substitutional variant involves the substitution of a naturally occurring amino acid residue for a non-naturally occurring amino acid residue. Non-naturally occurring amino acid residues can be incorporated, e.g., through tRNA recoding, or through any of the methods as described, e.g., in WO 2016154675A1, which is incorporated herein by reference.

[0441] One type of substitutional variant involves substituting one or more hypervariable region residues of a parent antibody (e.g., a humanized or human antibody). Generally, the resulting variant(s) selected for further development will have modified (e.g., improved) biological properties relative to the parent antibody from which they are generated. A convenient way for generating such substitutional variants involves affinity maturation using phage display, yeast display, or mammalian display. Briefly, several hypervariable region sites (e.g., 6-7 sites) are mutated to generate all possible amino acid substitutions at each site. The antibodies thus generated are displayed from filamentous phage particles as fusions to at least part of a phage coat protein (e.g., the gene III product of M13) packaged within each particle. The phage-displayed variants are then screened for their biological activity (e.g., binding affinity). In order to identify candidate hypervariable region sites for modification, scanning mutagenesis (e.g., alanine scanning) can be performed to identify hypervariable region residues contributing significantly to antigen binding. Alternatively, or additionally, it may be beneficial to analyze a crystal structure of the antigen-antibody complex to identify contact points between the antibody and antigen. Such contact residues and neighboring residues are candidates for substitution according to techniques known in the art, including those elaborated herein. Once such variants are generated, the panel of variants is subjected to screening using techniques known in the art, including those described herein,

and antibodies with superior properties in one or more relevant assays may be selected for further development.

[0442] Nucleic acid molecules encoding amino acid sequence variants of the masked cytokines are prepared by a variety of methods known in the art. These methods include, but are not limited to, isolation from a natural source (in the case of naturally occurring amino acid sequence variants) or preparation by oligonucleotide-mediated (or site-directed) mutagenesis, PCR mutagenesis, and cassette mutagenesis of an earlier prepared variant or a non-variant version of the antibody, for example.

[0443] It may be desirable to introduce one or more amino acid modifications in an Fc region of antibodies of the invention, thereby generating an Fc region variant. The Fc region variant may comprise a human Fc region sequence (e.g., a human IgG1, IgG2, IgG3 or IgG4 Fc region) comprising an amino acid modification (e.g. a substitution) at one or more amino acid positions including that of a hinge cysteine.

[0444] In some embodiments, a masked cytokine provided herein includes an antibody or fragment thereof having an IgG1, IgG2, IgG3, or IgG4 isotype with enhanced effector function. In some embodiments, a masked cytokine provided herein includes an antibody or fragment thereof having an IgG1 isotype with enhanced effector function. In some embodiments, a masked cytokine provided herein (e.g., a masked IL-2 polypeptide or functional fragment thereof or a masked IL-15 polypeptide or functional fragment thereof) has an IgG1 isotype with enhanced effector function. In some embodiments, the masked cytokine is afucosylated. In some embodiments, the masked cytokine has increased levels of mannose moieties. In some embodiments, the masked cytokine has increased levels of bisecting glycan moieties. In some embodiments, the IgG1 comprises amino acid mutations.

[0445] In some embodiments, a masked cytokine provided herein includes an antibody having an IgG1 isotype (e.g., a human IgG1 isotype). In some embodiments, the IgG1 comprises one or more amino acid substitutions that enhance effector function. In one embodiment, the IgG1 comprises the amino acid substitutions S298A, E333A, and K334A wherein the amino acid residues are numbered according to the EU index as in Kabat. In one embodiment, the IgG1 comprises the amino acid substitutions S239D and I332E wherein the amino acid residues are numbered according to the EU index as in Kabat. In one embodiment, the IgG1 comprises the amino acid substitutions S239D, A330L, and I332E wherein the amino acid residues are numbered according to the EU index as in Kabat. In one embodiment, the IgG1 comprises the amino acid substitutions P247I and A339D or A339Q wherein the amino acid residues are numbered according to the EU index as in Kabat. In one embodiment, the IgG1 comprises the amino acid substitutions D280H, K290S with or without S298D or S298V wherein the amino acid residues are numbered according to the EU index as in Kabat. In one embodiment, the IgG1 comprises the amino acid substitutions F243L, R292P, and Y300L wherein the amino acid residues are numbered according to the EU index as in Kabat. In one embodiment, the IgG1 comprises the amino acid substitutions F243L, R292P, Y300L, and P396L wherein the amino acid residues are numbered

according to the EU index as in Kabat. In one embodiment, the IgG1 comprises the amino acid substitutions F243L, R292P, Y300L, V305I, and P396L wherein the amino acid residues are numbered according to the EU index as in Kabat. In one embodiment, the IgG1 comprises the amino acid substitutions G236A, S239D, and I332E wherein the amino acid residues are numbered according to the EU index as in Kabat. In one embodiment, the IgG1 comprises the amino acid substitutions K326A and E333A wherein the amino acid residues are numbered according to the EU index as in Kabat. In one embodiment, the IgG1 comprises the amino acid substitutions K326W and E333S wherein the amino acid residues are numbered according to the EU index as in Kabat. In one embodiment, the IgG1 comprises the amino acid substitutions K290E, S298G, T299A, with or without K326E wherein the amino acid residues are numbered according to the EU index as in Kabat. In one embodiment, the IgG1 comprises the amino acid substitutions K290N, S298G, T299A, with or without K326E wherein the amino acid residues are numbered according to the EU index as in Kabat. In one embodiment, the IgG1 comprises the amino acid substitution K334V wherein the amino acid residues are numbered according to the EU index as in Kabat. In one embodiment, the IgG1 comprises the amino acid substitutions L235S, S239D, and K334V wherein the amino acid residues are numbered according to the EU index as in Kabat. In one embodiment, the IgG1 comprises the amino acid substitutions K334V and Q331M, S239D, F243V, E294L, or S298T wherein the amino acid residues are numbered according to the EU index as in Kabat. In one embodiment, the IgG1 comprises the amino acid substitutions E233L, Q311M, and K334V wherein the amino acid residues are numbered according to the EU index as in Kabat. In one embodiment, the IgG1 comprises the amino acid substitutions L234I, Q311M, and K334V wherein the amino acid residues are numbered according to the EU index as in Kabat. In one embodiment, the IgG1 comprises the amino acid substitutions K334V and S298T, A330M, or A330F wherein the amino acid residues are numbered according to the EU index as in Kabat. In one embodiment, the IgG1 comprises the amino acid substitutions K334V, Q311M, and either A330M or A330F wherein the amino acid residues are numbered according to the EU index as in Kabat. In one embodiment, the IgG1 comprises the amino acid substitutions K334V, S298T, and either A330M or A330F wherein the amino acid residues are numbered according to the EU index as in Kabat. In one embodiment, the IgG1 comprises the amino acid substitutions K334V, S239D, and either A330M or S298T wherein the amino acid residues are numbered according to the EU index as in Kabat. In one embodiment, the IgG1 comprises the amino acid substitutions L234Y, Y296W, and K290Y, F243V, or E294L wherein the amino acid residues are numbered according to the EU index as in Kabat. In one embodiment, the IgG1 comprises the amino acid substitutions Y296W and either L234Y or K290Y wherein the amino acid residues are numbered according to the EU index as in Kabat. In one embodiment, the IgG1 comprises the amino acid substitutions S239D, A330S, and I332E wherein the amino acid residues are numbered according to the EU index as in Kabat.

[0446] In some embodiments, the IgG1 comprises one or more amino acid substitutions that decrease or inhibit effector function. In one embodiment, the IgG1 comprises the amino acid substitution N297A, N297G, or N297Q wherein the amino acid residues are numbered according to the EU index as in Kabat. In one embodiment, the IgG1 comprises the amino acid substitution L234A or L235A wherein the amino acid residues are numbered according to the EU index as in Kabat. In one embodiment, the IgG1 comprises the amino acid substitutions C220S, C226S, C229S, and P238S wherein the amino acid residues are numbered according to the EU index as in Kabat. In one embodiment, the IgG1 comprises the amino acid substitutions C226S, C229S, E233P, L234V, and L235A wherein the amino acid residues are numbered according to the EU index as in Kabat. In one embodiment, the IgG1 comprises the amino acid substitutions L234F, L235E, and P331S wherein the amino acid residues are numbered according to the EU index as in Kabat. In one embodiment, the IgG1 comprises the amino acid substitutions S267E and L328F wherein the amino acid residues are numbered according to the EU index as in Kabat.

[0447] In accordance with this description and the teachings of the art, it is contemplated that in some embodiments, an antibody or fragment thereof of the masked cytokine may comprise one or more alterations as compared to the wild type counterpart antibody, e.g. in the Fc region. For example, it is thought that certain alterations can be made in the Fc region that would result in altered (i.e., either improved or diminished) C1q binding and/or Complement Dependent Cytotoxicity (CDC), e.g., as described in WO99/51642. See also Duncan & Winter Nature 322:738-40 (1988); U.S. Pat. No. 5,648,260; U.S. Pat. No. 5,624,821; and WO94/29351 concerning other examples of Fc region variants. WO00/42072 (Presta) and WO 2004/056312 (Lowman) describe antibody variants with improved or diminished binding to FcRs. The content of these patent publications are specifically incorporated herein by reference. *See also* Shields et al. J. Biol. Chem. 9(2): 6591-6604 (2001). Antibodies with increased half-lives and improved binding to the neonatal Fc receptor (FcRn), which is responsible for the transfer of maternal IgGs to the fetus (Guyer et al., J. Immunol. 117:587 (1976) and Kim et al., J. Immunol. 24:249 (1994)), are described in US2005/0014934A1 (Hinton et al.). These antibodies comprise an Fc region with one or more substitutions therein which improve binding of the Fc region to FcRn. Polypeptide variants with altered Fc region amino acid sequences and increased or decreased C1q binding capability are described in U.S. Pat. No. 6,194,551B1, WO99/51642. The contents of those patent publications are specifically incorporated herein by reference. See, also, Idusogie et al. J. Immunol. 164: 4178-4184 (2000).

B. Masked Cytokine-Drug Conjugates

[0448] The invention also provides masked cytokine-drug conjugates (MCDCs) comprising a masked cytokine provided herein, which can be any masked cytokine disclosed herein, conjugated to one or more agents. In some embodiments, the one or more agents is a cytotoxic agent, such as a chemotherapeutic agent or drug, growth inhibitory agent, toxin (e.g., protein toxin, enzymatically active

toxin of bacterial, fungal, plant, or animal origin, or fragments thereof), or radioactive isotopes. In some embodiments, the one or more agents is an immune stimulant.

[0449] In some embodiments, the one or more drugs conjugated to the masked cytokine includes, but is not limited to, a maytansinoid (see U.S. Patent Nos. 5,208,020, 5,416,064 and European Patent EP 0 425 235 B1); an auristatin such as monomethylauristatin drug moieties DE and DF (MMAE and MMAF) (see U.S. Patent Nos. 5,635,483 and 5,780,588, and 7,498,298); a dolastatin; a calicheamicin or derivative thereof (see U.S. Patent Nos. 5,712,374, 5,714,586, 5,739,116, 5,767,285, 5,770,701, 5,770,710, 5,773,001, and 5,877,296; Hinman et al., Cancer Res. 53:3336-3342 (1993); and Lode et al., Cancer Res. 58:2925-2928 (1998)); an anthracycline such as daunomycin or doxorubicin (see Kratz et al., Current Med. Chem. 13:477-523 (2006); Jeffrey et al., Bioorganic & Med. Chem. Letters 16:358-362 (2006); Torgov et al., Bioconj. Chem. 16:717-721 (2005); Nagy et al., Proc. Natl. Acad. Sci. USA 97:829-834 (2000); Dubowchik et al., Bioorg. & Med. Chem. Letters 12:1529-1532 (2002); King et al., J. Med. Chem. 45:4336-4343 (2002); and U.S. Patent No. 6,630,579); methotrexate; vindesine; a taxane such as docetaxel, paclitaxel, larotaxel, tesetaxel, and ortataxel; a trichothecene; and CC1065.

[0450] In another embodiment, the one or more drugs conjugated to the masked cytokine includes, but is not limited to, an inhibitor of tubulin polymerization (e.g., maytansinoids and auristatins), DNA damaging agents (e.g., pyrrolobenzodiazepine (PBD) dimers, calicheamicins, duocarmycins and indolinobenzodiazepine dimers), and DNA synthesis inhibitors (e.g., exatecan derivative Dxd).

[0451] In another embodiment, a masked cytokine-drug conjugate comprises a masked cytokine as described herein conjugated to an enzymatically active toxin or fragment thereof, including, but not limited to, diphtheria A chain, nonbinding active fragments of diphtheria toxin, exotoxin A chain (from Pseudomonas aeruginosa), ricin A chain, abrin A chain, modeccin A chain, alpha-sarcin, Aleurites fordii proteins, dianthin proteins, Phytolaca americana proteins (PAPI, PAPII, and PAP-S), momordica charantia inhibitor, curcin, crotin, sapaonaria officinalis inhibitor, gelonin, mitogellin, restrictocin, phenomycin, enomycin, and the tricothecenes.

[0452] In another embodiment, a masked cytokine-drug conjugate comprises a masked cytokine as described herein conjugated to a radioactive atom to form a radioconjugate. A variety of radioactive isotopes are available for the production of radioconjugates. Examples include At211, I131, I125, Y90, Re186, Re188, Sm153, Bi212, P32, Pb212 and radioactive isotopes of Lu. When the radioconjugate is used for detection, it may comprise a radioactive atom for scintigraphic studies, for example tc99m or I123, or a spin label for nuclear magnetic resonance (NMR) imaging (also known as magnetic resonance imaging, mri), such as iodine-123 again, iodine-131, indium-111, fluorine-19, carbon-13, nitrogen-15, oxygen-17, gadolinium, manganese or iron.

[0453] In some embodiments, a masked cytokine-drug conjugate comprises a masked cytokine as described herein conjugated to one or more immune stimulants. In some embodiments, the immune stimulant is a stimulator of interferon genes (STING) agonist or a toll-like receptor (TLR) agonist.

[0454] The STING agonist can be any agonist of STING. In some embodiments, the STING agonist is a cyclic dinucleotide (CDN). The CDN can be any CDN or derivative or variant thereof. In some embodiments, the STING agonist is a CDN selected from the group consisting of cGAMP, c-di-AMP, c-di-GMP, cAIMP, and c-di-IMP. In some embodiments, the STING agonist is a derivative or variant of a CDN selected from the group consisting of cGAMP, c-di-AMP, c-di-GMP, cAIMP, and c-di-IMP. In some embodiments, the STING agonist is 4-(2-chloro-6-fluorobenzyl)-N-(furan-2-ylmethyl)-3-oxo-3,4-dihydro-2H-benzo[b][1,4]thiazine-6-carboxamide, or a derivative or variant thereof. *See, e.g.*, Sali et al. (2015) PloS Pathog., 11(12): e1005324.

[0455] The TLR agonist can be an agonist of any TLR, such as TLR1, TLR2, TLR3, TLR4, TLR5, TLR6, TLR7, TLR8, TLR9, or TLR10. In some embodiments, the TLR agonist is an agonist of a TLR expressed on the cell surface, such as TLR1, TLR2, TLR4, or TLR5. In some embodiments, the TLR agonist is an agonist of a TLR expressed intracellularly, such as TLR3, TLR7, TLR8, TLR9, or TLR10.

[0456] Conjugates of a masked cytokine and a cytotoxic agent may be made using a variety of bifunctional protein coupling agents such as N-succinimidyl-3-(2-pyridyldithio) propionate (SPDP), succinimidyl-4-(N-maleimidomethyl) cyclohexane-1-carboxylate (SMCC), iminothiolane (IT), bifunctional derivatives of imidoesters (such as dimethyl adipimidate HCl), active esters (such as disuccinimidyl suberate), aldehydes (such as glutaraldehyde), bis-azido compounds (such as bis (p-azidobenzoyl) hexanediamine), bis-diazonium derivatives (such as bis-(p-diazoniumbenzoyl)-ethylenediamine), diisocyanates (such as toluene 2,6-diisocyanate), and bis-active fluorine compounds (such as 1,5-difluoro-2,4-dinitrobenzene). For example, a ricin immunotoxin can be prepared as described in Vitetta et al., Science 238:1098 (1987). Carbon-14-labeled 1-isothiocyanatobenzyl-3-methyldiethylene triaminepentaacetic acid (MX-DTPA) is an exemplary chelating agent for conjugation of radionucleotide to an antibody. *See* WO94/11026. The linker may be a "cleavable linker" facilitating release of a cytotoxic drug in the cell. For example, an acid-labile linker, peptidase-sensitive linker, photolabile linker, dimethyl linker or disulfide-containing linker (Chari et al., Cancer Res. 52:127-131 (1992); U.S. Patent No. 5,208,020) may be used.

[0457] The MCDCs herein expressly contemplate, but are not limited to such conjugates prepared with cross-linker reagents including, but not limited to, BMPS, EMCS, GMBS, HBVS, LC-SMCC, MBS, MPBH, SBAP, SIA, SIAB, SMCC, SMPB, SMPH, sulfo-EMCS, sulfo-GMBS, sulfo-KMUS, sulfo-MBS, sulfo-SIAB, sulfo-SMCC, and sulfo-SMPB, and SVSB (succinimidyl-(4-vinylsulfone)benzoate) which are commercially available (e.g., from Pierce Biotechnology, Inc., Rockford, IL., U.S.A).

C. Vectors, Host Cells, and Recombinant Methods

[0458] For recombinant production of a masked cytokine of the invention, the one or more nucleic acids encoding it is isolated and inserted into a replicable vector for further cloning (amplification of the

DNA) or for expression. DNA encoding the masked cytokine, including components thereof, is readily isolated and sequenced using conventional procedures. Many vectors are available. The choice of vector depends in part on the host cell to be used. Generally, host cells are of either prokaryotic or eukaryotic (generally mammalian) origin. It will be appreciated that constant regions of any isotype of antibody or fragment thereof, when applicable, can be used for this purpose, including IgG, IgM, IgA, IgD, and IgE constant regions, and that such constant regions can be obtained from any human or animal species. In some embodiments, one vector is used to encode the masked cytokine. In some embodiments, more than one vector is used to encode the masked cytokine.

1. Generating Masked Cytokines Using Prokaryotic Host Cells

a. Vector Construction

[0459] Polynucleotide sequences encoding polypeptide components of the masked cytokines of the invention can be obtained using standard recombinant techniques. Desired polynucleotide sequences of an antibody or antibody fragment thereof may be isolated and sequenced from antibody producing cells such as hybridoma cells. Alternatively, polynucleotides can be synthesized using nucleotide synthesizer or PCR techniques, or obtained from other sources. Once obtained, sequences encoding the components of the masked cytokine are inserted into a recombinant vector capable of replicating and expressing heterologous polynucleotides in prokaryotic hosts. Many vectors that are available and known in the art can be used for the purpose of the present invention. Selection of an appropriate vector will depend mainly on the size of the nucleic acids to be inserted into the vector and the particular host cell to be transformed with the vector. Each vector contains various components, depending on its function (amplification or expression of heterologous polynucleotide, or both) and its compatibility with the particular host cell in which it resides. The vector components generally include, but are not limited to: an origin of replication, a selection marker gene, a promoter, a ribosome binding site (RBS), a signal sequence, the heterologous nucleic acid insert and a transcription termination sequence.

[0460] In general, plasmid vectors containing replicon and control sequences which are derived from species compatible with the host cell are used in connection with these hosts. The vector ordinarily carries a replication site, as well as marking sequences which are capable of providing phenotypic selection in transformed cells. For example, E. coli is typically transformed using pBR322, a plasmid derived from an E. coli species. pBR322 contains genes-encoding ampicillin (Amp) and tetracycline (Tet) resistance and thus provides easy means for identifying transformed cells. pBR322, its derivatives, or other microbial plasmids or bacteriophage may also contain, or be modified to contain, promoters which can be used by the microbial organism for expression of endogenous proteins. Examples of pBR322 derivatives used for expression of particular antibodies are described in detail in Carter et al., U.S. Pat. No. 5,648,237.

[0461] In addition, phage vectors containing replicon and control sequences that are compatible with the host microorganism can be used as transforming vectors in connection with these hosts. For example, bacteriophage such as λGEM.TM.-11 may be utilized in making a recombinant vector which can be used to transform susceptible host cells such as E. coli LE392.

[0462] The expression vector of the invention may comprise two or more promoter-cistron pairs, encoding each of the polypeptide components. A promoter is an untranslated regulatory sequence located upstream (5′) to a cistron that modulates its expression. Prokaryotic promoters typically fall into two classes, inducible and constitutive. Inducible promoter is a promoter that initiates increased levels of transcription of the cistron under its control in response to changes in the culture condition, e.g. the presence or absence of a nutrient or a change in temperature.

[0463] A large number of promoters recognized by a variety of potential host cells are well known. The selected promoter can be operably linked to cistron DNA encoding either chain of the masked cytokine by removing the promoter from the source DNA via restriction enzyme digestion and inserting the isolated promoter sequence into the vector of the invention. Both the native promoter sequence and many heterologous promoters may be used to direct amplification and/or expression of the target genes. In some embodiments, heterologous promoters are utilized, as they generally permit greater transcription and higher yields of expressed target gene as compared to the native target polypeptide promoter.

[0464] Promoters suitable for use with prokaryotic hosts include the PhoA promoter, the β-galactamase and lactose promoter systems, a tryptophan (trp) promoter system and hybrid promoters such as the tac or the trc promoter. However, other promoters that are functional in bacteria (such as other known bacterial or phage promoters) are suitable as well. Their nucleotide sequences have been published, thereby enabling a skilled worker operably to ligate them to cistrons encoding, for example, the target light and heavy chains for masked cytokines comprising a light and heavy chain (Siebenlist et al. (1980) Cell 20: 269) using linkers or adaptors to supply any required restriction sites.

[0465] In one aspect of the invention, each cistron within the recombinant vector comprises a secretion signal sequence component that directs translocation of the expressed polypeptides across a membrane. In general, the signal sequence may be a component of the vector, or it may be a part of the target polypeptide DNA that is inserted into the vector. The signal sequence selected for the purpose of this invention should be one that is recognized and processed (i.e. cleaved by a signal peptidase) by the host cell. For prokaryotic host cells that do not recognize and process the signal sequences native to the heterologous polypeptides, the signal sequence is substituted by a prokaryotic signal sequence selected, for example, from the group consisting of the alkaline phosphatase, penicillinase, Ipp, or heat-stable enterotoxin II (STII) leaders, LamB, PhoE, PelB, OmpA and MBP. In one embodiment of the invention, the signal sequences used in both cistrons of the expression system are STII signal sequences or variants thereof.

[0466] In another aspect, the production of the polypeptide components according to the invention can occur in the cytoplasm of the host cell, and therefore does not require the presence of secretion signal sequences within each cistron. In that regard, for embodiments comprising immunoglobulin light and heavy chains, for example, the light and heavy chains are expressed with or without the sequences for the masking moiety, linker sequence, etc., folded and assembled to form functional immunoglobulins within the cytoplasm. Certain host strains (e.g., the E. coli trxB-strains) provide cytoplasm conditions that are favorable for disulfide bond formation, thereby permitting proper folding and assembly of expressed protein subunits. Proba and Pluckthun Gene, 159:203 (1995).

[0467] Masked cytokines of the invention can also be produced by using an expression system in which the quantitative ratio of expressed polypeptide components can be modulated in order to maximize the yield of secreted and properly assembled antibodies of the invention. Such modulation is accomplished at least in part by simultaneously modulating translational strengths for the polypeptide components.

[0468] Prokaryotic host cells suitable for expressing masked cytokines of the invention include Archaebacteria and Eubacteria, such as Gram-negative or Gram-positive organisms. Examples of useful bacteria include Escherichia (e.g., E. coli), Bacilli (e.g., B. subtilis), Enterobacteria, Pseudomonas species (e.g., P. aeruginosa), Salmonella typhimurium, Serratia marcescans, Klebsiella, Proteus, Shigella, Rhizobia, Vitreoscilla, or Paracoccus. In one embodiment, gram-negative cells are used. In one embodiment, E. coli cells are used as hosts for the invention. Examples of E. coli strains include strain W3110 (Bachmann, Cellular and Molecular Biology, vol. 2 (Washington, D.C.: American Society for Microbiology, 1987), pp. 1190-1219; ATCC Deposit No. 27,325) and derivatives thereof, including strain 33D3 having genotype W3110 ΔfhuA (ΔtonA) ptr3 lac Iq lacL8 ΔompTΔ(nmpc-fepE) degP41 kanR (U.S. Pat. No. 5,639,635). Other strains and derivatives thereof, such as E. coli 294 (ATCC 31,446), E. coli B, E. coliλ 1776 (ATCC 31,537) and E. coli RV308(ATCC 31,608) are also suitable. These examples are illustrative rather than limiting. Methods for constructing derivatives of any of the above-mentioned bacteria having defined genotypes are known in the art and described in, for example, Bass et al., Proteins, 8:309-314 (1990). It is generally necessary to select the appropriate bacteria taking into consideration replicability of the replicon in the cells of a bacterium. For example, E. coli, Serratia, or Salmonella species can be suitably used as the host when well-known plasmids such as pBR322, pBR325, pACYC177, or pKN410 are used to supply the replicon. Typically, the host cell should secrete minimal amounts of proteolytic enzymes, and additional protease inhibitors may desirably be incorporated in the cell culture.

b. Masked Cytokine Production

[0469] Host cells are transformed with the above-described expression vectors and cultured in conventional nutrient media modified as appropriate for inducing promoters, selecting transformants, or amplifying the genes encoding the desired sequences.

[0470] Transformation means introducing DNA into the prokaryotic host so that the DNA is replicable, either as an extrachromosomal element or by chromosomal integrant. Depending on the host cell used, transformation is done using standard techniques appropriate to such cells. The calcium treatment employing calcium chloride is generally used for bacterial cells that contain substantial cell-wall barriers. Another method for transformation employs polyethylene glycol/DMSO. Yet another technique used is electroporation.

[0471] Prokaryotic cells used to produce the masked cytokines of the invention are grown in media known in the art and suitable for culture of the selected host cells. Examples of suitable media include luria broth (LB) plus necessary nutrient supplements. In some embodiments, the media also contains a selection agent, chosen based on the construction of the expression vector, to selectively permit growth of prokaryotic cells containing the expression vector. For example, ampicillin is added to media for growth of cells expressing ampicillin resistant gene.

[0472] Any necessary supplements besides carbon, nitrogen, and inorganic phosphate sources may also be included at appropriate concentrations introduced alone or as a mixture with another supplement or medium such as a complex nitrogen source. Optionally, the culture medium may contain one or more reducing agents selected from the group consisting of glutathione, cysteine, cystamine, thioglycollate, dithioerythritol and dithiothreitol.

[0473] The prokaryotic host cells are cultured at suitable temperatures. In certain embodiments, for E. coli growth, growth temperatures range from about 20° C. to about 39° C.; from about 25° C. to about 37° C.; or about 30° C. The pH of the medium may be any pH ranging from about 5 to about 9, depending mainly on the host organism. In certain embodiments, for E. coli, the pH is from about 6.8 to about 7.4, or about 7.0.

[0474] If an inducible promoter is used in the expression vector of the invention, protein expression is induced under conditions suitable for the activation of the promoter. In one aspect of the invention, PhoA promoters are used for controlling transcription of the polypeptides. Accordingly, the transformed host cells are cultured in a phosphate-limiting medium for induction. In certain embodiments, the phosphate-limiting medium is the C.R.A.P. medium (see, e.g., Simmons et al., J. Immunol. Methods (2002), 263:133-147). A variety of other inducers may be used, according to the vector construct employed, as is known in the art.

[0475] In one embodiment, the expressed masked cytokines of the present invention are secreted into and recovered from the periplasm of the host cells. Protein recovery typically involves disrupting the microorganism, generally by such means as osmotic shock, sonication or lysis. Once cells are disrupted, cell debris or whole cells may be removed by centrifugation or filtration. The proteins may be

further purified, for example, by affinity resin chromatography. Alternatively, proteins can be transported into the culture media and isolated therein. Cells may be removed from the culture and the culture supernatant being filtered and concentrated for further purification of the proteins produced. The expressed polypeptides can be further isolated and identified using commonly known methods such as polyacrylamide gel electrophoresis (PAGE) and Western blot assay.

[0476] In one aspect of the invention, masked cytokine production is conducted in large quantity by a fermentation process. Various large-scale fed-batch fermentation procedures are available for production of recombinant proteins. Large-scale fermentations have at least 1000 liters of capacity, and in certain embodiments, about 1,000 to 100,000 liters of capacity. These fermentors use agitator impellers to distribute oxygen and nutrients, especially glucose. Small scale fermentation refers generally to fermentation in a fermentor that is no more than approximately 100 liters in volumetric capacity, and can range from about 1 liter to about 100 liters.

[0477] In a fermentation process, induction of protein expression is typically initiated after the cells have been grown under suitable conditions to a desired density, e.g., an OD550 of about 180-220, at which stage the cells are in the early stationary phase. A variety of inducers may be used, according to the vector construct employed, as is known in the art and described above. Cells may be grown for shorter periods prior to induction. Cells are usually induced for about 12-50 hours, although longer or shorter induction time may be used.

[0478] To improve the production yield and quality of the polypeptides of the invention, various fermentation conditions can be modified. For example, to improve the proper assembly and folding of, for example, secreted antibody polypeptides, additional vectors overexpressing chaperone proteins, such as Dsb proteins (DsbA, DsbB, DsbC, DsbD and or DsbG) or FkpA (a peptidylprolyl cis,trans-isomerase with chaperone activity) can be used to co-transform the host prokaryotic cells. The chaperone proteins have been demonstrated to facilitate the proper folding and solubility of heterologous proteins produced in bacterial host cells. Chen et al. (1999) J. Biol. Chem. 274:19601-19605; Georgiou et al., U.S. Pat. No. 6,083,715; Georgiou et al., U.S. Pat. No. 6,027,888; Bothmann and Pluckthun (2000) J. Biol. Chem. 275:17100-17105; Ramm and Pluckthun (2000) J. Biol. Chem. 275:17106-17113; Arie et al. (2001) Mol. Microbiol. 39:199-210.

[0479] To minimize proteolysis of expressed heterologous proteins (especially those that are proteolytically sensitive), certain host strains deficient for proteolytic enzymes can be used for the present invention. For example, host cell strains may be modified to effect genetic mutation(s) in the genes encoding known bacterial proteases such as Protease III, OmpT, DegP, Tsp, Protease I, Protease Mi, Protease V, Protease VI and combinations thereof. Some E. coli protease-deficient strains are available and described in, for example, Joly et al. (1998), supra; Georgiou et al., U.S. Pat. No. 5,264,365; Georgiou et al., U.S. Pat. No. 5,508,192; Hara et al., Microbial Drug Resistance, 2:63-72 (1996).

[0480] In some embodiments, E. coli strains deficient for proteolytic enzymes and transformed with plasmids overexpressing one or more chaperone proteins are used as host cells in the expression system of the invention.

c. Masked Cytokine Purification

[0481] In some embodiments, the masked cytokine produced herein is further purified to obtain preparations that are substantially homogeneous for further assays and uses. Standard protein purification methods known in the art can be employed. The following procedures are exemplary of suitable purification procedures: fractionation on immunoaffinity or ion-exchange columns, ethanol precipitation, reverse phase HPLC, chromatography on silica or on a cation-exchange resin such as DEAE, chromatofocusing, SDS-PAGE, ammonium sulfate precipitation, and gel filtration using, for example, Sephadex G-75.

[0482] In some embodiments, Protein A immobilized on a solid phase is used for immunoaffinity purification of the masked cytokines of the invention. Protein A is a 41 kD cell wall protein from Staphylococcus aureas which binds with a high affinity to the Fc region of antibodies. Lindmark et al (1983) J. Immunol. Meth. 62:1-13. The solid phase to which Protein A is immobilized can be a column comprising a glass or silica surface, or a controlled pore glass column or a silicic acid column. In some applications, the column is coated with a reagent, such as glycerol, to possibly prevent nonspecific adherence of contaminants.

[0483] As the first step of purification, a preparation derived from the cell culture as described above can be applied onto a Protein A immobilized solid phase to allow specific binding of the masked cytokine of interest to Protein A. The solid phase would then be washed to remove contaminants non-specifically bound to the solid phase. Finally, the masked cytokine of interest is recovered from the solid phase by elution.

[0484] Other methods of purification that provide for high affinity binding to a component of the masked cytokine can be employed in accordance with standard protein purification methods known in the art.

2. Generating Masked Cytokines Using Eukaryotic Host Cells

[0485] A vector for use in a eukaryotic host cell generally includes one or more of the following non-limiting components: a signal sequence, an origin of replication, one or more marker genes, an enhancer element, a promoter, and a transcription termination sequence.

a. Signal Sequence Component

[0486] A vector for use in a eukaryotic host cell may also contain a signal sequence or other polypeptide having a specific cleavage site at the N-terminus of the mature protein or polypeptide of

interest. The heterologous signal sequence selected may be one that is recognized and processed (i.e., cleaved by a signal peptidase) by the host cell. In mammalian cell expression, mammalian signal sequences as well as viral secretory leaders, for example, the herpes simplex gD signal, are available. The DNA for such a precursor region is ligated in reading frame to DNA encoding the masked cytokine.

b. Origin of Replication

[0487] Generally, an origin of replication component is not needed for mammalian expression vectors. For example, the SV40 origin may typically be used only because it contains the early promoter.

c. Selection Gene Component

[0488] Expression and cloning vectors may contain a selection gene, also termed a selectable marker. Typical selection genes encode proteins that (a) confer resistance to antibiotics or other toxins, e.g., ampicillin, neomycin, methotrexate, or tetracycline, (b) complement auxotrophic deficiencies, where relevant, or (c) supply critical nutrients not available from complex media.

[0489] One example of a selection scheme utilizes a drug to arrest growth of a host cell. Those cells that are successfully transformed with a heterologous gene produce a protein conferring drug resistance and thus survive the selection regimen. Examples of such dominant selection use the drugs neomycin, mycophenolic acid and hygromycin.

[0490] Another example of suitable selectable markers for mammalian cells are those that enable the identification of cells competent to take up the masked cytokine encoding nucleic acid, such as DHFR, thymidine kinase, metallothionein-I and -II, primate metallothionein genes, adenosine deaminase, ornithine decarboxylase, etc.

[0491] For example, in some embodiments, cells transformed with the DHFR selection gene are first identified by culturing all of the transformants in a culture medium that contains methotrexate (Mtx), a competitive antagonist of DHFR. In some embodiments, an appropriate host cell when wild-type DHFR is employed is the Chinese hamster ovary (CHO) cell line deficient in DHFR activity (e.g., ATCC CRL-9096).

[0492] Alternatively, host cells (particularly wild-type hosts that contain endogenous DHFR) transformed or co-transformed with DNA sequences encoding a masked cytokine, wild-type DHFR protein, and another selectable marker such as aminoglycoside 3′-phosphotransferase (APH) can be selected by cell growth in medium containing a selection agent for the selectable marker such as an aminoglycosidic antibiotic, e.g., kanamycin, neomycin, or G418. See U.S. Pat. No. 4,965,199. Host cells may include NS0, including cell lines deficient in glutamine synthetase (GS). Methods for the use of GS as a selectable marker for mammalian cells are described in U.S. Pat. No. 5,122,464 and U.S. Pat. No. 5,891,693.

d. Promoter Component

[0493] Expression and cloning vectors usually contain a promoter that is recognized by the host organism and is operably linked to nucleic acid encoding a masked cytokine of interest, which can be any masked cytokine described herein. Promoter sequences are known for eukaryotes. For example, virtually all eukaryotic genes have an AT-rich region located approximately 25 to 30 bases upstream from the site where transcription is initiated. Another sequence found 70 to 80 bases upstream from the start of transcription of many genes is a CNCAAT region where N may be any nucleotide. At the 3′ end of most eukaryotic genes is an AATAAA sequence that may be the signal for addition of the poly A tail to the 3′ end of the coding sequence. In certain embodiments, any or all of these sequences may be suitably inserted into eukaryotic expression vectors.

[0494] Transcription from vectors in mammalian host cells is controlled, for example, by promoters obtained from the genomes of viruses such as polyoma virus, fowlpox virus, adenovirus (such as Adenovirus 2), bovine papilloma virus, avian sarcoma virus, cytomegalovirus, a retrovirus, hepatitis-B virus and Simian Virus 40 (SV40), from heterologous mammalian promoters, e.g., the actin promoter or an immunoglobulin promoter, from heat-shock promoters, provided such promoters are compatible with the host cell systems.

[0495] The early and late promoters of the SV40 virus are conveniently obtained as an SV40 restriction fragment that also contains the SV40 viral origin of replication. The immediate early promoter of the human cytomegalovirus is conveniently obtained as a HindIII E restriction fragment. A system for expressing DNA in mammalian hosts using the bovine papilloma virus as a vector is disclosed in U.S. Pat. No. 4,419,446. A modification of this system is described in U.S. Pat. No. 4,601,978. See also Reyes et al., Nature 297:598-601 (1982), describing expression of human β-interferon cDNA in murine cells under the control of a thymidine kinase promoter from herpes simplex virus. Alternatively, the Rous Sarcoma Virus long terminal repeat can be used as the promoter.

e. Enhancer Element Component

[0496] Transcription of DNA encoding a masked cytokine of this invention by higher eukaryotes is often increased by inserting an enhancer sequence into the vector. Many enhancer sequences are now known from mammalian genes (globin, elastase, albumin, α-fetoprotein, and insulin). Typically, however, one will use an enhancer from a eukaryotic cell virus. Examples include the SV40 enhancer on the late side of the replication origin (bp 100-270), the human cytomegalovirus early promoter enhancer, the murine cytomegalovirus early promoter enhancer, the polyoma enhancer on the late side of the replication origin, and adenovirus enhancers. *See also* Yaniv, Nature 297:17-18 (1982) (describing enhancer elements for activation of eukaryotic promoters). The enhancer may be spliced into the vector

at a position 5′ or 3′ to the masked cytokine-encoding sequence, but is generally located at a site 5′ from the promoter.

f. Transcription Termination Component

[0497] Expression vectors used in eukaryotic host cells may also contain sequences necessary for the termination of transcription and for stabilizing the mRNA. Such sequences are commonly available from the 5′ and, occasionally 3′, untranslated regions of eukaryotic or viral DNAs or cDNAs. These regions contain nucleotide segments transcribed as polyadenylated fragments in the untranslated portion of the mRNA encoding a masked cytokine. One useful transcription termination component is the bovine growth hormone polyadenylation region. *See* WO94/11026 and the expression vector disclosed therein.

g. Selection and Transformation of Host Cells

[0498] Suitable host cells for cloning or expressing the DNA in the vectors herein include higher eukaryote cells described herein, including vertebrate host cells. Propagation of vertebrate cells in culture (tissue culture) has become a routine procedure. Examples of useful mammalian host cell lines are monkey kidney CV1 line transformed by SV40 (COS-7, ATCC CRL 1651); human embryonic kidney line (293 or 293 cells subcloned for growth in suspension culture, Graham et al., J. Gen Virol. 36:59 (1977)); baby hamster kidney cells (BHK, ATCC CCL 10); Chinese hamster ovary cells/-DHFR (CHO, Urlaub et al., Proc. Natl. Acad. Sci. USA 77:4216 (1980)); murine sertoli cells (TM4, Mather, Biol. Reprod. 23:243-251 (1980)); monkey kidney cells (CV1 ATCC CCL 70); African green monkey kidney cells (VERO-76, ATCC CRL-1587); human cervical carcinoma cells (HELA, ATCC CCL 2); canine kidney cells (MDCK, ATCC CCL 34); buffalo rat liver cells (BRL 3A, ATCC CRL 1442); human lung cells (W138, ATCC CCL 75); human liver cells (Hep G2, HB 8065); murine mammary tumor (MMT 060562, ATCC CCL51); TRI cells (Mather et al., Annals N.Y. Acad. Sci. 383:44-68 (1982)); MRC 5 cells; FS4 cells; and a human hepatoma line (Hep G2).

[0499] Host cells are transformed with the above-described-expression or cloning vectors for masked cytokine production and cultured in conventional nutrient media modified as appropriate for inducing promoters, selecting transformants, or amplifying the genes encoding the desired sequences.

h. Culturing Host Cells

[0500] The host cells used to produce masked cytokines of this invention may be cultured in a variety of media. Commercially available media such as Ham's F10 (Sigma), Minimal Essential Medium ((MEM), Sigma), RPMI-1640 (Sigma), and Dulbecco's Modified Eagle's Medium ((DMEM), Sigma) are suitable for culturing the host cells. In addition, any of the media described in Ham et al., Meth. Enz. 58:44 (1979), Barnes et al., Anal. Biochem. 102:255 (1980), U.S. Pat. No. 4,767,704; 4,657,866;

4,927,762; 4,560,655; or 5,122,469; WO 90/03430; WO 87/00195; or U.S. Pat. Re. 30,985 may be used as culture media for the host cells. Any of these media may be supplemented as necessary with hormones and/or other growth factors (such as insulin, transferrin, or epidermal growth factor), salts (such as sodium chloride, calcium, magnesium, and phosphate), buffers (such as HEPES), nucleotides (such as adenosine and thymidine), antibiotics (such as GENTAMYCIN™ drug), trace elements (defined as inorganic compounds usually present at final concentrations in the micromolar range), and glucose or an equivalent energy source. Any other supplements may also be included at appropriate concentrations that would be known to those skilled in the art. The culture conditions, such as temperature, pH, and the like, are those previously used with the host cell selected for expression, and will be apparent to the ordinarily skilled artisan.

i. Purification of Masked Cytokines

[0501] When using recombinant techniques, the masked cytokines can be produced intracellularly, or directly secreted into the medium. If the masked cytokine is produced intracellularly, as a first step, the particulate debris, either host cells or lysed fragments, may be removed, for example, by centrifugation or ultrafiltration. Where the masked cytokine is secreted into the medium, supernatants from such expression systems may be first concentrated using a commercially available protein concentration filter, for example, an Amicon or Millipore Pellicon ultrafiltration unit. A protease inhibitor such as PMSF may be included in any of the foregoing steps to inhibit proteolysis, and antibiotics may be included to prevent the growth of adventitious contaminants.

[0502] The masked cytokine composition prepared from the cells can be purified using, for example, hydroxylapatite chromatography, gel electrophoresis, dialysis, and affinity chromatography, with affinity chromatography being a convenient technique. The suitability of protein A as an affinity ligand depends on the species and isotype of any immunoglobulin Fc domain, if any, that is present in the masked cytokine. Protein A can be used to purify antibodies that are based on human IgG1, IgG2, or IgG4 heavy chains (Lindmark et al., J. Immunol. Methods 62:1-13 (1983)). Protein G is recommended for all murine isotypes and for human γ3 (Guss et al., EMBO J. 5:15671575 (1986)). The matrix to which the affinity ligand is attached may be agarose, but other matrices are available. Mechanically stable matrices such as controlled pore glass or poly(styrenedivinyl)benzene allow for faster flow rates and shorter processing times than can be achieved with agarose. Where the masked cytokine comprises a CH3 domain, the Bakerbond ABX™ resin (J. T. Baker, Phillipsburg, N.J.) is useful for purification. Other techniques for protein purification such as fractionation on an ion-exchange column, ethanol precipitation, Reverse Phase HPLC, chromatography on silica, chromatography on heparin SEPHAROSE™ chromatography on an anion or cation exchange resin (such as a polyaspartic acid column), chromatofocusing, SDS-PAGE, and ammonium sulfate precipitation are also available depending on the masked cytokine to be recovered.

[0503] Following any preliminary purification step(s), the mixture comprising the masked cytokine of interest and contaminants may be subjected to further purification, for example, by low pH hydrophobic interaction chromatography using an elution buffer at a pH between about 2.5-4.5, performed at low salt concentrations (e.g., from about 0-0.25M salt).

[0504] In general, various methodologies for preparing masked cytokines for use in research, testing, and clinical use are well-established in the art, consistent with the above-described methodologies and/or as deemed appropriate by one skilled in the art for a particular masked cytokine of interest.

III. Compositions

[0505] In some aspects, also provided herein are compositions comprising any of the masked cytokines described herein. In some embodiments, the composition comprises any of the exemplary embodiments of masked cytokine described herein. In some embodiments, the composition comprises a dimer of any of the masked cytokines described herein. In some embodiments, the composition is a pharmaceutical composition. In some embodiments, the composition comprises a masked cytokine and further comprises one or more of the components as described in detail below. For example, in some embodiments, the composition comprises one or more pharmaceutically acceptable carriers, excipients, stabilizers, buffers, preservatives, tonicity agents, non-ionic surfactants or detergents, or other therapeutic agents or active compounds, or combinations thereof. The various embodiments of the composition are sometimes referred to herein as formulations.

[0506] Therapeutic formulations are prepared for storage by mixing the active ingredient having the desired degree of purity with optional pharmaceutically acceptable carriers, excipients or stabilizers (Remington: The Science and Practice of Pharmacy, 20th Ed., Lippincott Williams & Wiklins, Pub., Gennaro Ed., Philadelphia, Pa. 2000). Acceptable carriers, excipients, or stabilizers are nontoxic to recipients at the dosages and concentrations employed, and include buffers, antioxidants including ascorbic acid, methionine, Vitamin E, sodium metabisulfite; preservatives, isotonicifiers, stabilizers, metal complexes (e.g. Zn-protein complexes); chelating agents such as EDTA and/or non-ionic surfactants.

[0507] Buffers can be used to control the pH in a range which optimizes the therapeutic effectiveness, especially if stability is pH dependent. Buffers can be present at concentrations ranging from about 50 mM to about 250 mM. Suitable buffering agents for use with the present invention include both organic and inorganic acids and salts thereof. For example, citrate, phosphate, succinate, tartrate, fumarate, gluconate, oxalate, lactate, acetate. Additionally, buffers may be comprised of histidine and trimethylamine salts such as Tris.

[0508] Preservatives can be added to prevent microbial growth, and are typically present in a range from about 0.2%-1.0% (w/v). Examples of suitable preservatives commonly used with therapeutics

include octadecyldimethylbenzyl ammonium chloride; hexamethonium chloride; benzalkonium halides (e.g., chloride, bromide, iodide), benzethonium chloride; thimerosal, phenol, butyl or benzyl alcohol; alkyl parabens such as methyl or propyl paraben; catechol; resorcinol; cyclohexanol, 3-pentanol, m-cresol, o-cresol, p-cresol, methyl p-hydroxybenzoate, propyl p-hydroxybenzoate, 2-phenoxyethanol, butyl p- hydroxybenzoate, 2-phenylethanol, ethanol, chlorobutanol, thiomerosal, bronopol, benzoic acid, imidurea, chlorohexidine, sodium dehydroacetate, chlorocresol, ethyl p-hydroxybenzoate, and chlorphenesine (3p-chlorphenoxypropane-1 ,2- diol).

[0509] Tonicity agents, sometimes known as "stabilizers" can be present to adjust or maintain the tonicity of liquid in a composition. When used with large, charged biomolecules such as proteins and antibodies, they are often termed "stabilizers" because they can interact with the charged groups of the amino acid side chains, thereby lessening the potential for inter and intra-molecular interactions. Tonicity agents can be present in any amount between about 0.1% to about 25% by weight or between about 1 to about 5% by weight, taking into account the relative amounts of the other ingredients. In some embodiments, tonicity agents include polyhydric sugar alcohols, trihydric or higher sugar alcohols, such as glycerin, erythritol, arabitol, xylitol, sorbitol and mannitol.

[0510] Additional excipients include agents which can serve as one or more of the following: (1) bulking agents, (2) solubility enhancers, (3) stabilizers and (4) and agents preventing denaturation or adherence to the container wall. Such excipients include: polyhydric sugar alcohols (enumerated above); amino acids such as alanine, glycine, glutamine, asparagine, histidine, arginine, lysine, ornithine, leucine, 2-phenylalanine, glutamic acid, threonine, etc.; organic sugars or sugar alcohols such as sucrose, lactose, lactitol, trehalose, stachyose, mannose, sorbose, xylose, ribose, ribitol, myoinisitose, myoinisitol, galactose, galactitol, glycerol, cyclitols (e.g., inositol), polyethylene glycol; sulfur containing reducing agents, such as urea, glutathione, thioctic acid, sodium thioglycolate, thioglycerol, α-monothioglycerol and sodium thio sulfate; low molecular weight proteins such as human serum albumin, bovine serum albumin, gelatin or other immunoglobulins; hydrophilic polymers such as polyvinylpyrrolidone; monosaccharides (e.g., xylose, mannose, fructose, glucose; disaccharides (e.g., lactose, maltose, sucrose); trisaccharides such as raffinose; and polysaccharides such as dextrin or dextran.

[0511] Non-ionic surfactants or detergents (also known as "wetting agents") can be present to help solubilize the therapeutic agent as well as to protect the therapeutic protein against agitation-induced aggregation, which also permits the formulation to be exposed to shear surface stress without causing denaturation of the active therapeutic protein or antibody. Non-ionic surfactants are present in a range of about 0.05 mg/ml to about 1.0 mg/ml or about 0.07 mg/ml to about 0.2 mg/ml. In some embodiments, non-ionic surfactants are present in a range of about 0.001% to about 0.1% w/v or about 0.01% to about 0.1% w/v or about 0.01% to about 0.025% w/v.

[0512] Suitable non-ionic surfactants include polysorbates (20, 40, 60, 65, 80, etc.), polyoxamers (184, 188, etc.), PLURONIC® polyols, TRITON®, polyoxyethylene sorbitan monoethers (TWEEN®-

20, TWEEN®-80, etc.), lauromacrogol 400, polyoxyl 40 stearate, polyoxyethylene hydrogenated castor oil 10, 50 and 60, glycerol monostearate, sucrose fatty acid ester, methyl celluose and carboxymethyl cellulose. Anionic detergents that can be used include sodium lauryl sulfate, dioctyle sodium sulfosuccinate and dioctyl sodium sulfonate. Cationic detergents include benzalkonium chloride or benzethonium chloride.

[0513] In order for the formulations to be used for in vivo administration, they must be sterile. The formulation may be rendered sterile by filtration through sterile filtration membranes. The therapeutic compositions herein generally are placed into a container having a sterile access port, for example, an intravenous solution bag or vial having a stopper pierceable by a hypodermic injection needle.

[0514] The route of administration is in accordance with known and accepted methods, such as by single or multiple bolus or infusion over a long period of time in a suitable manner, e.g., injection or infusion by subcutaneous, intravenous, intraperitoneal, intramuscular, intraarterial, intralesional or intraarticular routes, topical administration, inhalation or by sustained release or extended-release means.

[0515] Any of the masked cytokines described herein can be used alone or in combination with other therapeutic agents such is in the methods described herein. The term "in combination with" encompasses two or more therapeutic agents (e.g., a masked cytokine and a therapeutic agent) that are included in the same or separate formulations. In some embodiments, "in combination with" refers to "simultaneous" administration, in which case administration of the masked cytokine of the invention occurs simultaneously to the administration of the one or more additional therapeutic agents (e.g., at the same time or within one hour between administration(s) of the masked cytokine and administration of the one or more additional therapeutic agents). In some embodiments, "in combination with" refers to sequential administration, in which case administration of the masked cytokine of the invention occurs prior to and/or following, administration of the one or more additional therapeutic agents (e.g., greater than one hour between administration(s) of the masked cytokine and administration of the one or more additional therapeutic agents). Agents contemplated herein include, but are not limited to, a cytotoxic agent, a cytokine, an agent targeting an immune checkpoint molecule, an agent targeting an immune stimulatory molecule, a growth inhibitory agent, an immune stimulatory agent, an anti-inflammatory agent, or an anti-cancer agent.

[0516] The formulation herein may also contain more than one active compound as necessary for the particular indication being treated, preferably those with complementary activities that do not adversely affect each other. Alternatively, or in addition, the composition may comprise a cytotoxic agent, cytokine, agent targeting an immune checkpoint molecule or stimulatory molecule, growth inhibitory agent, an immune stimulatory agent, an anti-inflammatory agent, or an anti-cancer agent. Such molecules are suitably present in combination in amounts that are effective for the purpose intended.

[0517] The formulation may be presented in any suitable state, such as a liquid formulation, a solid state (lyophilized) formulation, or a frozen formulation. Approaches for preparing each of these types of formulations for therapeutic use are well known in the art.

IV. Methods of Treatment

[0518] Provided herein are methods for treating or preventing a disease in a subject comprising administering to the subject an effective amount of any masked cytokine described herein or compositions thereof. In some embodiments, methods are provided for treating or preventing a disease in a subject comprising administering to the subject an effective amount of a masked cytokine. In some embodiments, methods are provided for treating or preventing a disease in a subject comprising administering to the subject an effective amount of any embodiment of a masked cytokine described herein. In some embodiments, methods are provided for treating or preventing a disease in a subject comprising administering to the subject any composition described herein. In some embodiments, the subject (e.g., a human patient) has been diagnosed with a neoplastic disorder (e.g., cancer) or is at risk of developing such a disorder.

[0519] For the prevention or treatment of disease, the appropriate dosage of an active agent will depend on the type of disease to be treated, as defined herein, the severity and course of the disease, whether the agent is administered for preventive or therapeutic purposes, previous therapy, the subject's clinical history and response to the agent, and the discretion of the attending physician. The agent is suitably administered to the subject at one time or over a series of treatments.

[0520] In some embodiments of the methods described herein, an interval between administrations of a masked cytokine described herein is about one week or longer. In some embodiments of the methods described herein, an interval between administrations of a masked cytokine described herein is about two days or longer, about three days or longer, about four days or longer, about five days or longer, or about six days or longer. In some embodiments of the methods described herein, an interval between administrations of a masked cytokine described herein is about one week or longer, about two weeks or longer, about three weeks or longer, or about four weeks or longer. In some embodiments of the methods described herein, an interval between administrations of a masked cytokine described herein is about one month or longer, about two months or longer, or about three months or longer. As used herein, an interval between administrations refers to the time period between one administration of the masked cytokine and the next administration of the masked cytokine. As used herein, an interval of about one month includes four weeks. In some embodiments, the treatment includes multiple administrations of the masked cytokine, wherein the interval between administrations may vary. For example, in some embodiments, the interval between the first administration and the second administration is about one week, and the intervals between the subsequent administrations are about two weeks. In some embodiments, the interval between the first administration and the second administration is about two

days, three days, four days, or five days, or six days, and the intervals between the subsequent administrations are about one week.

[0521] In some embodiments, the masked cytokine is administered on multiple occasions over a period of time. The dosage that is administered to the subject on multiple occasions can, in some embodiments, be the same dosage for each administration, or, in some embodiments, the masked cytokine can be administered to the subject at two or more different dosages. For example, in some embodiments, a masked cytokine is initially administered at one dosage on one or more occasions and is later administered at a second dosage on one or more occasions beginning at a later time point.

[0522] In some embodiments, a masked cytokine described herein is administered at a flat dose. In some embodiments, a masked cytokine described herein is administered to a subject at a dosage from about 25 mg to about 500 mg per dose. In some embodiments, the masked cytokine is administered to a subject at a dosage of about 25mg to about 50mg, about 50mg to about 75mg, about 75mg to about 100mg, about 100mg to about 125mg, about 125mg to about 150mg, about 150mg to about 175mg, about 175mg to about 200mg, about 200mg to about 225mg, about 225mg to about 250mg, about 250mg to about 275mg, about 275mg to about 300mg, about 300mg to about 325mg, about 325mg to about 350mg, about 350mg to about 375mg, about 375mg to about 400mg, about 400mg to about 425mg, about 425mg to about 450mg, about 450mg, to about 475mg, or about 475mg to about 500mg per dose.

[0523] In some embodiments, a masked cytokine described herein is administered to a subject at a dosage based on the subject's weight or body surface area (BSA). Depending on the type and severity of the disease, about 1 μg/kg to 15 mg/kg (e.g. 0.1mg/kg-10mg/kg) of masked cytokine can be an initial candidate dosage for administration to the patient, whether, for example, by one or more separate administrations, or by continuous infusion. One typical daily dosage might range from about 1 μg/kg to 100 mg/kg or more, depending on the factors mentioned above. For repeated administrations over several days or longer, depending on the condition, the treatment would generally be sustained until a desired suppression of disease symptoms occurs. One exemplary dosage of the masked cytokine would be in the range from about 0.05 mg/kg to about 10 mg/kg. Thus, one or more doses of about 0.5 mg/kg, 2.0 mg/kg, 4.0 mg/kg or 10 mg/kg (or any combination thereof) may be administered to the patient. In some embodiments, a masked cytokine described herein is administered to a subject at a dosage from about 0.1 mg/kg to about 10 mg/kg or about 1.0 mg/kg to about 10 mg/kg. In some embodiments, a masked cytokine described herein is administered to a subject at a dosage of about any of 0.1 mg/kg, 0.5 mg/kg, 1.0 mg/kg, 1.5 mg/kg, 2.0 mg/kg, 2.5 mg/kg, 3.0 mg/kg, 3.5 mg/kg, 4.0 mg/kg, 4.5 mg/kg, 5.0 mg/kg, 5.5 mg/kg, 6.0 mg/kg, 6.5 mg/kg, 7.0 mg/kg, 7.5 mg/kg, 8.0 mg/kg, 8.5 mg/kg, 9.0 mg/kg, 9.5 mg/kg, or 10.0 mg/kg. In some embodiments, a masked cytokine described herein is administered to a subject at a dosage of about or at least about 0.1 mg/kg, about or at least about 0.5 mg/kg, about or at least about 1.0 mg/kg, about or at least about 1.5 mg/kg, about or at least about 2.0 mg/kg, about or at least about 2.5 mg/kg, about or at least about 3.0 mg/kg, about or at least about 3.5 mg/kg, about or at

least about 4.0 mg/kg, about or at least about 4.5 mg/kg, about or at least about 5.0 mg/kg, about or at least about 5.5 mg/kg, about or at least about 6.0 mg/kg, about or at least about 6.5 mg/kg, about or at least about 7.0 mg/kg, about or at least about 7.5 mg/kg, about or at least about 8.0 mg/kg, about or at least about 8.5 mg/kg, about or at least about 9.0 mg/kg, about or at least about 9.5 mg/kg, about or at least about 10.0 mg/kg, about or at least about 15.0 mg/kg, about or at least about 20mg/kg, about or at least about 30mg/kg, about or at least about 40mg/kg, about or at least about 50mg/kg, about or at least about 60mg/kg, about or at least about 70mg/kg, about or at least about 80mg/kg, about or at least about 90mg/kg, or about or at least about 100mg/kg. Any of the dosing frequencies described above may be used.

[0524] In some embodiments, a masked IL-2 polypeptide described herein is administered at a flat dose. In some embodiments, a masked IL-2 polypeptide described herein is administered to a subject at a dosage from about 25 mg to about 500 mg per dose. In some embodiments, the masked IL-2 polypeptide is administered to a subject at a dosage of about 25mg to about 50mg, about 50mg to about 75mg, about 75mg to about 100mg, about 100mg to about 125mg, about 125mg to about 150mg, about 150mg to about 175mg, about 175mg to about 200mg, about 200mg to about 225mg, about 225mg to about 250mg, about 250mg to about 275mg, about 275mg to about 300mg, about 300mg to about 325mg, about 325mg to about 350mg, about 350mg to about 375mg, about 375mg to about 400mg, about 400mg to about 425mg, about 425mt to about 450mg, about 450mg, to about 475mg, or about 475mg to about 500mg per dose.

[0525] In some embodiments, a masked IL-2 polypeptide described herein is administered to a subject at a dosage based on the subject's weight or body surface area (BSA). Depending on the type and severity of the disease, about 1 µg/kg to 15 mg/kg (e.g. 0.1mg/kg-10mg/kg) of masked IL-2 polypeptide can be an initial candidate dosage for administration to the patient, whether, for example, by one or more separate administrations, or by continuous infusion. One typical daily dosage might range from about 1 µg/kg to 100 mg/kg or more, depending on the factors mentioned above. For repeated administrations over several days or longer, depending on the condition, the treatment would generally be sustained until a desired suppression of disease symptoms occurs. One exemplary dosage of the masked IL-2 polypeptide would be in the range from about 0.05 mg/kg to about 10 mg/kg. Thus, one or more doses of about 0.5 mg/kg, 2.0 mg/kg, 4.0 mg/kg or 10 mg/kg (or any combination thereof) may be administered to the patient. In some embodiments, a masked IL-2 polypeptide described herein is administered to a subject at a dosage from about 0.1 mg/kg to about 10 mg/kg or about 1.0 mg/kg to about 10 mg/kg. In some embodiments, a masked IL-2 polypeptide described herein is administered to a subject at a dosage of about any of 0.1 mg/kg, 0.5 mg/kg, 1.0 mg/kg, 1.5 mg/kg, 2.0 mg/kg, 2.5 mg/kg, 3.0 mg/kg, 3.5 mg/kg, 4.0 mg/kg, 4.5 mg/kg, 5.0 mg/kg, 5.5 mg/kg, 6.0 mg/kg, 6.5 mg/kg, 7.0 mg/kg, 7.5 mg/kg, 8.0 mg/kg, 8.5 mg/kg, 9.0 mg/kg, 9.5 mg/kg, or 10.0 mg/kg. In some embodiments, a masked IL-2 polypeptide described herein is administered to a subject at a dosage of about or at least about 0.1 mg/kg,

about or at least about 0.5 mg/kg, about or at least about 1.0 mg/kg, about or at least about 1.5 mg/kg, about or at least about 2.0 mg/kg, about or at least about 2.5 mg/kg, about or at least about 3.0 mg/kg, about or at least about 3.5 mg/kg, about or at least about 4.0 mg/kg, about or at least about 4.5 mg/kg, about or at least about 5.0 mg/kg, about or at least about 5.5 mg/kg, about or at least about 6.0 mg/kg, about or at least about 6.5 mg/kg, about or at least about 7.0 mg/kg, about or at least about 7.5 mg/kg, about or at least about 8.0 mg/kg, about or at least about 8.5 mg/kg, about or at least about 9.0 mg/kg, about or at least about 9.5 mg/kg, about or at least about 10.0 mg/kg, about or at least about 15.0 mg/kg, about or at least about 20mg/kg, about or at least about 30mg/kg, about or at least about 40mg/kg, about or at least about 50mg/kg, about or at least about 60mg/kg, about or at least about 70mg/kg, about or at least about 80mg/kg, about or at least about 90mg/kg, or about or at least about 100mg/kg. Any of the dosing frequencies described above may be used.

[0526] In some embodiments, a masked IL-15 polypeptide described herein is administered at a flat dose. In some embodiments, a masked IL-15 polypeptide described herein is administered to a subject at a dosage from about 25 mg to about 500 mg per dose. In some embodiments, the masked IL-15 polypeptide is administered to a subject at a dosage of about 25mg to about 50mg, about 50mg to about 75mg, about 75mg to about 100mg, about 100mg to about 125mg, about 125mg to about 150mg, about 150mg to about 175mg, about 175mg to about 200mg, about 200mg to about 225mg, about 225mg to about 250mg, about 250mg to about 275mg, about 275mg to about 300mg, about 300mg to about 325mg, about 325mg to about 350mg, about 350mg to about 375mg, about 375mg to about 400mg, about 400mg to about 425mg, about 425mg to about 450mg, about 450mg, to about 475mg, or about 475mg to about 500mg per dose.

[0527] In some embodiments, a masked IL-15 polypeptide described herein is administered to a subject at a dosage based on the subject's weight or body surface area (BSA). Depending on the type and severity of the disease, about 1 µg/kg to 15 mg/kg (e.g. 0.1mg/kg-10mg/kg) of masked IL-15 polypeptide can be an initial candidate dosage for administration to the patient, whether, for example, by one or more separate administrations, or by continuous infusion. One typical daily dosage might range from about 1 µg/kg to 100 mg/kg or more, depending on the factors mentioned above. For repeated administrations over several days or longer, depending on the condition, the treatment would generally be sustained until a desired suppression of disease symptoms occurs. Thus, one or more doses of about 0.5 mg/kg, 2.0 mg/kg, 4.0 mg/kg or 10 mg/kg (or any combination thereof) may be administered to the patient. In some embodiments, a masked IL-15 polypeptide described herein is administered to a subject at a dosage from about 25 mg to about 500 mg per dose. In some embodiments, a masked IL-15 polypeptide described herein is administered to a subject at a dosage from about 0.1 mg/kg to about 10 mg/kg or about 1.0 mg/kg to about 10 mg/kg. In some embodiments, a masked IL-15 polypeptide described herein is administered to a subject at a dosage of about any of 0.1 mg/kg, 0.5 mg/kg, 1.0 mg/kg, 1.5 mg/kg, 2.0 mg/kg, 2.5 mg/kg, 3.0 mg/kg, 3.5 mg/kg, 4.0 mg/kg, 4.5 mg/kg, 5.0 mg/kg, 5.5 mg/kg, 6.0 mg/kg, 6.5

mg/kg, 7.0 mg/kg, 7.5 mg/kg, 8.0 mg/kg, 8.5 mg/kg, 9.0 mg/kg, 9.5 mg/kg, or 10.0 mg/kg. In some embodiments, a masked IL-15 polypeptide described herein is administered to a subject at a dosage of about or at least about 0.1 mg/kg, about or at least about 0.5 mg/kg, about or at least about 1.0 mg/kg, about or at least about 1.5 mg/kg, about or at least about 2.0 mg/kg, about or at least about 2.5 mg/kg, about or at least about 3.0 mg/kg, about or at least about 3.5 mg/kg, about or at least about 4.0 mg/kg, about or at least about 4.5 mg/kg, about or at least about 5.0 mg/kg, about or at least about 5.5 mg/kg, about or at least about 6.0 mg/kg, about or at least about 6.5 mg/kg, about or at least about 7.0 mg/kg, about or at least about 7.5 mg/kg, about or at least about 8.0 mg/kg, about or at least about 8.5 mg/kg, about or at least about 9.0 mg/kg, about or at least about 9.5 mg/kg, about or at least about 10.0 mg/kg, about or at least about 15.0 mg/kg, about or at least about 20mg/kg, about or at least about 30mg/kg, about or at least about 40mg/kg, about or at least about 50mg/kg, about or at least about 60mg/kg, about or at least about 70mg/kg, about or at least about 80mg/kg, about or at least about 90mg/kg, or about or at least about 100mg/kg. Any of the dosing frequencies described above may be used.

[0528] A method of treatment contemplated herein is the treatment of a disorder or disease with any of the masked cytokines or compositions described herein. In some embodiments, the method of treatment uses any masked IL-2 polypeptide described herein, or any masked IL-15 polypeptide described herein, or any of the compositions comprising a masked cytokine described herein. Disorders or diseases that are treatable with the formulations of this present invention include leukemia, lymphoma, head and neck cancer, colorectal cancer, prostate cancer, pancreatic cancer, melanoma, breast cancer, neuroblastoma, lung cancer, ovarian cancer, osteosarcoma, bladder cancer, cervical cancer, liver cancer, kidney cancer, skin cancer (e.g., Merkel cell carcinoma) or testicular cancer.

[0529] In some embodiments, provided herein is a method of treatment or prevention of a cancer by administration of any masked cytokines or compositions described herein. In some embodiments, provided herein is a method of treatment or prevention of a cancer by administration of a masked IL-2 polypeptide, or a masked IL-15 polypeptide, or any of the compositions comprising a masked cytokine described herein. As used herein, the term "cancer" refers to all types of cancer, neoplasm or malignant tumors found in mammals, including leukemias, lymphomas, melanomas, neuroendocrine tumors, carcinomas and sarcomas. Exemplary cancers that may be treated with a masked cytokine, pharmaceutical composition, or method provided herein, include lymphoma, sarcoma, bladder cancer, bone cancer, brain tumor, cervical cancer, colon cancer, esophageal cancer, gastric cancer, head and neck cancer, kidney cancer, myeloma, thyroid cancer, leukemia, prostate cancer, breast cancer (e.g. triple negative, ER positive, ER negative, chemotherapy resistant, Herceptin resistant, HER2 positive, doxorubicin resistant, tamoxifen resistant, ductal carcinoma, lobular carcinoma, primary, metastatic), ovarian cancer, pancreatic cancer, liver cancer (e.g. hepatocellular carcinoma), lung cancer (e.g. non-small cell lung carcinoma, squamous cell lung carcinoma, adenocarcinoma, large cell lung carcinoma, small cell lung carcinoma, carcinoid, sarcoma), glioblastoma multiforme, glioma, melanoma, prostate

cancer, castration-resistant prostate cancer, breast cancer, triple negative breast cancer, glioblastoma, ovarian cancer, lung cancer, squamous cell carcinoma (e.g., head, neck, or esophagus), colorectal cancer, leukemia, acute myeloid leukemia, lymphoma, B cell lymphoma, or multiple myeloma. Additional examples include, cancer of the thyroid, endocrine system, brain, breast, cervix, colon, head & neck, esophagus, liver, kidney, lung, non-small cell lung, melanoma, mesothelioma, ovary, sarcoma, stomach, uterus or Medulloblastoma, Hodgkin's Disease, Non-Hodgkin's Lymphoma, multiple myeloma, neuroblastoma, glioma, glioblastoma multiforme, ovarian cancer, rhabdomyosarcoma, primary thrombocytosis, primary macroglobulinemia, primary brain tumors, cancer, malignant pancreatic insulanoma, malignant carcinoid, urinary bladder cancer, premalignant skin lesions, testicular cancer, lymphomas, thyroid cancer, neuroblastoma, esophageal cancer, genitourinary tract cancer, malignant hypercalcemia, endometrial cancer, adrenal cortical cancer, neoplasms of the endocrine or exocrine pancreas, medullary thyroid cancer, medullary thyroid carcinoma, melanoma, colorectal cancer, papillary thyroid cancer, hepatocellular carcinoma, Paget's Disease of the Nipple, Phyllodes Tumors, Lobular Carcinoma, Ductal Carcinoma, cancer of the pancreatic stellate cells, cancer of the hepatic stellate cells, or prostate cancer.

[0530] In some embodiments, provided herein is a method of treatment or prevention of a leukemia by administration of any masked cytokine or composition described herein. The term "leukemia" refers broadly to progressive, malignant diseases of the blood-forming organs and is generally characterized by a distorted proliferation and development of leukocytes and their precursors in the blood and bone marrow. Leukemia is generally clinically classified on the basis of (1) the duration and character of the disease-acute or chronic; (2) the type of cell involved; myeloid (myelogenous), lymphoid (lymphogenous), or monocytic; and (3) the increase or non-increase in the number abnormal cells in the blood-leukemic or aleukemic (subleukemic). Exemplary leukemias that may be treated with a compound, pharmaceutical composition, or method provided herein include, for example, acute nonlymphocytic leukemia, chronic lymphocytic leukemia, acute granulocytic leukemia, chronic granulocytic leukemia, acute promyelocytic leukemia, adult T-cell leukemia, aleukemic leukemia, a leukocythemic leukemia, basophylic leukemia, blast cell leukemia, bovine leukemia, chronic myelocytic leukemia, leukemia cutis, embryonal leukemia, eosinophilic leukemia, Gross' leukemia, hairy-cell leukemia, hemoblastic leukemia, hemocytoblastic leukemia, histiocytic leukemia, stem cell leukemia, acute monocytic leukemia, leukopenic leukemia, lymphatic leukemia, lymphoblastic leukemia, lymphocytic leukemia, lymphogenous leukemia, lymphoid leukemia, lymphosarcoma cell leukemia, mast cell leukemia, megakaryocytic leukemia, micromyeloblastic leukemia, monocytic leukemia, myeloblastic leukemia, myelocytic leukemia, myeloid granulocytic leukemia, myelomonocytic leukemia, Naegeli leukemia, plasma cell leukemia, multiple myeloma, plasmacytic leukemia, promyelocytic leukemia, Rieder cell leukemia, Schilling's leukemia, stem cell leukemia, subleukemic leukemia, or undifferentiated cell leukemia.

[0531] In some embodiments, provided herein is a method of treatment or prevention of a sarcoma by administration of any masked cytokine or composition described herein. The term "sarcoma" generally refers to a tumor which is made up of a substance like the embryonic connective tissue and is generally composed of closely packed cells embedded in a fibrillar or homogeneous substance. Sarcomas that may be treated with a compound, pharmaceutical composition, or method provided herein include a chondrosarcoma, fibrosarcoma, lymphosarcoma, melanosarcoma, myxosarcoma, osteosarcoma, Abemethy's sarcoma, adipose sarcoma, liposarcoma, alveolar soft part sarcoma, ameloblastic sarcoma, botryoid sarcoma, chloroma sarcoma, chorio carcinoma, embryonal sarcoma, Wilms' tumor sarcoma, endometrial sarcoma, stromal sarcoma, Ewing's sarcoma, fascial sarcoma, fibroblastic sarcoma, giant cell sarcoma, granulocytic sarcoma, Hodgkin's sarcoma, idiopathic multiple pigmented hemorrhagic sarcoma, immunoblastic sarcoma of B cells, lymphoma, immunoblastic sarcoma of T-cells, Jensen's sarcoma, Kaposi's sarcoma, Kupffer cell sarcoma, angiosarcoma, leukosarcoma, malignant mesenchymoma sarcoma, parosteal sarcoma, reticulocytic sarcoma, Rous sarcoma, serocystic sarcoma, synovial sarcoma, or telangiectaltic sarcoma.

[0532] In some embodiments, provided herein is a method of treatment or prevention of a melanoma by administration of any masked cytokine or composition described herein. The term "melanoma" is taken to mean a tumor arising from the melanocytic system of the skin and other organs. Melanomas that may be treated with a compound, pharmaceutical composition, or method provided herein include, for example, acral-lentiginous melanoma, amelanotic melanoma, benign juvenile melanoma, Cloudman's melanoma, S91 melanoma, Harding-Passey melanoma, juvenile melanoma, lentigo maligna melanoma, malignant melanoma, nodular melanoma, subungal melanoma, or superficial spreading melanoma.

[0533] In some embodiments, provided herein is a method of treatment or prevention of a carcinoma by administration of any masked cytokine or composition described herein. The term "carcinoma" refers to a malignant new growth made up of epithelial cells tending to infiltrate the surrounding tissues and give rise to metastases. Exemplary carcinomas that may be treated with a compound, pharmaceutical composition, or method provided herein include, for example, medullary thyroid carcinoma, familial medullary thyroid carcinoma, acinar carcinoma, acinous carcinoma, adenocystic carcinoma, adenoid cystic carcinoma, carcinoma adenomatosum, carcinoma of adrenal cortex, alveolar carcinoma, alveolar cell carcinoma, basal cell carcinoma, carcinoma basocellulare, basaloid carcinoma, basosquamous cell carcinoma, bronchioalveolar carcinoma, bronchiolar carcinoma, bronchogenic carcinoma, cerebriform carcinoma, cholangiocellular carcinoma, chorionic carcinoma, colloid carcinoma, comedo carcinoma, corpus carcinoma, cribriform carcinoma, carcinoma en cuirasse, carcinoma cutaneum, cylindrical carcinoma, cylindrical cell carcinoma, duct carcinoma, ductal carcinoma, carcinoma durum, embryonal carcinoma, encephaloid carcinoma, epiermoid carcinoma, carcinoma epitheliale adenoides, exophytic carcinoma, carcinoma ex ulcere, carcinoma fibrosum, gelatiniforni carcinoma, gelatinous carcinoma, giant cell carcinoma, carcinoma gigantocellulare, glandular carcinoma, granulosa cell carcinoma, hair-

matrix carcinoma, hematoid carcinoma, hepatocellular carcinoma, Hurthle cell carcinoma, hyaline carcinoma, hypernephroid carcinoma, infantile embryonal carcinoma, carcinoma in situ, intraepidermal carcinoma, intraepithelial carcinoma, Krompecher's carcinoma, Kulchitzky-cell carcinoma, large-cell carcinoma, lenticular carcinoma, carcinoma lenticulare, lipomatous carcinoma, lobular carcinoma, lymphoepithelial carcinoma, carcinoma medullare, medullary carcinoma, melanotic carcinoma, carcinoma molle, mucinous carcinoma, carcinoma muciparum, carcinoma mucocellulare, mucoepidermoid carcinoma, carcinoma mucosum, mucous carcinoma, carcinoma myxomatodes, nasopharyngeal carcinoma, oat cell carcinoma, carcinoma ossificans, osteoid carcinoma, papillary carcinoma, periportal carcinoma, preinvasive carcinoma, prickle cell carcinoma, pultaceous carcinoma, renal cell carcinoma of kidney, reserve cell carcinoma, carcinoma sarcomatodes, schneiderian carcinoma, scirrhous carcinoma, carcinoma scroti, signet-ring cell carcinoma, carcinoma simplex, small-cell carcinoma, solanoid carcinoma, spheroidal cell carcinoma, spindle cell carcinoma, carcinoma spongiosum, squamous carcinoma, squamous cell carcinoma, string carcinoma, carcinoma telangiectaticum, carcinoma telangiectodes, transitional cell carcinoma, carcinoma tuberosum, tubular carcinoma, tuberous carcinoma, verrucous carcinoma, or carcinoma villosum.

[0534] In some embodiments, provided herein is a method of treatment or prevention of metastatic cancer by administration of any masked cytokine or composition described herein. As used herein, the terms “metastasis,” “metastatic,” and “metastatic cancer” can be used interchangeably and refer to the spread of a neoplastic disease or disorder, e.g., cancer, from one organ or another non-adjacent organ or body part. Cancer occurs at an originating site, e.g., breast, which site is referred to as a primary tumor, e.g., primary breast cancer. Some cancer cells in the primary tumor or originating site acquire the ability to penetrate and infiltrate surrounding normal tissue in the local area and/or the ability to penetrate the walls of the lymphatic system or vascular system circulating through the system to other sites and tissues in the body. A second clinically detectable tumor formed from cancer cells of a primary tumor is referred to as a metastatic or secondary tumor. When cancer cells metastasize, the metastatic tumor and its cells are presumed to be similar to those of the original tumor. Thus, if lung cancer metastasizes to the breast, the secondary tumor at the site of the breast consists of abnormal lung cells and not abnormal breast cells. The secondary tumor in the breast is referred to a metastatic lung cancer. Thus, the phrase metastatic cancer refers to a disease in which a subject has or had a primary tumor and has one or more secondary tumors. The phrases non-metastatic cancer or subjects with cancer that is not metastatic refers to diseases in which subjects have a primary tumor but not one or more secondary tumors. For example, metastatic lung cancer refers to a disease in a subject with or with a history of a primary lung tumor and with one or more secondary tumors at a second location or multiple locations, e.g., in the breast.

[0535] In some embodiments, provided herein is a method of treatment or prevention of a cancer by administration of any masked cytokine or composition described herein in combination with an anti-cancer agent. The anti-cancer agent can be any agent capable of reducing cancer growth, interfering with

cancer cell replication, directly or indirectly killing cancer cells, reducing metastasis, reducing tumor blood supply, or reducing cell survival. In some embodiments, the anti-cancer agent is selected from the group consisting of a PD-1 inhibitor, an EGFR inhibitor, a HER2 inhibitor , a VEGFR inhibitor, a CTLA-4 inhibitor, a BTLA inhibitor, a B7H4 inhibitor, a B7H3 inhibitor, a CSFIR inhibitor, an HVEM inhibitor, a CD27 inhibitor, a KIR inhibitor, an NKG2A inhibitor, an NKG2D agonist, a TWEAK inhibitor, an ALK inhibitor, a CD52 targeting antibody, a CCR4 targeting antibody, a PD-L1 inhibitor, a KIT inhibitor, a PDGFR inhibitor, a BAFF inhibitor, an HDAC inhibitor, a VEGF ligand inhibitor, a CD19 targeting molecule, a FOLR1 targeting molecule, a DLL3 targeting molecule, a DKK1 targeting molecule, a MUC1 targeting molecule, a MUC16 targeting molecule, a PSMA targeting molecule, an MSLN targeting molecule, an NY-ESO-1 targeting molecule, a B7H3 targeting molecule, a B7H4 targeting molecule, a BCMA targeting molecule, a CD29 targeting molecule, a CD151targeting molecule, a CD123 targeting molecule, a CD33 targeting molecule, a CD37 targeting molecule, a CDH19 targeting molecule, a CEA targeting molecule, a Claudin 18.2 targeting molecule, a CLEC12A targeting molecule, an EGFRVIII targeting molecule, an EPCAM targeting molecule, an EPHA2 targeting molecule, an FCRH5 targeting molecule, an FLT3 targeting molecule, a GD2 targeting molecule, a glypican 3 targeting molecule, a gpA33 targeting molecule, a GPRC5D targeting molecule, an IL-23R targeting molecule, an IL-1RAP targeting molecule, a MCSP targeting molecule, a RON targeting molecule, a ROR1 targeting molecule, a STEAP2 targeting molecule, a TfR targeting molecule, a CD166 targeting molecule, a TPBG targeting molecule, a TROP2 targeting molecule, a proteasome inhibitor, an ABL inhibitor, a CD30 inhibitor, a FLT3 inhibitor, a MET inhibitor, a RET inhibitor, an IL-1β inhibitor, a MEK inhibitor, a ROS1 inhibitor, a BRAF inhibitor, a CD38 inhibitor, a RANKL inhibitor, a B4GALNT1 inhibitor, a SLAMF7 inhibitor, an IDH2 inhibitor, an mTOR inhibitor, a CD20 targeting antibody, a BTK inhibitor, a PI3K inhibitor, a FLT3 inhibitor, a PARP inhibitor, a CDK4 inhibitor, a CDK6 inhibitor, an FGFR inhibitor, a RAF inhibitor, a JAK1 inhibitor, a JAK2 inhibitor, a JAK3 inhibitor, an IL-6 inhibitor, a IL-17 inhibitor, a Smoothened inhibitor, an IL-6R inhibitor, a BCL2 inhibitor, a PTCH inhibitor, a PIGF inhibitor, a TGFB inhibitor, a CD28 agonist, a CD3 agonist, CD40 agonist, a GITR agonist, a OX40 agonist, a VISTA agonist, a CD137 agonist, a LAG3 inhibitor, a TIM3 inhibitor, a TIGIT inhibitor, and an IL-2R inhibitor.

[0536] In some embodiments, provided herein is a method of treatment or prevention of a cancer by administration of any masked cytokine described herein in combination with an anti-inflammatory agent. The anti-inflammatory agent can be any agent capable of preventing, counteracting, inhibiting, or otherwise reducing inflammation.

[0537] In some embodiments, the anti-inflammatory agent is a cyclooxygenase (COX) inhibitor. The COX inhibitor can be any agent that inhibits the activity of COX-1 and/or COX-2. In some embodiments, the COX inhibitor selectively inhibits COX-1 (i.e., the COX inhibitor inhibits the activity of COX-1 more than it inhibits the activity of COX-2). In some embodiments, the COX inhibitor

selectively inhibits COX-2 (i.e., the COX inhibitor inhibits the activity of COX-2 more than it inhibits the activity of COX-1). In some embodiments, the COX inhibitor inhibits both COX-1 and COX-2.

[0538] In some embodiments, the COX inhibitor is a selective COX-1 inhibitor and is selected from the group consisting of SC-560, FR122047, P6, mofezolac, TFAP, flurbiprofen, and ketoprofen. In some embodiments, the COX inhibitor is a selective COX-2 inhibitor and is selected from the group consisting of celecoxib, rofecoxib, meloxicam, piroxicam, deracoxib, parecoxib, valdecoxib, etoricoxib, a chromene derivative, a chroman derivative, N-(2-cyclohexyloxynitrophenyl) methane sulfonamide, parecoxib, lumiracoxib, RS 57067, T-614, BMS-347070, JTE-522, S-2474, SVT- 2016, CT-3, ABT-963, SC-58125, nimesulide, flosulide, NS-398, L- 745337, RWJ-63556, L-784512, darbufelone, CS-502, LAS-34475, LAS- 34555, S-33516, diclofenac, mefenamic acid, and SD-8381. In some embodiments, the COX inhibitor is selected from the group consisting of ibuprofen, naproxen, ketorolac, indomethacin, aspirin, naproxen, tolmetin, piroxicam, and meclofenamate. In some embodiments, the COX inhibitor is selected from the group consisting of SC-560, FR122047, P6, mofezolac, TFAP, flurbiprofen, ketoprofen, celecoxib, rofecoxib, meloxicam, piroxicam, deracoxib, parecoxib, valdecoxib, etoricoxib, a chromene derivative, a chroman derivative, N-(2-cyclohexyloxynitrophenyl) methane sulfonamide, parecoxib, lumiracoxib, RS 57067, T-614, BMS-347070, JTE-522, S-2474, SVT- 2016, CT-3, ABT-963, SC-58125, nimesulide, flosulide, NS-398, L- 745337, RWJ-63556, L-784512, darbufelone, CS-502, LAS-34475, LAS- 34555, S-33516, diclofenac, mefenamic acid, SD-8381, ibuprofen, naproxen, ketorolac, indomethacin, aspirin, naproxen, tolmetin, piroxicam, and meclofenamate.

[0539] In some embodiments, the anti-inflammatory agent is an NF-κB inhibitor. The NF-κB inhibitor can be any agent that inhibits the activity of the NF-κB pathway. In some embodiments, the NF-κB inhibitor is selected from the group consisting of an IKK complex inhibitor, an IκB degradation inhibitor, an NF-κB nuclear translocation inhibitor, a p65 acetylation inhibitor, an NF-κB DNA binding inhibitor, an NF-κB transactivation inhibitor, and a p53 induction inhibitor.

[0540] In some embodiments, the IKK complex inhibitor is selected from the group consisting of TPCA-1, NF-κB Activation Inhibitor VI (BOT-64), BMS-345541, amlexanox, SC-514 (GK-01140), IMD-0354, and IKK-16. In some embodiments, the IκB degradation inhibitor is selected from the group consisting of BAY-11-7082, MG-115, MG-132, lactacystin, epoxomicin, parthenolide, carfilzomib, and MLN-4924 (pevonedistat). In some embodiments, the NF-κB nuclear translocation inhibitor is selected from the group consisting of JSH-23 and rolipram. In some embodiments, the p65 acetylation inhibitor is selected from the group consisting of gallic acid and anacardic acid. In some embodiments, the NF-κB DNA binding inhibitor is selected from the group consisting of GYY-4137, p-XSC, CV-3988, and prostaglandin E2 (PGE2). In some embodiments, the NF-κB transactivation inhibitor is selected from the group consisting of LY-294002, wortmannin, and mesalamine. In some embodiments, the p53 induction inhibitor is selected from the group consisting of quinacrine and flavopiridol. In some embodiments, the NF-κB inhibitor is selected from the group consisting of TPCA-1, NF-κB Activation Inhibitor VI (BOT-

64), BMS-345541, amlexanox, SC-514 (GK-01140), IMD-0354, IKK-16, BAY-11-7082, MG-115, MG-132, lactacystin, epoxomicin, parthenolide, carfilzomib, MLN-4924 (pevonedistat), JSH-23 rolipram, gallic acid, anacardic acid, GYY-4137, p-XSC, CV-3988, prostaglandin E2 (PGE2), LY-294002, wortmannin, mesalamine, quinacrine, and flavopiridol.

[0541] In some embodiments, provided herein is a method of treatment or prevention of a cancer by administration of any masked cytokine or composition described herein in combination with an anti-cancer therapeutic protein. The anti-cancer therapeutic protein can be any therapeutic protein capable of reducing cancer growth, interfering with cancer cell replication, directly or indirectly killing cancer cells, reducing metastasis, reducing tumor blood supply, or reducing cell survival. Exemplary anti-cancer therapeutic proteins may come in the form of an antibody or fragment thereof, an antibody derivative, a bispecific antibody, a chimeric antigen receptor (CAR) T cell, a fusion protein, or a bispecific T-cell engager (BiTE).

[0542] In some embodiments, provided herein is a method of treatment or prevention of an inflammatory or autoimmune disease by administration of any masked cytokine or composition described herein. The term "inflammatory disease" refers to a disease caused by, resulting from, or resulting in, inflammation. The term "autoimmune disease" refers to a disease in which the subject's own immune system attacks its own cells or tissues.

[0543] In some embodiments, the inflammatory or autoimmune disease is selected from the group consisting of atherosclerosis, obesity, inflammatory bowel disease (IBD), rheumatoid arthritis, allergic encephalitis, psoriasis, atopic skin disease, osteoporosis, peritonitis, hepatitis, lupus, celiac disease, Sjogren's syndrome, polymyalgia rheumatica, multiple sclerosis (MS), ankylosing spondylitis, type 1 diabetes mellitus, alopecia areata, vasculitis, and temporal arteritis, graft versus host disease (GVHD), asthma, COPD, a paraneoplastic autoimmune disease, cartilage inflammation, juvenile arthritis, juvenile rheumatoid arthritis, pauciarticular juvenile rheumatoid arthritis, polyarticular juvenile rheumatoid arthritis, systemic onset juvenile rheumatoid arthritis, juvenile ankylosing spondylitis, juvenile enteropathic arthritis, juvenile reactive arthritis, juvenile Reiter's Syndrome, SEA Syndrome (Seronegativity, Enthesopathy, Arthropathy Syndrome), juvenile dermatomyositis , juvenile psoriatic arthritis, juvenile Scleroderma, juvenile systemic lupus erythematosus, juvenile vasculitis, pauciarticular rheumatoid arthritis, systemic onset rheumatoid arthritis, enteropathic arthritis, reactive arthritis, Reiter's Syndrome, dermatomyositis, psoriatic arthritis, Scleroderma, vasculitis, myolitis, polymyolitis, dermatomyolitis, polyarteritis nodossa, Wegener's granulomatosis, arteritis, ploymyalgia rheumatica, sarcoidosis, Sclerosis, primary biliary Sclerosis, Sclerosing cholangitis, psoriasis, plaque psoriasis, guttate psoriasis, inverse psoriasis, pustular psoriasis, erythrodermic psoriasis, dermatitis, atopic dermatitis, atherosclerosis, Still's disease, Systemic Lupus Erythematosus (SLE), myasthenia gravis, Crohn's disease, ulcerative colitis, celiac disease, rhinosinusitis, rhinosinusitis with polyps, eosinophilic esophogitis, eosinophilic bronchitis, Guillain-Barre disease, thyroiditis (e.g., Graves' disease), Addison's

disease, Raynaud's phenomenon, autoimmune hepatitis, transplantation rejection, kidney damage, hepatitis C-induced vasculitis, and spontaneous loss of pregnancy.

V. Articles of Manufacture or Kits

[0544] In another aspect, an article of manufacture or kit is provided which comprises any masked cytokine described herein. The article of manufacture or kit may further comprise instructions for use of the cytokines in the methods of the invention. Thus, in certain embodiments, the article of manufacture or kit comprises instructions for the use of a masked cytokine in methods for treating or preventing a disorder (e.g., a cancer) in an individual comprising administering to the individual an effective amount of a masked cytokine. For example, in certain embodiments, the article of manufacture or kit comprises instructions for the use of a masked IL-2 polypeptide in methods for treating or preventing a disorder (e.g., a cancer) in an individual comprising administering to the individual an effective amount of a masked IL-2 polypeptide. In certain embodiments, the individual is a human. In some embodiments, the individual has a disease selected from the group consisting of include leukemia, lymphoma, head and neck cancer, colorectal cancer, prostate cancer, pancreatic cancer, melanoma, breast cancer, neuroblastoma, lung cancer, ovarian cancer, osteosarcoma, bladder cancer, cervical cancer, liver cancer, kidney cancer, skin cancer or testicular cancer.

[0545] The article of manufacture or kit may further comprise a container. Suitable containers include, for example, bottles, vials (e.g., dual chamber vials), syringes (such as single or dual chamber syringes), test tubes, and intravenous (IV) bags. The container may be formed from a variety of materials such as glass or plastic. The container holds the formulation. In some embodiments, the formulation is a lyophilized formulation. In some embodiments, the formulation is a frozen formulation. In some embodiments, the formulation is a liquid formulation.

[0546] The article of manufacture or kit may further comprise a label or a package insert, which is on or associated with the container, may indicate directions for reconstitution and/or use of the formulation. The label or package insert may further indicate that the formulation is useful or intended for subcutaneous, intravenous, or other modes of administration for treating or preventing a disorder (e.g., a cancer) in an individual. The container holding the formulation may be a single-use vial or a multi-use vial, which allows for repeat administrations of the reconstituted formulation. The article of manufacture or kit may further comprise a second container comprising a suitable diluent. The article of manufacture or kit may further include other materials desirable from a commercial, therapeutic, and user standpoint, including other buffers, diluents, filters, needles, syringes, and package inserts with instructions for use.

[0547] In a specific embodiment, the present invention provides kits for a single dose-administration unit. Such kits comprise a container of an aqueous formulation of therapeutic cytokine, including both

single or multi-chambered pre-filled syringes. Exemplary pre-filled syringes are available from Vetter GmbH, Ravensburg, Germany.

[0548] The article of manufacture or kit herein optionally further comprises a container comprising a second medicament, wherein the masked cytokine is a first medicament, and which article or kit further comprises instructions on the label or package insert for treating the subject with the second medicament, in an effective amount.

[0549] In another embodiment, provided herein is an article of manufacture or kit comprising the formulations described herein for administration in an auto-injector device. An auto-injector can be described as an injection device that upon activation, will deliver its contents without additional necessary action from the patient or administrator. They are particularly suited for self-medication of therapeutic formulations when the delivery rate must be constant and the time of delivery is greater than a few moments.

VI. DEFINITIONS

[0550] Unless defined otherwise, all terms of art, notations and other technical and scientific terms or terminology used herein are intended to have the same meaning as is commonly understood by one of ordinary skill in the art to which the claimed subject matter pertains. In some cases, terms with commonly understood meanings are defined herein for clarity and/or for ready reference, and the inclusion of such definitions herein should not necessarily be construed to represent a substantial difference over what is generally understood in the art.

[0551] It is to be understood that this invention is not limited to particular compositions or biological systems, which can, of course, vary. It is also to be understood that the terminology used herein is for the purpose of describing particular embodiments only, and is not intended to be limiting. As used in this specification and the appended claims, the singular forms "a," "an," and "the" include plural referents unless the content clearly dictates otherwise. Thus, for example, reference to "an IL-2 polypeptide" optionally includes a combination of two or more such polypeptides, and the like.

[0552] The term "about" as used herein refers to the usual error range for the respective value readily known to the skilled person in this technical field. Reference to "about" a value or parameter herein includes (and describes) embodiments that are directed to that value or parameter per se.

[0553] It is understood that aspects and embodiments of the invention described herein include "comprising," "consisting," and "consisting essentially of" aspects and embodiments.

[0553a] In the claims which follow and in the description of the invention, except where the context requires otherwise due to express language or necessary implication, the word "comprise" or variations such as "comprises" or "comprising" is used in an inclusive sense, i.e. to specify the presence of the

stated features but not to preclude the presence or addition of further features in various embodiments of the invention.

[0554] As used herein, the term "and/or" refers to any one of the items, any combination of the items, or all of the items with which the term is associated. For instance, the phrase "A, B, and/or C" is intended to encompass each of the following embodiments: A, B, and C; A, B, or C; A or B; A or C; B or

C; A and B; A and C; B and C; A and B or C; B and A or C; C and A or B; A (alone); B (alone); and C (alone).

[0555] The term "antibody" includes polyclonal antibodies, monoclonal antibodies (including full length antibodies which have an immunoglobulin Fc region), antibody compositions with polyepitopic specificity, multispecific antibodies (e.g., bispecific antibodies, diabodies, and single-chain molecules, as well as antibody fragments (e.g., Fab, F(ab')2, and Fv). The term "immunoglobulin" (Ig) is used interchangeably with "antibody" herein.

[0556] The term "diabodies" refers to small antibody fragments with two antigen-binding sites, which comprise a heavy chain variable (VH) domain connected to a light chain variable (VL) domain in the same polypeptide chain (VH-VL).

[0557] The basic 4-chain antibody unit is a heterotetrameric glycoprotein composed of two identical light (L) chains and two identical heavy (H) chains. An IgM antibody consists of 5 of the basic heterotetramer units along with an additional polypeptide called a J chain, and contains 10 antigen binding sites, while IgA antibodies comprise from 2-5 of the basic 4-chain units which can polymerize to form polyvalent assemblages in combination with the J chain. In the case of IgGs, the 4-chain unit is generally about 150,000 daltons. Each L chain is linked to an H chain by one covalent disulfide bond, while the two H chains are linked to each other by one or more disulfide bonds depending on the H chain isotype. Each H and L chain also has regularly spaced intrachain disulfide bridges. Each H chain has at the N-terminus, a variable domain (VH) followed by three constant domains (CH) for each of the α and γ chains and four CH domains for μ and ε isotypes. Each L chain has at the N-terminus, a variable domain (VL) followed by a constant domain at its other end. The VL is aligned with the VH and the CL is aligned with the first constant domain of the heavy chain (CH1). Particular amino acid residues are believed to form an interface between the light chain and heavy chain variable domains. The pairing of a VH and VL together forms a single antigen-binding site. For the structure and properties of the different classes of antibodies, see e.g., Basic and Clinical Immunology, 8th Edition, Daniel P. Sties, Abba I. Terr and Tristram G. Parsolw (eds), Appleton & Lange, Norwalk, CT, 1994, page 71 and Chapter 6.

[0558] The L chain from any vertebrate species can be assigned to one of two clearly distinct types, called kappa and lambda, based on the amino acid sequences of their constant domains. Depending on the amino acid sequence of the constant domain of their heavy chains (CH), immunoglobulins can be assigned to different classes or isotypes. There are five classes of immunoglobulins: IgA, IgD, IgE, IgG and IgM, having heavy chains designated α, δ, ε, γ and μ, respectively. The γ and α classes are further divided into subclasses on the basis of relatively minor differences in the CH sequence and function, e.g., humans express the following subclasses: IgG1, IgG2, IgG3, IgG4, IgA1 and IgA2. IgG1 antibodies can exist in multiple polymorphic variants termed allotypes (reviewed in Jefferis and Lefranc 2009. mAbs Vol 1 Issue 4 1-7) any of which are suitable for use in the invention. Common allotypic variants in human populations are those designated by the letters a,f,n,z.

[0559] An "isolated" antibody is one that has been identified, separated and/or recovered from a component of its production environment (e.g., naturally or recombinantly). In some embodiments, the isolated polypeptide is free of association with all other components from its production environment. Contaminant components of its production environment, such as that resulting from recombinant transfected cells, are materials that would typically interfere with research, diagnostic or therapeutic uses for the antibody, and may include enzymes, hormones, and other proteinaceous or non-proteinaceous solutes. In some embodiments, the polypeptide is purified: (1) to greater than 95% by weight of antibody as determined by, for example, the Lowry method, and in some embodiments, to greater than 99% by weight; (1) to a degree sufficient to obtain at least 15 residues of N-terminal or internal amino acid sequence by use of a spinning cup sequenator, or (3) to homogeneity by SDS-PAGE under non-reducing or reducing conditions using Coomassie blue or silver stain. Isolated antibody includes the antibody in situ within recombinant cells since at least one component of the antibody's natural environment will not be present. Ordinarily, however, an isolated polypeptide or antibody is prepared by at least one purification step.

[0560] The term "monoclonal antibody" as used herein refers to an antibody obtained from a population of substantially homogeneous antibodies, i.e., the individual antibodies comprising the population are identical except for possible naturally occurring mutations and/or post-translation modifications (e.g., isomerizations, amidations) that may be present in minor amounts. In some embodiments, monoclonal antibodies have a C-terminal cleavage at the heavy chain and/or light chain. For example, 1, 2, 3, 4, or 5 amino acid residues are cleaved at the C-terminus of heavy chain and/or light chain. In some embodiments, the C-terminal cleavage removes a C-terminal lysine from the heavy chain. In some embodiments, monoclonal antibodies have an N-terminal cleavage at the heavy chain and/or light chain. For example, 1, 2, 3, 4, or 5 amino acid residues are cleaved at the N-terminus of heavy chain and/or light chain. In some embodiments truncated forms of monoclonal antibodies can be made by recombinant techniques. In some embodiments, monoclonal antibodies are highly specific, being directed against a single antigenic site. In some embodiments, monoclonal antibodies are highly specific, being directed against multiple antigenic sites (such as a bispecific antibody or a multispecific antibody). The modifier "monoclonal" indicates the character of the antibody as being obtained from a substantially homogeneous population of antibodies, and is not to be construed as requiring production of the antibody by any particular method. For example, the monoclonal antibodies to be used in accordance with the present invention may be made by a variety of techniques, including, for example, the hybridoma method, recombinant DNA methods, phage-display technologies, and technologies for producing human or human-like antibodies in animals that have parts or all of the human immunoglobulin loci or genes encoding human immunoglobulin sequences.

[0561] The terms "full-length antibody," "intact antibody" or "whole antibody" are used interchangeably to refer to an antibody in its substantially intact form, as opposed to an antibody

fragment. Specifically, whole antibodies include those with heavy and light chains including an Fc region. The constant domains may be native sequence constant domains (e.g., human native sequence constant domains) or amino acid sequence variants thereof. In some cases, the intact antibody may have one or more effector functions.

[0562] An "antibody fragment" comprises a portion of an intact antibody, such as the antigen binding region and/or the variable region of the intact antibody, and/or the constant region of the intact antibody. Examples of an antibody fragment include the Fc region of the antibody, a portion of the Fc region, or a portion of the antibody comprising the Fc region. Examples of antigen-binding antibody fragments include domain antibodies (dAbs), Fab, Fab', F(ab')2 and Fv fragments; diabodies; linear antibodies (see U.S. Pat. No. 5,641,870, Example 2; Zapata et al., Protein Eng. 8(10): 1057-1062 [1995]); single-chain antibody molecules, and multispecific antibodies formed from antibody fragments. Single heavy chain antibodies or single light chain antibodies can be engineered, or in the case of the heavy chain, can be isolated from camelids, shark, libraries or mice engineered to produce single heavy chain molecules.

[0563] Papain digestion of antibodies produced two identical antigen-binding fragments, called "Fab" fragments, and a residual "Fc" fragment, a designation reflecting the ability to crystallize readily. The Fab fragment consists of an entire L chain along with the variable region domain of the H chain (VH), and the first constant domain of one heavy chain (CH1). Each Fab fragment is monovalent with respect to antigen binding, i.e., it has a single antigen-binding site. Pepsin treatment of an antibody yields a single large F(ab')2 fragment which roughly corresponds to two disulfide linked Fab fragments having different antigen-binding activity and is still capable of cross-linking antigen. Fab' fragments differ from Fab fragments by having a few additional residues at the carboxy terminus of the CH1 domain including one or more cysteines from the antibody hinge region. Fab'-SH is the designation herein for Fab' in which the cysteine residue(s) of the constant domains bear a free thiol group. F(ab')2 antibody fragments originally were produced as pairs of Fab' fragments which have hinge cysteines between them. Other chemical couplings of antibody fragments are also known. The Fc fragment comprises the carboxy-terminal portions of both H chains held together by disulfides. The effector functions of antibodies are determined by sequences and glycan in the Fc region, the region which is also recognized by Fc receptors (FcR) found on certain types of cells.

[0564] The term "Fc region" herein is used to define a C-terminal region of an immunoglobulin heavy chain, including native-sequence Fc regions and variant Fc regions. Although the boundaries of the Fc region of an immunoglobulin heavy chain might vary, the human IgG heavy-chain Fc region is usually defined to stretch from an amino acid residue at position Cys226, or from Pro230, to the carboxyl-terminus thereof. Suitable native-sequence Fc regions for use in the antibodies of the invention include human IgG1, IgG2, IgG3 and IgG4.

[0565] The term "cytokine" refers to a secreted polypeptide or active fragment or mutant thereof that modulates the activity of cells, particularly cells of the immune system. Examples of cytokines include, for instance, chemokines, interferons, interleukins, lymphokines, and tumor necrosis factors. The term encompasses any cytokine protein, or a functional fragment or variant thereof. The term encompasses any native cytokine from any vertebrate source, including mammals such as primates (e.g., humans) and rodents (e.g., rats and mice), unless otherwise indicated. The term encompasses an unprocessed form of the cytokine as well as any form of the cytokine that results from processing in a cell. The term also encompasses naturally occurring variants of a cytokine. The term also encompasses non-naturally occurring variants of a cytokine, such as truncations, deletions, forms where the cytokine is linked to another molecule, and variants caused by at least one amino acid change to the amino acid sequence (e.g., by substitution, addition, or deletion). In some aspects, the variants or homologs have at least 90%, 95%, 96%, 97%, 98%, 99% or 100% amino acid sequence identity across the whole sequence or a portion of the sequence (e.g., a 50, 100, 125, or 150 or more continuous amino acid portion) compared to a naturally occurring cytokine polypeptide.

[0566] The term "IL-2" or "IL-2 polypeptide" as used herein refers to any interleukin-2 (IL-2) protein, or a functional fragment or variant thereof. The term encompasses any native IL-2 from any vertebrate source, including mammals such as primates (e.g., humans) and rodents (e.g., rats and mice), unless otherwise indicated. The term encompasses unprocessed IL-2 (e.g., a full length, precursor form of IL-2 that consists of amino acid residues 1-153) as well as any form of IL-2 that results from processing in the cell (e.g., a mature form of IL-2 that consists of amino acid residues 21-153). As such, the term encompasses a protein encoded by the amino acid sequence of SEQ ID NO: 160, as well as sequence variants thereof. The term also encompasses naturally occurring variants of IL-2. The term also encompasses non-naturally occurring variants of IL-2, such as truncations, deletions, forms where IL-2 is linked to another molecule, and variants caused by at least one amino acid change to the amino acid sequence (e.g., by substitution, addition, or deletion). In some aspects, the variants or homologs have at least 90%, 95%, 96%, 97%, 98%, 99% or 100% amino acid sequence identity across the whole sequence or a portion of the sequence (e.g., a 50, 100, or 133 continuous amino acid portion) compared to a naturally occurring IL-2 polypeptide, such as an IL-2 polypeptide encoded by the amino acid sequence of SEQ ID NO: 159 or 160. As such, the term "IL-2" or "IL-2 polypeptide" includes an IL-2 protein comprising the amino acid sequence of any one of SEQ ID NOs: 1-8, 159, 160, 230, 243-251, 260, 775-792, and 813-822, including variants thereof, such as variants created by one or more amino acid substitutions to the amino acid sequence of any one of SEQ ID NOs: 1-8, 159, 160, 230, 243-251, 260, 775-792, and 813-822.

[0567] The term "IL-15" or "IL-15 polypeptide" as used herein refers to any interleukin-15 (IL-15) protein, or a functional fragment or variant thereof. The term encompasses any native IL-15 from any vertebrate source, including mammals such as primates (e.g., humans) and rodents (e.g., rats and mice),

unless otherwise indicated. The term encompasses unprocessed IL-15 (e.g., a full length, precursor form of IL-15 that consists of amino acid residues 1-162) as well as any form of IL-15 that results from processing in the cell (e.g., a mature form of IL-15 that consists of amino acid residues 49-162). As such, the term encompasses a protein encoded by the amino acid sequence of SEQ ID NO: 167, as well as sequence variants thereof. The term also encompasses naturally occurring variants of IL-15. The term also encompasses non-naturally occurring variants of IL-15, such as truncations, deletions, forms where IL-15 is linked to another molecule, and variants caused by at least one amino acid change to the amino acid sequence (e.g., by substitution, addition, or deletion). In some aspects, the variants or homologs have at least 90%, 95%, 96%, 97%, 98%, 99% or 100% amino acid sequence identity across the whole sequence or a portion of the sequence (e.g., a 50, 100, or 114 continuous amino acid portion) compared to a naturally occurring IL-15 polypeptide, such as an IL-15 polypeptide encoded by the amino acid sequence of SEQ ID NO: 166 or 167. As such, the term "IL-15" or "IL-15 polypeptide" includes an IL-15 protein comprising the amino acid sequence of SEQ ID NO: 166 or 167, including variants thereof, such as variants created by one or more amino acid substitutions to the amino acid sequence of SEQ ID NO: 166 or 167.

[0568] "Functional fragments" of a cytokine comprise a portion of a full length cytokine protein which retains or has modified cytokine receptor binding capability (e.g., within at least 50%, 80%, 90%, 95%, 96%, 97%, 98%, 99% or 100% activity compared to the full length cytokine protein). The full length cytokine protein can be a full length cytokine protein of a wildtype cytokine protein, or it can be a full length cytokine protein of a modified variant of a cytokine protein, such as a full length cytokine that has been modified by one or more amino acid substitutions. Cytokine receptor binding capability can be shown, for example, by the capability of a cytokine to bind to the cytokine's cognate receptor or a component thereof (e.g., one or more chain(s) of a heterotrimeric receptor complex). As used herein, "full length" can refer to the full length of a cytokine in its unprocessed (i.e., precursor) form or it's processed (i.e., mature) form. The term also encompasses a portion of a full length protein which retains or has modified cytokine receptor binding capability (e.g., within at least 50%, 80%, 90%, 95%, 96%, 97%, 98%, 99% or 100% activity compared to the full length cytokine protein) and has been further modified to include one or more modifications to the amino acid sequence, such as one or more amino acid deletions, additions, or substitutions. Thus, a functional fragment of a cytokine not only encompasses a portion of a full length cytokine protein, but it also encompasses a variant of a portion of a full length cytokine protein. For instance, a functional fragment of an IL-2 polypeptide comprises a portion of a full length IL-2 protein which retains or has modified IL-2R binding capability (e.g., within at least 50%, 80%, 90%, 95%, 96%, 97%, 98%, 99% or 100% activity compared to full length wildtype IL-2). IL-2R binding capability can be shown, for example, by the capability to bind to the IL-2Rα chain, the IL-2Rβ chain, and/or the IL-2Rγ chain of the IL-2R, either individually or in combination with one another. A functional fragment of IL-2 includes, for example, an IL-2 protein that comprises amino

acid residues 21-153 of the full length IL-2 sequence of SEQ ID NO: 159, as well as variants thereof, such as variants that include one or more substitutions to the amino acid sequence. As such, a functional fragment of IL-2 includes, for example, an IL-2 protein comprising the amino acid sequence of any one of SEQ ID NOs: 1-8, 160, 230, 243-251, 260, 775-792, and 813-822. A functional fragment of IL-15 includes, for example, an IL-15 protein comprising the amino acid sequence of SEQ ID NO: 167.

[0569] The term "activatable" as used herein to describe any cytokine or functional fragment thereof means a cytokine or functional fragment thereof has been modified to comprise a masking moiety, and, in some embodiments, other components, that allow for activation of the cytokine or functional fragment thereof in a preferred environment. For example, a cytokine or functional fragment thereof that has been modified to comprise an masking moiety for activation in a preferred environment may be referred to herein as an "activatable cytokine," or "masked cytokine," or "activatable masked cytokine." As such, the term "masked cytokine" includes any cytokine or functional fragment thereof that has been modified to comprise a masking moiety, and, in some embodiments, other components, such as a cleavable peptide, that allow for activation of the cytokine or functional fragment thereof in a preferred environment.

[0570] The term "masking moiety" as used herein refers to a peptide capable of binding to, or otherwise exhibiting an affinity for, a cytokine or functional fragment thereof such that the masking moiety blocks, occludes, inhibits (e.g., decreases) or otherwise prevents (e.g., masks) the activity or binding of the cytokine or functional fragment thereof to its cognate receptor or protein. In some embodiments, the masking moiety is a cytokine receptor, or a subunit or functional fragment thereof.

[0571] The term "cytokine receptor" as used herein refers to any receptor within the art that binds to one or more cytokine(s) including, but not limited to, receptors of IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, IL-13, IL-14, IL-15, IL-16, IL-17, IL-18, IL-19, IL-20, IL-21, IL-22, IL-23, IL-24, IL-25, IL-26, IL-27, IL-28A, IL-28B, IL-29, IL-30, IL-31, IL-32, IL-33, IL-34, IL-35, IL-36, IL-37, granulocyte-macrophage colony-stimulating factor (GM-CSF), macrophage colony-stimulating factor (M-CSF), tumor necrosis factor alpha (TNF-α), transforming growth factor beta (TGF-β), IFN-γ (gamma), CD252, CD154, CD178, CD70, CD153, 4-1BB-L, TRAIL, RANKL, APO3L, CD256, CD257, CD258, TL1, AITRL, EDA1, interferon (IFN)-α (alpha), IFN-β (beta), IFN-γ (gamma), growth hormone (GH), erythropoietin (EPO), prolactin (PRL), leukemia inhibitory factor (LIF), oncostatin (OSM), and thrombopoietin (TPO). Some cytokine receptors function, in whole or in part, as heteromeric complexes of more than one subunit, or as homomeric complexes. The term also encompasses subunits of cytokine receptors that are capable of binding to one or more cytokine(s) either individually or when in complex with one or more other cytokine receptor subunits (e.g., as a heteromeric or homomeric complex). As such, reference to a "cytokine receptor" that is a heteromeric complex of three subunits, for example, includes reference to the heteromeric complex comprising all three subunits, as well as reference to each subunit individually or in various combinations with one another. Non-limiting examples of cytokine

receptors include CXCR1, CXCR2, CXCR3, CXCR4, CXCR5, CXCR6, CXCR7, CCR1, CCR2, CCR3, CCR4, CCR5, CCR6, CCR7, CCR8, CCR9, CCR10, CCR11, XCR1, CX3CR1, IL-1RAP, IL-1RAPL1, IL-1RAPL2, IL-1RL1, IL-1RL2, IL-1R1, IL-1R2, IL-2R, IL-2Rα, IL-2Rβ, IL-2Rγ, IL-3Rα, IL-4R, IL-5Rα, IL-6R, IL-6ST, IL-7R, IL-9R, IL-10Rα, IL-10Rβ, IL-11Rα, IL-12Rβ1, IL-12Rβ2, IL-13Rα1, IL-13Rα2, IL-15Rα, IL-17RA, IL-17RB, IL-17RC, IL-17RD, IL-17RE, IL-18RAP, IL-18R1, IL-20Rα, IL-20Rβ, IL-21R, IL-22Rα1, IL-22Rα2, IL-23R, IL-27Rα, IL-28Rα, IL-31RA, IFNAR1, IFNAR2, IFNGR1, IFNGR2, IFNLR1, GMRα (CD116), CD131, GHR, PRLR, EPOR, LIFR (CD118), OSMRβ, TPO-R (CD110), CSF-1R, EDAR, TNFRSF1A, TNFRSF1B, LTBR, TNFRSF4, CD40, FAS, TNFRSF6B, CD27, TNFRSF8, TNFRSF9, TNFRSF10A, TNFRSF10B, TNFRSF10C, TNFRSF10D, TNFRSF11A, TNFRSF11B, TNFRSF12A, TNFRSF13B, TNFRSF13C, TNFRSF14, NGFR, TNFRSF17, TNFRSF18, TNFRSF19, RELT, TNFRSF21, TNFRSF25, and EDA2R.

[0572] The term "IL-2R" or "IL-2 receptor" or "IL-2 cytokine receptor" as used herein refers to the high-affinity IL-2 receptor complex that comprises three separate and non-covalently linked chains: the IL-2Rα chain (also referred to as CD25), the IL-2Rβ chain (also referred to as CD122), and the IL-2Rγ chain (also referred to as CD132). IL-2 is capable of binding to the IL-2Rα chain. IL-2 is also capable of binding to the IL-2Rα chain in combination with the IL-2Rβ chain. IL-2 is also capable of binding to the IL-2Rα chain in combination with the IL-2Rβ and IL-2Rγ chains with highest affinity. In some cases, the term also encompasses the IL-2Rα chain, the IL-2Rβ chain, or the IL-2Rγ chain, or combinations thereof.

[0573] The term "IL-15R" or "IL-15 receptor" or "IL-15 cytokine receptor" as used herein refers to the high-affinity IL-15 receptor complex that comprises three separate and non-covalently linked chains: the IL-15Rα chain, the IL-2Rβ chain, and the IL-2Rγ chain. IL-15 is capable of binding to the IL-15Rα chain, to the heterodimer of the IL-2Rβ chain and the IL-2Rγ chain, and to the IL-15Rα chain in combination with the IL-2Rβ chain and the IL-2Rγ chain. In some cases, the term also encompasses the IL-15Rα chain, the IL-2Rβ chain, or the IL-2Rγ chain, or combinations thereof.

[0574] The term "half-life extension domain" refers to a domain that is linked to a target component (e.g., a cytokine or functional fragment thereof, or a masking moiety) for the purpose of extending the half-life of the target component in serum. The term "half-life extension domain" encompasses, for example, antibodies, antibody fragments, bispecific antibodies, albumin, binding proteins (e.g., albumin-binding proteins and IgG-binding proteins), polyamino acid sequences, and antibody derivatives (e.g., scFvs, scFcs, dual-variable-domains, and antibody derivatives based on the CrossMab approach).

[0575] "Percent (%) amino acid sequence identity" with respect to a reference polypeptide sequence is defined as the percentage of amino acid residues in a candidate sequence that are identical with the amino acid residues in the reference polypeptide sequence, after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity, and not considering any conservative substitutions as part of the sequence identity. Alignment for purposes of determining

percent amino acid sequence identity can be achieved in various ways that are within the skill in the art, for instance, using publicly available computer software such as BLAST, BLAST-2, ALIGN or Megalign (DNASTAR) software. Those skilled in the art can determine appropriate parameters for aligning sequences, including any algorithms needed to achieve maximal alignment over the full length of the sequences being compared. For example, the % amino acid sequence identity of a given amino acid sequence A to, with, or against a given amino acid sequence B (which can alternatively be phrased as a given amino acid sequence A that has or comprises a certain % amino acid sequence identity to, with, or against a given amino acid sequence B) is calculated as follows:

100 times the fraction X/Y

where X is the number of amino acid residues scored as identical matches by the sequence in that program's alignment of A and B, and where Y is the total number of amino acid residues in B. It will be appreciated that where the length of amino acid sequence A is not equal to the length of amino acid sequence B, the % amino acid sequence identity of A to B will not equal the % amino acid sequence identity of B to A.

[0576] Antibody "effector functions" refer to those biological activities attributable to the Fc region (a native sequence Fc region or amino acid sequence variant Fc region) of an antibody, and vary with the antibody isotype. Examples of antibody effector functions include: C1q binding and complement dependent cytotoxicity; Fc receptor binding; antibody-dependent cell-mediated cytotoxicity (ADCC); phagocytosis; down regulation of cell surface receptors (e.g., B cell receptors); and B cell activation.

[0577] "Binding affinity" as used herein refers to the strength of the non-covalent interactions between a single binding site of a molecule (e.g., a cytokine) and its binding partner (e.g., a cytokine receptor). In some embodiments, the affinity of a binding protein (e.g., a cytokine) can generally be represented by a dissociation constant (Kd). Affinity can be measured by common methods known in the art, including those described herein.

[0578] An "isolated" nucleic acid molecule encoding the cytokine polypeptides described herein is a nucleic acid molecule that is identified and separated from at least one contaminant nucleic acid molecule with which it is ordinarily associated in the environment in which it was produced. In some embodiments, the isolated nucleic acid is free of association with all components associated with the production environment. The isolated nucleic acid molecules encoding the polypeptides and cytokine polypeptides herein is in a form other than in the form or setting in which it is found in nature. Isolated nucleic acid molecules therefore are distinguished from nucleic acid encoding the polypeptides and cytokine polypeptides herein existing naturally in cells.

[0579] The term "pharmaceutical formulation" refers to a preparation that is in such form as to permit the biological activity of the active ingredient to be effective, and that contains no additional components that are unacceptably toxic to a subject to which the formulation would be administered. Such formulations are sterile.

[0580] "Carriers" as used herein include pharmaceutically acceptable carriers, excipients, or stabilizers that are nontoxic to the cell or mammal being exposed thereto at the dosages and concentrations employed. Often the physiologically acceptable carrier is an aqueous pH buffered solution. Examples of physiologically acceptable carriers include buffers such as phosphate, citrate, and other organic acids; antioxidants including ascorbic acid; low molecular weight (less than about 10 residues) polypeptide; proteins, such as serum albumin, gelatin, or immunoglobulins; hydrophilic polymers such as polyvinylpyrrolidone; amino acids such as glycine, glutamine, asparagine, arginine or lysine; monosaccharides, disaccharides, and other carbohydrates including glucose, mannose, or dextrins; chelating agents such as EDTA; sugar alcohols such as mannitol or sorbitol; salt-forming counterions such as sodium; and/or nonionic surfactants such as TWEEN™, polyethylene glycol (PEG), and PLURONICS™.

[0581] As used herein, the term "treatment" refers to clinical intervention designed to alter the natural course of the individual or cell being treated during the course of clinical pathology. Desirable effects of treatment include decreasing the rate of disease progression, ameliorating or palliating the disease state, and remission or improved prognosis. An individual is successfully "treated", for example, if one or more symptoms associated with a disorder (e.g., a neoplastic disease) are mitigated or eliminated. For example, an individual is successfully "treated" if treatment results in increasing the quality of life of those suffering from a disease, decreasing the dose of other medications required for treating the disease, reducing the frequency of recurrence of the disease, lessening severity of the disease, delaying the development or progression of the disease, and/or prolonging survival of individuals.

[0582] As used herein, "in conjunction with" or "in combination with" refers to administration of one treatment modality in addition to another treatment modality. As such, "in conjunction with" or "in combination with" refers to administration of one treatment modality before, during or after administration of the other treatment modality to the individual.

[0583] As used herein, the term "prevention" includes providing prophylaxis with respect to occurrence or recurrence of a disease in an individual. An individual may be predisposed to, susceptible to a disorder, or at risk of developing a disorder, but has not yet been diagnosed with the disorder. In some embodiments, masked cytokines described herein are used to delay development of a disorder.

[0584] As used herein, an individual "at risk" of developing a disorder may or may not have detectable disease or symptoms of disease, and may or may not have displayed detectable disease or symptoms of disease prior to the treatment methods described herein. "At risk" denotes that an individual has one or more risk factors, which are measurable parameters that correlate with development of the disease, as known in the art. An individual having one or more of these risk factors has a higher probability of developing the disorder than an individual without one or more of these risk factors.

[0585] An "effective amount" refers to at least an amount effective, at dosages and for periods of time necessary, to achieve the desired or indicated effect, including a therapeutic or prophylactic result.

An effective amount can be provided in one or more administrations. A "therapeutically effective amount" is at least the minimum concentration required to effect a measurable improvement of a particular disorder. A therapeutically effective amount herein may vary according to factors such as the disease state, age, sex, and weight of the patient, and the ability of the antibody to elicit a desired response in the individual. A therapeutically effective amount may also be one in which any toxic or detrimental effects of the masked cytokine are outweighed by the therapeutically beneficial effects. A "prophylactically effective amount" refers to an amount effective, at the dosages and for periods of time necessary, to achieve the desired prophylactic result. Typically, but not necessarily, since a prophylactic dose is used in subjects prior to or at the earlier stage of disease, the prophylactically effective amount can be less than the therapeutically effective amount.

[0586] "Chronic" administration refers to administration of the medicament(s) in a continuous as opposed to acute mode, so as to main the initial therapeutic effect (activity) for an extended period of time. "Intermittent" administration is treatment that is not consecutively done without interruption, but rather is cyclic in nature.

[0587] As used herein, an "individual" or a "subject" is a mammal. A "mammal" for purposes of treatment includes humans, domestic and farm animals, and zoo, sports, or pet animals, such as dogs, horses, rabbits, cattle, pigs, hamsters, gerbils, mice, ferrets, rats, cats, etc. In some embodiments, the individual or subject is human.

VII. EXEMPLARY EMBODIMENTS

[0588] Among the provided embodiments are:

1. A masked cytokine comprising:

a) a masking moiety; and

b) a cytokine or functional fragment thereof,

wherein the masking moiety is linked to the cytokine or functional fragment thereof via a first linker.

2. The masked cytokine of embodiment 1, further comprising a half-life extension domain that is linked to either the masking moiety or the cytokine or functional fragment thereof.

3. The masked cytokine of embodiment 2, wherein the half-life extension domain is linked to either the masking moiety or the cytokine or functional fragment thereof via a second linker.

4. The masked cytokine of embodiment 2 or embodiment 3, wherein:

i) the masked cytokine comprises in an N to C-terminal or in a C to N-terminal direction: a) the masking moiety; b) the first linker; c) the cytokine or functional fragment thereof; and d) the half-life extension domain;

ii) the masked cytokine comprises in an N to C-terminal or in a C to N-terminal direction: a) the masking moiety; b) the first linker; c) the cytokine or functional fragment thereof; d) the second linker and e) the half-life extension domain;

iii) the masked cytokine comprises in an N to C-terminal or in a C to N-terminal direction: a) the cytokine or functional fragment thereof; b) the first linker; c) the masking moiety; and d) the half-life extension domain; or

iv) the masked cytokine comprises in an N to C-terminal or in a C to N-terminal direction: a) the cytokine or functional fragment thereof; b) the first linker; c) the masking moiety; d) the second linker; and e) the half-life extension domain.

5. The masked cytokine of any one of embodiments 1-4, wherein the cytokine or functional fragment thereof is an IL-2 polypeptide or functional fragment thereof.

6. The masked cytokine of embodiment 5, wherein the IL-2 polypeptide or functional fragment thereof comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 1-8, 160, 230, 243-251, 260, 775-792, and 813-822.

7. The masked cytokine of embodiment 5, wherein the IL-2 polypeptide or functional fragment thereof comprises an amino acid sequence produced by introducing one or more amino acid substitutions into the amino acid sequence of the IL-2 polypeptide or functional fragment thereof that reduces the affinity of the IL-2 polypeptide or functional fragment thereof for CD25 (IL-2Rα).

8. The masked cytokine of embodiment 7, wherein the amino acid sequence is produced by introducing one or more of the following amino acid substitutions into any one of SEQ ID NOs: 1-8, 160, 243-251, 260, 775-792, and 813-822: R38A, F42A, F42K, F42E, K43A, Y45A, Y45N, Y45R, E62A, E62R, E62S, and L72G.

9. The masked cytokine of embodiment 5, wherein the IL-2 polypeptide or functional fragment thereof comprises an amino acid sequence produced by introducing one or more amino acid substitutions into the amino acid sequence of the IL-2 polypeptide or functional fragment thereof that increases the affinity of the IL-2 polypeptide or functional fragment thereof for IL-2Rβ or IL-2Rγ.

10. The masked cytokine of embodiment 9, wherein the amino acid sequence is produced by introducing one or more of the following amino acid substitutions into any one of SEQ ID NOs: 1-8, 160, 243-251, 260, 775-792, and 813-822: H16I, L18C, D20A, D20L, D20F, N29L, L80F, R81D, L85V, I86V, and I92F.

11. The masked cytokine of embodiment 7 or embodiment 8, wherein the amino acid sequence is produced by further introducing one or more amino acid substitutions that increase the affinity of the IL-2 polypeptide or functional fragment thereof for IL-2Rβ or IL-2Rγ.

12. The masked cytokine of embodiment 11, wherein the one or more amino acid substitutions that increase the affinity of the IL-2 polypeptide or functional fragment thereof for IL-2Rβ or IL-2Rγ is selected from the group consisting of H16I, L18C, D20A, D20L, D20F, N29L, L80F, R81D, L85V, I86V, and I92F.

13. The masked cytokine of embodiment 5, wherein the IL-2 polypeptide or functional fragment thereof comprises an amino acid sequence produced by introducing one or more amino acid substitutions into the amino acid sequence of the IL-2 polypeptide or functional fragment thereof that stabilizes the IL-2 polypeptide or functional fragment thereof.

14. The masked cytokine of embodiment 13, wherein the amino acid sequence is produced by introducing one of the following amino acid substitutions into any one of SEQ ID NOs: 1-8, 160, 243-251, 260, 775-792, and 813-822: C125S, C125A, and C125G.

15. The masked cytokine of any one of embodiments 7-12, wherein the amino acid sequence is produced by further introducing one or more amino acid substitutions that stabilize the IL-2 polypeptide or functional fragment thereof.

16. The masked cytokine of embodiment 15, wherein the one or more amino acid substitutions that stabilize the IL-2 polypeptide or functional fragment thereof is the amino acid substitution C125S, C125A, or C125G.

17. The masked cytokine of any one of embodiments 5-16, wherein the masking moiety comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 9, 10, 161-165, 187-218, 221-229, 231, 261, 826 and 827.

18. The masked cytokine of any one of embodiments 1-4, wherein the cytokine or functional fragment thereof is an IL-15 polypeptide or functional fragment thereof.

19. The masked cytokine of embodiment 18, wherein the IL-15 polypeptide or functional fragment thereof comprises the amino acid sequence of SEQ ID NO: 167.

20. The masked cytokine of embodiment 18 or embodiment 19, wherein the masking moiety comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 10, 161-165, 219-229, 232-234, 261, and 823-827.

21. The masked cytokine of embodiment 18 or embodiment 19, wherein the masking moiety comprises an amino acid sequence produced by introducing one or more of the following amino acid substitutions into the amino acid sequence of any one of SEQ ID NOs: 232-234, and 823-825: R24A, R26A, K34A, S40A, L42A, and P67A.

22. The masked cytokine of any one of embodiments 2-21, wherein the half-life extension domain is an antibody or fragment thereof.

23. The masked cytokine of embodiment 22, wherein the antibody or fragment thereof comprises either a heavy chain polypeptide or a light chain polypeptide.

24. The masked cytokine of embodiment 23, wherein the heavy chain polypeptide comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 158, 168, and 169.

25. The masked cytokine of embodiment 23, wherein the heavy chain polypeptide comprises one or more amino acid substitutions altering effector function.

26. The masked cytokine of embodiment 25, wherein the heavy chain polypeptide:

a) is an IgG1 heavy chain polypeptide and comprises the amino acid substitution(s):

i) N297A, N297G, or N297Q;

ii) L234A and L235A;

iii) C220S, C226S, C229S, and P238S;

iv) C226S, C229S, E233P, L234V, and L235A;

v) L234F, L235E, and P331S;

vi) S267E and L328F;

vii) D265A;

viii) L234A, L235A, and P329G;

b) is an IgG2 heavy chain polypeptide and comprises the amino acid substitution(s):

i) V234A and G237A;

ii) H268Q, V309L, A330S, and A331S; or

iii) V234A, G237A, P238S, H268A, V309L, A330S, and P331S; or

e) is an IgG4 heavy chain polypeptide and comprises the amino acid substitution(s):

i) L235A, G237A, and E318A;

ii) S228P, L234A, and L235A;

iii) H268Q, V309L, A330S, and P331S; or

iv) S228P and L235A, numbered according to the Kabat EU numbering system.

27. The masked cytokine of embodiment 25, wherein the heavy chain polypeptide comprises one or more amino acid substitutions enhancing effector function.

28. The masked cytokine of embodiment 27, wherein the heavy chain polypeptide is an IgG1 heavy chain polypeptide and comprises the amino acid substitution(s):

a) S298A, E333A, and K334A;

b) S239D and I332E;

c) S239D, A330L, and I332E;

d) P247I and A339D or A339Q;

e) D280H and K290S;

f) D280H, K290S, and either S298D or S298V;

g) F243L, R292P, and Y300L;

h) F243L, R292P, Y300L, and P396L;

i) F243L, R292P, Y300L, V305I, and P396L;

j) G236A, S239D, and I332E;

k) K326A and E333A;

l) K326W and E333S;

m) K290E, S298G, and T299A;

n) K290E, S298G, T299A, and K326E;

o) K290N, S298G, and T299A;

p) K290N, S298G, T299A, and K326E;

q) K334V;

r) L235S, S239D, and K334V;

s) K334V and Q331M, S239D, F243V, E294L, or S298T;

t) E233L, Q311M, and K334V;

u) L234I, Q311M, and K334V;

v) K334V and S298T, A330M, or A330F;

w) K334V, Q311M, and either A330M or A330F;

x) K334V, S298T, and either A330M or A330F;

y) K334V, S239D, and either A330M or S298T;

z) L234Y, Y296W, and K290Y, F243V, or E294L;

aa) Y296W and either L234Y or K290Y;

ab) S239D, A330S, and I332E,

ac) V264I;

ad) F243L and V264I;

ae) L328M;

af) I332E;

ag) L328M and I332E;

ah) V264I and I332E;

ai) S239E and I332E;

aj) S239Q and I332E;

ak) S239E;

al) A330Y;

am) I332D;

an) L328I and I332E;

ao) L328Q and I332E;

ap) V264T;

aq) V240I;

ar) V266I;

as) S239D;

at) S239D and I332D;

au) S239D and I332N;

av) S239D and I332Q;

aw) S239E and I332D;

ax) S239E and I332N;

ay) S239E and I332Q;

az) S239N and I332D;

ba) S239N and I332E;

bb) S239Q and I332D;

bc) A330Y and I332E;

bd) V264I, A330Y, and I332E;

be) A330L and I332E;

bf) V264I, A330L, and I332E;

bg) L234E, L234Y, or L234I;

bh) L235D, L235S, L235Y, or L235I;

bi) S239T;

bj) V240M;

bk) V264Y;

bl) A330I;

bm) N325T;

bn) I332E and L328D, L328V, L328T, or L328I;

bo) V264I, I332E, and either S239E or S239Q;

bp) S239E, V264I, A330Y, and I332E;

bq) A330Y, I332E, and either S239D or S239N;

br) A330L, I332E, and either S239D or S239N;

bs) V264I, S298A, and I332E;

bt) S298A, I332E, and either S239D or S239N;

bu) S239D, V264I, and I332E;

bv) S239D, V264I, S298A, and I332E;

bw) S239D, V264I, A330L, and I332E;

bx) S239D, I332E, and A330I;

by) P230A;

bz) P230A, E233D, and I332E;

ca) E272Y;

cb) K274T, K274E, K274R, K274L, or K274Y;

cd) F275W;

ce) N276L;

cf) Y278T;

cg) V302I;

ch) E318R;

ci) S324D, S324I or S324V;

cj) K326I or K326T;

ck) T335D, T335R, or T335Y;

cl) V240I and V266I;

cm) S239D, A330Y, I332E, and L234I;

cn) S239D, A330Y, I332E, and L235D;

co) S239D, A330Y, I332E, and V240I;

cp) S239D, A330Y, I332E, and V264T; or

cq) S239D, A330Y, I332E, and either K326E or K326T, numbered according to the Kabat EU numbering system.

29. The masked cytokine of embodiment 23, wherein the light chain polypeptide comprises the amino acid sequence of SEQ ID NO: 157 or 170.

30. The masked cytokine of embodiment 22, wherein the antibody or fragment thereof is a Fragment crystallizable domain (Fc domain) or fragment thereof.

31. The masked cytokine of embodiment 30, wherein the Fc domain or fragment thereof comprises one or more amino acid substitutions altering effector function.

32. The masked cytokine of embodiment 31, wherein the Fc domain or functional fragment thereof:

a) is an IgG1 Fc domain or functional fragment thereof and comprises the amino acid substitution(s):

i) N297A, N297G, or N297Q;

ii) L234A and L235A;

iii) C220S, C226S, C229S, and P238S;

iv) C226S, C229S, E233P, L234V, and L235A;

v) L234F, L235E, and P331S;

vi) S267E and L328F;

vii) D265A;

viii) L234A, L235A, and P329G;

b) is an IgG2 Fc domain or functional fragment thereof and comprises the amino acid substitution(s):

i) V234A and G237A;

ii) H268Q, V309L, A330S, and A331S; or

iii) V234A, G237A, P238S, H268A, V309L, A330S, and P331S; or

e) is an IgG4 Fc domain or functional fragment thereof and comprises the amino acid substitution(s):

i) L235A, G237A, and E318A;

ii) S228P, L234A, and L235A;

iii) H268Q, V309L, A330S, and P331S; or

iv) S228P and L235A, numbered according to the Kabat EU numbering system.

33. The masked cytokine of embodiment 31, wherein the Fc domain or functional fragment thereof comprises one or more amino acid substitutions enhancing effector function.

34. The masked cytokine of embodiment 33, wherein the Fc domain or functional fragment thereof is an IgG1 Fc domain or functional fragment thereof and comprises the amino acid substitution(s):

a) S298A, E333A, and K334A;
b) S239D and I332E;
c) S239D, A330L, and I332E;
d) P247I and A339D or A339Q;
e) D280H and K290S;
f) D280H, K290S, and either S298D or S298V;
g) F243L, R292P, and Y300L;
h) F243L, R292P, Y300L, and P396L;
i) F243L, R292P, Y300L, V305I, and P396L;
j) G236A, S239D, and I332E;
k) K326A and E333A;
l) K326W and E333S;
m) K290E, S298G, and T299A;
n) K290E, S298G, T299A, and K326E;
o) K290N, S298G, and T299A;
p) K290N, S298G, T299A, and K326E;
q) K334V;
r) L235S, S239D, and K334V;
s) K334V and Q331M, S239D, F243V, E294L, or S298T;
t) E233L, Q311M, and K334V;
u) L234I, Q311M, and K334V;
v) K334V and S298T, A330M, or A330F;
w) K334V, Q311M, and either A330M or A330F;
x) K334V, S298T, and either A330M or A330F;
y) K334V, S239D, and either A330M or S298T;
z) L234Y, Y296W, and K290Y, F243V, or E294L;
aa) Y296W and either L234Y or K290Y;
ab) S239D, A330S, and I332E,
ac) V264I;

ad) F243L and V264I;

ae) L328M;

af) I332E;

ag) L328M and I332E;

ah) V264I and I332E;

ai) S239E and I332E;

aj) S239Q and I332E;

ak) S239E;

al) A330Y;

am) I332D;

an) L328I and I332E;

ao) L328Q and I332E;

ap) V264T;

aq) V240I;

ar) V266I;

as) S239D;

at) S239D and I332D;

au) S239D and I332N;

av) S239D and I332Q;

aw) S239E and I332D;

ax) S239E and I332N;

ay) S239E and I332Q;

az) S239N and I332D;

ba) S239N and I332E;

bb) S239Q and I332D;

bc) A330Y and I332E;

bd) V264I, A330Y, and I332E;

be) A330L and I332E;

bf) V264I, A330L, and I332E;

bg) L234E, L234Y, or L234I;

bh) L235D, L235S, L235Y, or L235I;

bi) S239T;

bj) V240M;

bk) V264Y;

bl) A330I;

bm) N325T;

bn) I332E and L328D, L328V, L328T, or L328I;

bo) V264I, I332E, and either S239E or S239Q;

bp) S239E, V264I, A330Y, and I332E;

bq) A330Y, I332E, and either S239D or S239N;

br) A330L, I332E, and either S239D or S239N;

bs) V264I, S298A, and I332E;

bt) S298A, I332E, and either S239D or S239N;

bu) S239D, V264I, and I332E;

bv) S239D, V264I, S298A, and I332E;

bw) S239D, V264I, A330L, and I332E;

bx) S239D, I332E, and A330I;

by) P230A;

bz) P230A, E233D, and I332E;

ca) E272Y;

cb) K274T, K274E, K274R, K274L, or K274Y;

cd) F275W;

ce) N276L;

cf) Y278T;

cg) V302I;

ch) E318R;

ci) S324D, S324I or S324V;

cj) K326I or K326T;

ck) T335D, T335R, or T335Y;

cl) V240I and V266I;

cm) S239D, A330Y, I332E, and L234I;

cn) S239D, A330Y, I332E, and L235D;

co) S239D, A330Y, I332E, and V240I;

cp) S239D, A330Y, I332E, and V264T; or

cq) S239D, A330Y, I332E, and either K326E or K326T, numbered according to the Kabat EU numbering system.

35. The masked cytokine of any one of embodiments 30-32, wherein the Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 154.

36. The masked cytokine of any one of embodiments 2-21, wherein the half-life extension domain is an albumin polypeptide or fragment thereof.

37. The masked cytokine of embodiment 36, wherein the albumin polypeptide or fragment thereof comprises the amino acid sequence of SEQ ID NO: 171.

38. The masked cytokine of any one of embodiments 2-21, wherein the half-life extension domain is an albumin-binding protein or fragment thereof.

39. The masked cytokine of embodiment 38, wherein the albumin-binding protein or fragment thereof comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 172-174 and 252-259.

40. The masked cytokine of any one of embodiments 2-21, wherein the half-life extension domain is an IgG-binding protein or fragment thereof.

41. The masked cytokine of embodiment 40, wherein the IgG binding protein or functional fragment thereof comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 175-186.

42. The masked cytokine of any one of embodiments 2-21, wherein the half-life extension domain is a polyamino acid sequence.

43. The masked cytokine of embodiment 42, wherein the polyamino acid sequence is a PAS polypeptide or an XTEN polypeptide.

44. The masked cytokine of embodiment 43, wherein the PAS polypeptide comprises at least 25, at least 50, at least 100, at least 150, at least 200, at least 250, at least 300, at least 400, at least 500, at least 600, at least 700, at least 800, at least 900, at least 1000, at least 1100, at least 1200, at least 1300, at least 1500, at least 2000, at least 2500, or at least 3000 amino acid residues, wherein each amino acid residue is either a proline or an alanine residue.

45. The masked cytokine of embodiment 43, wherein the PAS polypeptide comprises at least 25, at least 50, at least 100, at least 150, at least 200, at least 250, at least 300, at least 400, at least 500, at least 600, at least 700, at least 800, at least 900, at least 1000, at least 1100, at least 1200, at least 1300, at least 1500, at least 2000, at least 2500, or at least 3000 amino acid residues, wherein each amino acid residue is selected from the group consisting of a proline, an alanine, and a serine residue.

46. The masked cytokine of embodiment 43, wherein the XTEN polypeptide comprises an amino acid sequence of about 25 to about 500, about 200 to about 1000, about 500 to about 1500, about 1000 to about 2000, or about 1500 to about 3000 amino acid residues, wherein at least about 70%, 75%, 80%, or 85% of the amino acid sequence consists of non-overlapping sequence motifs where each of the motifs has 5 to 100 amino acid residues, 5 to 50 amino acids residues, or 9 to 36 amino acid residues, and wherein at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% of each of the motifs consists of four, five, or six types of amino acid residues selected from the group consisting of glycine (G), alanine (A), serine (S), threonine (T), glutamate (E) and proline (P), and wherein the content of any one amino acid type in the full-length XTEN polypeptide does not exceed about 40%, about 35%, about 30%, about 25%, about 15%, about 10%, or about 8%.

47. The masked cytokine of any one of embodiments 1-46, wherein the masked cytokine further comprises one or more PEG polymer chains attached to the masked cytokine.

48. The masked cytokine of embodiment 47, wherein the one or more PEG polymer chains are attached to the cytokine or functional fragment thereof and/or the half-life extension domain.

49. The masked cytokine of any one of embodiments 1-48, wherein the masked cytokine is modified, or is further modified, by altering the amino acid sequence of the masked cytokine such that one or more additional N-linked and/or O-linked glycosylation sites are created.

50. The masked cytokine of embodiment 49, wherein the masked cytokine is modified, or is further modified, by altering the amino acid sequence of the masked cytokine such that one or more additional asparagine-X-serine (N-X-S) and/or asparagine-X-threonine (N-X-T) tripeptide sequence(s) is/are introduced into the amino acid sequence of the masked cytokine, wherein X is any amino acid except proline.

51. The masked cytokine of embodiment 49 or embodiment 50, wherein the masked cytokine is modified, or is further modified, by altering the amino acid sequence of the masked cytokine such that one or more additional serine or threonine residues is/are introduced into the amino acid sequence of the masked cytokine.

52. The masked cytokine of any one of embodiments 1-51, wherein the first linker comprises a first cleavable peptide.

53. The masked cytokine of any one of embodiments 1-52, where the first linker comprises a first N-terminal spacer domain and/or a first C-terminal spacer domain.

54. The masked cytokine of embodiment 53, wherein the first linker comprises:

a) the first N-terminal spacer domain, the first cleavable peptide, and the first C-terminal spacer domain;

b) the first N-terminal spacer domain and the first cleavable peptide;

c) the first N-terminal spacer domain and the first C-terminal spacer domain;

d) the first cleavable peptide and the first C-terminal spacer domain;

e) the first N-terminal spacer domain; or

f) the first C-terminal spacer domain.

55. The masked cytokine of embodiment 53 or embodiment 54, wherein the first cleavable peptide comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 96-153, 236-242, 264, 270-302, 306-317, 342-347, 356-415, 420-491, 494-501, 504-535, and 538-555.

56. The masked cytokine of any one of embodiments 53-55, wherein the first N-terminal spacer domain comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 20-95, 235, 268, 269, 303-305, 323-338, 340, 341, 727, 794, and 799.

57. The masked cytokine of any one of embodiments 53-55, wherein the first C-terminal spacer domain comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 20-95, 235, 268, 269, 303-305, 323-338, 340, 341, 727, 794, and 799.

58. The masked cytokine of embodiment 53 or embodiment 54, wherein the first cleavable peptide comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 96-153, 264, 270-302, 306-317, 342-347, 356-415, 420-491, 494-501, 504-535, and 538-555, and an amino acid sequence selected from the group consisting of SEQ ID NOs: 236-242.

59. The masked cytokine of embodiment 58, wherein the amino acid sequence selected from the group consisting of SEQ ID NOs: 96-153, 264, 270-302, 306-317, 342-347, 356-415, 420-491, 494-501, 504-535, and 538-555 comprises an N-terminus and a C-terminus, and the amino acid sequence selected from the group consisting of SEQ ID NOs: 236-242 is linked to the N-terminus or the C-terminus of the amino acid sequence selected from the group consisting of SEQ ID NOs: 96-153, 264, 270-302, 306-317, 342-347, 356-415, 420-491, 494-501, 504-535, and 538-555.

60. The masked cytokine of any one of embodiments 1-59, wherein the first linker comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 11-153, 235-242, 262-264, 268-320, 323-338, 340-354, 356-555, 668, 691, 724, 725, 727, 762-771, 794, and 797-812.

61. The masked cytokine of any one of embodiments 3-60, wherein the second linker comprises a second cleavable peptide.

62. The masked cytokine of any one of embodiments 3-61, wherein the second linker comprises a second N-terminal spacer domain and/or a second C-terminal spacer domain.

63. The masked cytokine of embodiment 62, wherein the second linker comprises:

a) the second N-terminal spacer domain, the second cleavable peptide, and second first C-terminal spacer domain;

b) the second N-terminal spacer domain and the second cleavable peptide;

c) the second N-terminal spacer domain and the second C-terminal spacer domain;

d) the second cleavable peptide and the second C-terminal spacer domain;

e) the second N-terminal spacer domain; or

f) the second C-terminal spacer domain.

64. The masked cytokine of any one of embodiments 61-63, wherein the second cleavable peptide comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 96-153, 236-242, 264, 270-302, 306-317, 342-347, 356-415, 420-491, 494-501, 504-535, and 538-555.

65. The masked cytokine of any one of embodiments 62-64, wherein the second N-terminal spacer domain comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 20-95, 235, 268, 269, 303-305, 323-338, 340, 341, 727, 794, and 799.

66. The masked cytokine of any one of embodiments 62-65, wherein the second C-terminal spacer domain comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 20-95, 235, 268, 269, 303-305, 323-338, 340, 341, 727, 794, and 799.

67. The masked cytokine of embodiment 62 or embodiment 63, wherein the second cleavable peptide comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 96-153, 264, 270-302, 306-317, 342-347, 356-415, 420-491, 494-501, 504-535, and 538-555, and an amino acid sequence selected from the group consisting of SEQ ID NOs: 236-242.

68. The masked cytokine of embodiment 67, wherein the amino acid sequence selected from the group consisting of SEQ ID NOs: 96-153, 264, 270-302, 306-317, 342-347, 356-415, 420-491, 494-501, 504-535, and 538-555 comprises an N-terminus and a C-terminus, and the amino acid sequence selected from the group consisting of SEQ ID NOs: 236-242 is linked to the N-terminus or the C-terminus of the amino acid sequence selected from the group consisting of SEQ ID NOs: 96-153, 264, 270-302, 306-317, 342-347, 356-415, 420-491, 494-501, 504-535, and 538-555.

69. The masked cytokine of any one of embodiments 3-68, wherein the second linker comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 11-153, 235-242, 262-264, 268-320, 323-338, 340-354, 356-555, 668, 691, 724, 725, 727, 762-771, 794, and 797-812.

70. A masked cytokine comprising:

a) a first masking moiety;

b) a cytokine or functional fragment thereof,

wherein the first masking moiety is linked to the cytokine or functional fragment thereof via a first linker; and

c) a second masking moiety,

wherein the second masking moiety is linked to the cytokine or functional fragment thereof via a second linker.

71. The masked cytokine of embodiment 70, further comprising a half-life extension domain that is linked to either the first masking moiety or the second masking moiety.

72. The masked cytokine of embodiment 71, wherein the half-life extension domain is linked to either the first masking moiety or the second masking moiety via a third linker.

73. The masked cytokine of embodiment 71 or embodiment 72, wherein:

i) the masked cytokine comprises in an N to C-terminal or in a C to N-terminal direction: a) the first masking moiety; b) the first linker; c) the cytokine or functional fragment thereof; d) the second linker; e) the second masking moiety; and f) the half-life extension domain;

ii) the masked cytokine comprises in an N to C-terminal or in a C to N-terminal direction: a) the first masking moiety; b) the first linker; c) the cytokine or functional fragment thereof; d) the second linker; e) the second masking moiety; f) the third linker; and g) the half-life extension domain;

iii) the masked cytokine comprises in an N to C-terminal or in a C to N-terminal direction: a) the second masking moiety; b) the second linker; c) the cytokine or functional fragment thereof; d) the first linker; e) the first masking moiety; and f) the half-life extension domain; or

iv) the masked cytokine comprises in an N to C-terminal or in a C to N-terminal direction: a) the second masking moiety; b) the second linker; c) the cytokine or functional fragment thereof; d) the first linker; e) the first masking moiety; f) the third linker; and g) the half-life extension domain.

74. The masked cytokine of any one of embodiments 70-73, wherein the cytokine or functional fragment thereof is an IL-2 polypeptide or functional fragment thereof.

75. The masked cytokine of embodiment 74, wherein the IL-2 polypeptide or functional fragment thereof comprises:

a) an amino acid sequence selected from the group consisting of SEQ ID NOs: 1-8, 160, 230, 243-251, 260, 775-792, and 813-822; or

b) an amino acid sequence produced by introducing one or more of the following amino acid substitutions into any one of SEQ ID NOs: 1-8, 160, 243-251, 260, 775-792, and 813-822: H16I, L18C, D20A, D20L, D20F, N29L, R38A, F42A, F42K, F42E, F43A, Y45A, Y45N, Y45R, E62A, E62R, E62S, L72G, L80F, R81D, L85V, I86V, I92F, and C125S.

76. The masked cytokine of embodiment 74 or embodiment 75, wherein the first masking moiety comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 9, 10, 161-165, 187-218, 221-229, 231, and 261, and the second masking moiety comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 9, 10, 161-165, 187-218, 221-229, 231, and 261, and wherein the amino acid sequence of the first masking moiety and the second masking moiety are different.

77. The masked cytokine of any one of embodiments 74-76, wherein:

a) the first masking moiety comprises the amino acid sequence of SEQ ID NO: 9 or 231, and the second masking moiety comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 10, 161-165, 187-218, 221-226, and 261; or

b) the first masking moiety comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 10, 161-165, 187-218, 221-226, and 261, and the second masking moiety comprises the amino acid sequence of SEQ ID NO: 9 or 231.

78. The masked cytokine of any one of embodiments 70-73, wherein the cytokine or functional fragment thereof is an IL-15 polypeptide or functional fragment thereof.

79. The masked cytokine of embodiment 78, wherein the IL-15 polypeptide or functional fragment thereof comprises the amino acid sequence of SEQ ID NO: 167.

80. The masked cytokine of embodiment 78 or embodiment 79, wherein:

a) the first masking moiety comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 232-234, and 823-825, and the second masking moiety comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 10, 161-165, 219-229, and 261;

b) the first masking moiety comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 10, 161-165, 219-229, and 261, and the second masking moiety comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 232-234, and 823-825;

c) the first masking moiety comprises an amino acid sequence produced by introducing one or more of the following amino acid substitutions into the amino acid sequence of any one of SEQ ID NOs: 232-234, and 823-825: R24A, R26A, K34A, S40A, L42A, and P67A, and the second masking moiety comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 10, 161-165, 219-229, and 261; or

d) the first masking moiety comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 10, 161-165, 219-229, and 261, and the second masking moiety comprises an amino acid sequence produced by introducing one or more of the following amino acid substitutions into the amino acid sequence of any one of SEQ ID NOs: 232-234, and 823-825: R24A, R26A, K34A, S40A, L42A, and P67A.

81. The masked cytokine of any one of embodiments 71-80, wherein the half-life extension domain is an antibody or fragment thereof.

82. The masked cytokine of embodiment 81, wherein the antibody or fragment thereof comprises either a heavy chain polypeptide or a light chain polypeptide.

83. The masked cytokine of embodiment 82, wherein the heavy chain polypeptide comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 158, 168, and 169.

84. The masked cytokine of embodiment 82, wherein the heavy chain polypeptide comprises one or more amino acid substitutions altering effector function.

85. The masked cytokine of embodiment 84, wherein the heavy chain polypeptide:

a) is an IgG1 heavy chain polypeptide and comprises the amino acid substitution(s):

i) N297A, N297G, or N297Q;

ii) L234A and L235A;

iii) C220S, C226S, C229S, and P238S;

iv) C226S, C229S, E233P, L234V, and L235A;

v) L234F, L235E, and P331S;

vi) S267E and L328F;

vii) D265A;

viii) L234A, L235A, and P329G;

b) is an IgG2 heavy chain polypeptide and comprises the amino acid substitution(s):

i) V234A and G237A;

ii) H268Q, V309L, A330S, and A331S; or

iii) V234A, G237A, P238S, H268A, V309L, A330S, and P331S; or

e) is an IgG4 heavy chain polypeptide and comprises the amino acid substitution(s):

i) L235A, G237A, and E318A;

ii) S228P, L234A, and L235A;

iii) H268Q, V309L, A330S, and P331S; or

iv) S228P and L235A, numbered according to the Kabat EU numbering system.

86. The masked cytokine of embodiment 84, wherein the heavy chain polypeptide comprises one or more amino acid substitutions enhancing effector function.

87. The masked cytokine of embodiment 86, wherein the heavy chain polypeptide is an IgG1 heavy chain polypeptide and comprises the amino acid substitution(s):

a) S298A, E333A, and K334A;

b) S239D and I332E;

c) S239D, A330L, and I332E;

d) P247I and A339D or A339Q;

e) D280H and K290S;

f) D280H, K290S, and either S298D or S298V;

g) F243L, R292P, and Y300L;

h) F243L, R292P, Y300L, and P396L;

i) F243L, R292P, Y300L, V305I, and P396L;

j) G236A, S239D, and I332E;

k) K326A and E333A;

l) K326W and E333S;

m) K290E, S298G, and T299A;

n) K290E, S298G, T299A, and K326E;

o) K290N, S298G, and T299A;

p) K290N, S298G, T299A, and K326E;

q) K334V;

r) L235S, S239D, and K334V;

s) K334V and Q331M, S239D, F243V, E294L, or S298T;

t) E233L, Q311M, and K334V;

u) L234I, Q311M, and K334V;

v) K334V and S298T, A330M, or A330F;

w) K334V, Q311M, and either A330M or A330F;

x) K334V, S298T, and either A330M or A330F;

y) K334V, S239D, and either A330M or S298T;

z) L234Y, Y296W, and K290Y, F243V, or E294L;

aa) Y296W and either L234Y or K290Y;

ab) S239D, A330S, and I332E,

ac) V264I;

ad) F243L and V264I;

ae) L328M;

af) I332E;

ag) L328M and I332E;

ah) V264I and I332E;

ai) S239E and I332E;

aj) S239Q and I332E;

ak) S239E;

al) A330Y;

am) I332D;

an) L328I and I332E;

ao) L328Q and I332E;

ap) V264T;

aq) V240I;

ar) V266I;

as) S239D;

at) S239D and I332D;

au) S239D and I332N;

av) S239D and I332Q;

aw) S239E and I332D;

ax) S239E and I332N;

ay) S239E and I332Q;

az) S239N and I332D;

ba) S239N and I332E;

bb) S239Q and I332D;

bc) A330Y and I332E;

bd) V264I, A330Y, and I332E;

be) A330L and I332E;

bf) V264I, A330L, and I332E;

bg) L234E, L234Y, or L234I;

bh) L235D, L235S, L235Y, or L235I;

bi) S239T;

bj) V240M;

bk) V264Y;

bl) A330I;

bm) N325T;

bn) I332E and L328D, L328V, L328T, or L328I;

bo) V264I, I332E, and either S239E or S239Q;

bp) S239E, V264I, A330Y, and I332E;

bq) A330Y, I332E, and either S239D or S239N;

br) A330L, I332E, and either S239D or S239N;

bs) V264I, S298A, and I332E;

bt) S298A, I332E, and either S239D or S239N;

bu) S239D, V264I, and I332E;

bv) S239D, V264I, S298A, and I332E;

bw) S239D, V264I, A330L, and I332E;

bx) S239D, I332E, and A330I;

by) P230A;

bz) P230A, E233D, and I332E;

ca) E272Y;

cb) K274T, K274E, K274R, K274L, or K274Y;

cd) F275W;

ce) N276L;

cf) Y278T;

cg) V302I;

ch) E318R;

ci) S324D, S324I or S324V;

cj) K326I or K326T;

ck) T335D, T335R, or T335Y;

cl) V240I and V266I;

cm) S239D, A330Y, I332E, and L234I;

cn) S239D, A330Y, I332E, and L235D;

co) S239D, A330Y, I332E, and V240I;

cp) S239D, A330Y, I332E, and V264T; or

cq) S239D, A330Y, I332E, and either K326E or K326T, numbered according to the Kabat EU numbering system.

88. The masked cytokine of embodiment 82, wherein the light chain polypeptide comprises the amino acid sequence of SEQ ID NO: 157 or 170.

89. The masked cytokine of embodiment 81, wherein the antibody or fragment thereof is a Fragment crystallizable domain (Fc domain) or fragment thereof.

90. The masked cytokine of embodiment 89, wherein the Fc domain or fragment thereof comprises one or more amino acid substitutions altering effector function.

91. The masked cytokine of embodiment 90, wherein the Fc domain or fragment thereof:

a) is an IgG1 Fc domain or fragment thereof and comprises the amino substitution(s):

i) N297A, N297G, or N297Q;

ii) L234A and L235A;

iii) C220S, C226S, C229S, and P238S;

iv) C226S, C229S, E233P, L234V, and L235A;

v) L234F, L235E, and P331S;

vi) S267E and L328F;

vii) D265A;

viii) L234A, L235A, and P329G;

b) is an IgG2 Fc domain or fragment thereof and comprises the amino acid substitution(s):

i) V234A and G237A;

ii) H268Q, V309L, A330S, and A331S; or

iii) V234A, G237A, P238S, H268A, V309L, A330S, and P331S; or

e) is an IgG4 Fc domain or fragment thereof and comprises the amino acid substitution(s):

i) L235A, G237A, and E318A;

ii) S228P, L234A, and L235A;

iii) H268Q, V309L, A330S, and P331S; or

iv) S228P and L235A, numbered according to the Kabat EU numbering system.

92. The masked cytokine of embodiment 90, wherein the Fc domain or fragment thereof comprises one or more amino acid substitutions enhancing effector function.

93. The masked cytokine of embodiment 92, wherein the Fc domain or fragment thereof is an IgG1 Fc domain or fragment thereof and comprises the amino acid substitution(s):

a) S298A, E333A, and K334A;

b) S239D and I332E;

c) S239D, A330L, and I332E;

d) P247I and A339D or A339Q;

e) D280H and K290S;

f) D280H, K290S, and either S298D or S298V;

g) F243L, R292P, and Y300L;

h) F243L, R292P, Y300L, and P396L;

i) F243L, R292P, Y300L, V305I, and P396L;

j) G236A, S239D, and I332E;

k) K326A and E333A;

l) K326W and E333S;

m) K290E, S298G, and T299A;

n) K290E, S298G, T299A, and K326E;

o) K290N, S298G, and T299A;

p) K290N, S298G, T299A, and K326E;

q) K334V;

r) L235S, S239D, and K334V;

s) K334V and Q331M, S239D, F243V, E294L, or S298T;

t) E233L, Q311M, and K334V;

u) L234I, Q311M, and K334V;

v) K334V and S298T, A330M, or A330F;

w) K334V, Q311M, and either A330M or A330F;

x) K334V, S298T, and either A330M or A330F;

y) K334V, S239D, and either A330M or S298T;

z) L234Y, Y296W, and K290Y, F243V, or E294L;

aa) Y296W and either L234Y or K290Y;

ab) S239D, A330S, and I332E,

ac) V264I;

ad) F243L and V264I;

ae) L328M;

af) I332E;

ag) L328M and I332E;

ah) V264I and I332E;

ai) S239E and I332E;

aj) S239Q and I332E;

ak) S239E;

al) A330Y;

am) I332D;

an) L328I and I332E;

ao) L328Q and I332E;

ap) V264T;

aq) V240I;

ar) V266I;

as) S239D;

at) S239D and I332D;

au) S239D and I332N;

av) S239D and I332Q;

aw) S239E and I332D;

ax) S239E and I332N;

ay) S239E and I332Q;

az) S239N and I332D;

ba) S239N and I332E;

bb) S239Q and I332D;

bc) A330Y and I332E;

bd) V264I, A330Y, and I332E;

be) A330L and I332E;

bf) V264I, A330L, and I332E;

bg) L234E, L234Y, or L234I;

bh) L235D, L235S, L235Y, or L235I;

bi) S239T;

bj) V240M;

bk) V264Y;

bl) A330I;

bm) N325T;

bn) I332E and L328D, L328V, L328T, or L328I;

bo) V264I, I332E, and either S239E or S239Q;

bp) S239E, V264I, A330Y, and I332E;

bq) A330Y, I332E, and either S239D or S239N;

br) A330L, I332E, and either S239D or S239N;

bs) V264I, S298A, and I332E;

bt) S298A, I332E, and either S239D or S239N;

bu) S239D, V264I, and I332E;

bv) S239D, V264I, S298A, and I332E;

bw) S239D, V264I, A330L, and I332E;

bx) S239D, I332E, and A330I;

by) P230A;

bz) P230A, E233D, and I332E;

ca) E272Y;

cb) K274T, K274E, K274R, K274L, or K274Y;

cd) F275W;

ce) N276L;

cf) Y278T;

cg) V302I;

ch) E318R;

ci) S324D, S324I or S324V;

cj) K326I or K326T;

ck) T335D, T335R, or T335Y;

cl) V240I and V266I;

cm) S239D, A330Y, I332E, and L234I;

cn) S239D, A330Y, I332E, and L235D;

co) S239D, A330Y, I332E, and V240I;

cp) S239D, A330Y, I332E, and V264T; or

cq) S239D, A330Y, I332E, and either K326E or K326T, numbered according to the Kabat EU numbering system.

94. The masked cytokine of embodiment 89, wherein the Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 154.

95. The masked cytokine of any one of embodiments 71-77, wherein the half-life extension domain is an albumin polypeptide or functional fragment thereof.

96. The masked cytokine of embodiment 95, wherein the albumin polypeptide or functional fragment thereof comprises the amino acid sequence of SEQ ID NO: 171.

97. The masked cytokine of any one of embodiments 71-77, wherein the half-life extension domain is an albumin-binding protein or functional fragment thereof.

98. The masked cytokine of embodiment 97, wherein the albumin-binding protein or functional fragment thereof comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 172-174 and 252-259.

99. The masked cytokine of any one of embodiments 71-77, wherein the half-life extension domain is an IgG-binding protein or functional fragment thereof.

100. The masked cytokine of embodiment 99, wherein the IgG-binding protein or functional fragment thereof comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 175-186.

101. The masked cytokine of any one of embodiments 71-77, wherein the half-life extension domain is a polyamino acid sequence.

102. The masked cytokine of embodiment 101, wherein the polyamino acid sequence is a PAS polypeptide or an XTEN polypeptide.

103. The masked cytokine of embodiment 102, wherein the PAS polypeptide comprises at least 25, at least 50, at least 100, at least 150, at least 200, at least 250, at least 300, at least 400, at least 500, at least 600, at least 700, at least 800, at least 900, at least 1000, at least 1100, at least 1200, at least 1300, at least 1500, at least 2000, at least 2500, or at least 3000 amino acid residues, wherein each amino acid residue is either a proline or an alanine residue.

104. The masked cytokine of embodiment 102, wherein the PAS polypeptide comprises at least 25, at least 50, at least 100, at least 150, at least 200, at least 250, at least 300, at least 400, at least 500, at least 600, at least 700, at least 800, at least 900, at least 1000, at least 1100, at least 1200, at least 1300, at least 1500, at least 2000, at least 2500, or at least 3000 amino acid residues, wherein each amino acid residue is selected from the group consisting of a proline, an alanine, and a serine residue.

105. The masked cytokine of embodiment 102, wherein the XTEN polypeptide comprises an amino acid sequence of about 25 to about 500, about 200 to about 1000, about 500 to about 1500, about 1000 to about 2000, or about 1500 to about 3000 amino acid residues, wherein at least about 70%, 75%, 80%, or 85% of the amino acid sequence consists of non-overlapping sequence motifs where each of the motifs has 5 to 100 amino acid residues, 5 to 50 amino acids residues, or 9 to 36 amino acid residues, and wherein at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% of each of the motifs consists of four, five, or six types of amino acid residues selected from the group consisting of glycine (G), alanine (A), serine (S), threonine (T), glutamate (E) and proline (P), and wherein the content of any one amino acid type in the full-length XTEN polypeptide does not exceed about 40%, about 35%, about 30%, about 25%, about 15%, about 10%, or about 8%.

106. The masked cytokine of any one of embodiments 70-105, wherein the masked cytokine further comprises one or more PEG polymer chains attached to the masked cytokine.

107. The masked cytokine of embodiment 106, wherein the one or more PEG polymer chains are attached to the cytokine or functional fragment thereof and/or the half-life extension domain.

108. The masked cytokine of any one of embodiments 70-107, wherein the masked cytokine is modified, or is further modified, by altering the amino acid sequence of the masked cytokine such that one or more additional N-linked and/or O-linked glycosylation sites are created.

109. The masked cytokine of embodiment 108, wherein the masked cytokine is modified, or is further modified, by altering the amino acid sequence of the masked cytokine such that one or more additional asparagine-X-serine (N-X-S) and/or asparagine-X-threonine (N-X-T) tripeptide sequence(s) is/are introduced into the amino acid sequence of the masked cytokine, wherein X is any amino acid except proline.

110. The masked cytokine of embodiment 108 or embodiment 109, wherein the masked cytokine is modified, or is further modified, by altering the amino acid sequence of the masked cytokine such that one or more additional serine or threonine residues is/are introduced into the amino acid sequence of the masked cytokine.

111. The masked cytokine of any one of embodiments 70-110, wherein the first linker comprises a first cleavable peptide.

112. The masked cytokine of any one of embodiments 70-111, where the first linker comprises a first N-terminal spacer domain and/or a first C-terminal spacer domain.

113. The masked cytokine of embodiment 112, wherein the first linker comprises:

a) the first N-terminal spacer domain, the first cleavable peptide, and the first C-terminal spacer domain;

b) the first N-terminal spacer domain and the first cleavable peptide;

c) the first N-terminal spacer domain and the first C-terminal spacer domain;

d) the first cleavable peptide and the first C-terminal spacer domain;

e) the first N-terminal spacer domain; or

f) the first C-terminal spacer domain.

114. The masked cytokine of any one of embodiments 111-113, wherein the first cleavable peptide comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 96-153, 236-242, 264, 270-302, 306-317, 342-347, 356-415, 420-491, 494-501, 504-535, and 538-555.

115. The masked cytokine of any one of embodiments 112-114, wherein the first N-terminal spacer domain comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 20-95, 235, 268, 269, 303-305, 323-338, 340, 341, 727, 794, and 799.

116. The masked cytokine of any one of embodiments 112-115, wherein the first C-terminal spacer domain comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 20-95, 235, 268, 269, 303-305, 323-338, 340, 341, 727, 794, and 799.

117. The masked cytokine of any one of embodiments 111-113, wherein the first cleavable peptide comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 96-153, 264, 270-302, 306-317, 342-347, 356-415, 420-491, 494-501, 504-535, and 538-555, and an amino acid sequence selected from the group consisting of SEQ ID NOs: 236-242.

118. The masked cytokine of embodiment 117, wherein the amino acid sequence selected from the group consisting of SEQ ID NOs: 96-153, 264, 270-302, 306-317, 342-347, 356-415, 420-491, 494-501, 504-535, and 538-555 comprises an N-terminus and a C-terminus, and the amino acid sequence selected from the group consisting of SEQ ID NOs: 236-242 is linked to the N-terminus or the C-terminus of the amino acid sequence selected from the group consisting of SEQ ID NOs: 96-153, 264, 270-302, 306-317, 342-347, 356-415, 420-491, 494-501, 504-535, and 538-555.

119. The masked cytokine of any one of embodiments 70-118, wherein the first linker comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 11-153, 235-242, 262-264, 268-320, 323-338, 340-354, 356-555, 668, 691, 724, 725, 727, 762-771, 794, and 797-812.

120. The masked cytokine of any one of embodiments 70-119, wherein the second linker comprises a second cleavable peptide.

121. The masked cytokine of any one of embodiments 70-120, wherein the second linker comprises a second N-terminal spacer domain and/or a second C-terminal spacer domain.

122. The masked cytokine of embodiment 121, wherein the second linker comprises:

a) the second N-terminal spacer domain, the second cleavable peptide, and second first C-terminal spacer domain;

b) the second N-terminal spacer domain and the second cleavable peptide;

c) the second N-terminal spacer domain and the second C-terminal spacer domain;

d) the second cleavable peptide and the second C-terminal spacer domain;

e) the second N-terminal spacer domain; or

f) the second C-terminal spacer domain.

123. The masked cytokine of any one of embodiments 120-122, wherein the second cleavable peptide comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 96-153, 236-242, 264, 270-302, 306-317, 342-347, 356-415, 420-491, 494-501, 504-535, and 538-555.

124. The masked cytokine of any one of embodiments 121-123, wherein the second N-terminal spacer domain comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 20-95, 235, 268, 269, 303-305, 323-338, 340, 341, 727, 794, and 799.

125. The masked cytokine of any one of embodiments 121-124, wherein the second C-terminal spacer domain comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 20-95, 235, 268, 269, 303-305, 323-338, 340, 341, 727, 794, and 799.

126. The masked cytokine of any one of embodiments 120-122, wherein the second cleavable peptide comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 96-153, 264, 270-302, 306-317, 342-347, 356-415, 420-491, 494-501, 504-535, and 538-555, and an amino acid sequence selected from the group consisting of SEQ ID NOs: 236-242.

127. The masked cytokine of embodiment 126, wherein the amino acid sequence selected from the group consisting of SEQ ID NOs: 96-153, 264, 270-302, 306-317, 342-347, 356-415, 420-491, 494-501, 504-535, and 538-555 comprises an N-terminus and a C-terminus, and the amino acid sequence selected from the group consisting of SEQ ID NOs: 236-242 is linked to the N-terminus or the C-terminus of the amino acid sequence selected from the group consisting of SEQ ID NOs: 96-153, 264, 270-302, 306-317, 342-347, 356-415, 420-491, 494-501, 504-535, and 538-555.

128. The masked cytokine of any one of embodiments 70-127, wherein the second linker comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 11-153, 235-242, 262-264, 268-320, 323-338, 340-354, 356-555, 668, 691, 724, 725, 727, 762-771, 794, and 797-812.

129. The masked cytokine of any one of embodiments 72-128, wherein the third linker comprises a third cleavable peptide.

130. The masked cytokine of any one of embodiments 72-129, wherein the third linker comprises a third N-terminal spacer domain and/or a third C-terminal spacer domain.

131. The masked cytokine of embodiment 130, wherein the third linker comprises:

a) the third N-terminal spacer domain, the third cleavable peptide, and third first C-terminal spacer domain;

b) the third N-terminal spacer domain and the third cleavable peptide;

c) the third N-terminal spacer domain and the third C-terminal spacer domain;

d) the third cleavable peptide and the third C-terminal spacer domain;

e) the third N-terminal spacer domain; or

f) the third C-terminal spacer domain.

132. The masked cytokine of any one of embodiments 129-131, wherein the third cleavable peptide comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 96-153, 236-242, 264, 270-302, 306-317, 342-347, 356-415, 420-491, 494-501, 504-535, and 538-555.

133. The masked cytokine of any one of embodiments 130-132, wherein the third N-terminal spacer domain comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 20-95, 235, 268, 269, 303-305, 323-338, 340, 341, 727, 794, and 799.

134. The masked cytokine of any one of embodiments 130-133, wherein the third C-terminal spacer domain comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 20-95, 235, 268, 269, 303-305, 323-338, 340, 341, 727, 794, and 799.

135. The masked cytokine of any one of embodiments 129-131, wherein the third cleavable peptide comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 96-153, 264, 270-302, 306-317, 342-347, 356-415, 420-491, 494-501, 504-535, and 538-555, and an amino acid sequence selected from the group consisting of SEQ ID NOs: 236-242.

136. The masked cytokine of embodiment 135, wherein the amino acid sequence selected from the group consisting of SEQ ID NOs: 96-153, 264, 270-302, 306-317, 342-347, 356-415, 420-491, 494-501, 504-535, and 538-555 comprises an N-terminus and a C-terminus, and the amino acid sequence selected from the group consisting of SEQ ID NOs: 236-242 is linked to the N-terminus or the C-terminus of the amino acid sequence selected from the group consisting of SEQ ID NOs: 96-153, 264, 270-302, 306-317, 342-347, 356-415, 420-491, 494-501, 504-535, and 538-555.

137. The masked cytokine of any one of embodiments 72-136, wherein the third linker comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 11-153, 235-242, 262-264, 268-320, 323-338, 340-354, 356-555, 668, 691, 724, 725, 727, 762-771, 794, and 797-812.

138. The masked cytokine of any one of embodiments 52-137, wherein the first cleavable peptide, the second cleavable peptide, and/or the third cleavable peptide is a substrate for a protease that is co-localized in a region or a tissue expressing a cytokine receptor.

139. The masked cytokine of embodiment 138, wherein the cytokine receptor is an IL-2 cytokine receptor or an IL-15 cytokine receptor.

140. The masked cytokine of any one of embodiments 1-139, wherein one or more of the first cleavable peptide, the second cleavable peptide, and the third cleavable peptide is cleaved by one or more enzyme selected from the group consisting of: ABHD12, ADAM12, ABHD12B, ABHD13, ABHD17A, ADAM19, ADAM20, ADAM21, ADAM28, ADAM30, ADAM33, ADAM8, ABHD17A, ADAMDEC1, ADAMTS1, ADAMTS10, ADAMTS12, ADAMTS13, ADAMTS14, ADAMTS15, ADAMTS16, ADAMTS17, ADAMTS18, ADAMTS19, ADAMTS2, ADAMTS20, ADAMTS3, ADAMTS4, ABHD17B, ADAMTS5, ADAMTS6, ADAMTS7, ADAMTS8, ADAMTS9, ADAMTSL1, ADAMTSL2, ADAMTSL3, ABHD17C, ADAMTSL5, ASTL, BMP1, CELA1, CELA2A, CELA2B, CELA3A, CELA3B, ADAM10, ADAM15, ADAM17, ADAM9, ADAMTS4, CTSE, CTSF,

ADAMTSL4, CMA1, CTRB1, CTRC, CTSO, CTRl, CTSA, CTSW, CTSB, CTSC, CTSD, ESP1, CTSG, CTSH, GZMA, GZMB, GZMH, CTSK, GZMM, CTSL, CTSS, CTSV, CTSZ, HTRA4, KLK10, KLK11, KLK13, KLK14, KLK2, KLK4, DPP4, KLK6, KLK7, KLKB1, ECE1, ECE2, ECEL1, MASP2, MEP1A, MEP1B, ELANE, FAP, GZMA, MMP11, GZMK, HGFAC, HPN, HTRA1, MMP11, MMP16, MMP17, MMP19, HTRA2, MMP20, MMP21, HTRA3, HTRA4, KEL, MMP23B, MMP24, MMP25, MMP26, MMP27, MMP28, KLK5, MMP3, MMP7, MMP8, MMP9, LGMN, LNPEP, MASP1, PAPPA, PAPPA2, PCSK1, NAPSA, PCSK5, PCSK6, MME, MMP1, MMP10, PLAT, PLAU, PLG, PRSS1, PRSS12, PRSS2, PRSS21, PRSS3, PRSS33, PRSS4, PRSS55, PRSS57, MMP12, PRSS8, PRSS9, PRTN3, MMP13, MMP14, ST14, TMPRSS10, TMPRSS11A, TMPRSS11D, TMPRSS11E, TMPRSS11F, TMPRSS12, TMPRSS13, MMP15, TMPRSS15, MMP2, TMPRSS2, TMPRSS3, TMPRSS4, TMPRSS5, TMPRSS6, TMPRSS7, TMPRSS9, NRDC, OVCH1, PAMR1, PCSK3, PHEX, TINAG, TPSAB1, TPSD1, and TPSG1.

141. The masked cytokine of any one of embodiments 2-69 and 71-140, wherein the half-life extension domain is conjugated to an agent.

142. The masked cytokine of embodiment 141, wherein the agent is an inhibitor of tubulin polymerization, a DNA damaging agent, or a DNA synthesis inhibitor.

143. The masked cytokine of embodiment 142, wherein the agent is a maytansinoid, an auristatin, a pyrrolobenzodiazepine (PBD) dimer, a calicheamicin, a duocarmycin, a indolinobenzodiazepine dimer or exatecan derivative Dxd.

144. The masked cytokine of embodiment 141, wherein the agent is an immune stimulant.

145. The masked cytokine of embodiment 144, wherein the immune stimulant is a stimulator of interferon genes (STING) agonist or a toll-like receptor (TLR) agonist.

146. The masked cytokine of embodiment 145, wherein the STING agonist is a cyclic dinucleotide (CDN).

147. The masked cytokine of embodiment 146, wherein the CDN is selected from the group consisting of cGAMP, c-di-AMP, c-di-GMP, cAIMP, c-di-IMP, 4-(2-chloro-6-fluorobenzyl)-N-(furan-2-ylmethyl)-3-oxo-3,4-dihydro-2H-benzo[b][1,4]thiazine-6-carboxamide.

148. The masked cytokine of embodiment 145, wherein the TLR agonist is an agonist of a TLR selected from the group consisting of TLR1, TLR2, TLR3, TLR4, TLR5, TLR6, TLR7, TLR8, TLR9, and TLR10.

149. A masked cytokine comprising:

a) a first half-life extension domain and a second half-life extension domain;

b) a masking moiety; and

c) a cytokine or functional fragment thereof,

wherein the masking moiety is linked to the first half-life extension domain,

wherein the cytokine or functional fragment thereof is linked to the second half-life extension domain, and

wherein the first half-life extension domain and the second half-life extension domain contain modifications promoting the association of the first and the second half-life extension domain.

150. The masked cytokine of embodiment 149, wherein the masking moiety is linked to the first half-life extension domain via a first linker; and/or wherein the cytokine or functional fragment thereof is linked to the second half-life extension domain via a second linker.

151. The masked cytokine of embodiment 149 or embodiment 150, wherein the cytokine or functional fragment thereof is an IL-2 polypeptide or functional fragment thereof.

152. The masked cytokine of embodiment 151, wherein the IL-2 polypeptide or functional fragment thereof comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 1-8, 160, 230, 243-251, 260, 775-792, and 813-822.

153. The masked cytokine of embodiment 151, wherein the IL-2 polypeptide or functional fragment thereof comprises an amino acid sequence produced by introducing one or more amino acid substitutions into the amino acid sequence of the IL-2 polypeptide or functional fragment thereof that reduces the affinity of the IL-2 polypeptide or functional fragment thereof for CD25 (IL-2Rα).

154. The masked cytokine of embodiment 153, wherein the amino acid sequence is produced by introducing one or more of the following amino acid substitutions into any one of SEQ ID NOs: 1-8, 160, 243-251, 260, 775-792, and 813-822: R38A, F42A, F42K, F42E, K43A, Y45A, Y45N, Y45R, E62A, E62R, E62S, and L72G.

155. The masked cytokine of embodiment 151, wherein the IL-2 polypeptide or functional fragment thereof comprises an amino acid sequence produced by introducing one or more amino acid substitutions into the amino acid sequence of the IL-2 polypeptide or functional fragment thereof that increases the affinity of the IL-2 polypeptide or functional fragment thereof for IL-2Rβ or IL-2Rγ.

156. The masked cytokine of embodiment 155, wherein the amino acid sequence is produced by introducing one or more of the following amino acid substitutions into any one of SEQ ID NOs: 1-8, 160, 243-251, 260, 775-792, and 813-822: H16I, L18C, D20A, D20L, D20F, N29L, L80F, R81D, L85V, I86V, and I92F.

157. The masked cytokine of embodiment 153 or embodiment 154, wherein the amino acid sequence is produced by further introducing one or more amino acid substitutions that increase the affinity of the IL-2 polypeptide or functional fragment thereof for IL-2Rβ or IL-2Rγ.

158. The masked cytokine of embodiment 157, wherein the one or more amino acid substitutions that increase the affinity of the IL-2 polypeptide or functional fragment thereof for IL-2Rβ or IL-2Rγ is selected from the group consisting of H16I, L18C, D20A, D20L, D20F, N29L, L80F, R81D, L85V, I86V, and I92F.

159. The masked cytokine of embodiment 151, wherein the IL-2 polypeptide or functional fragment thereof comprises an amino acid sequence produced by introducing one or more amino acid substitutions into the amino acid sequence of the IL-2 polypeptide or functional fragment thereof that stabilizes the IL-2 polypeptide or functional fragment thereof.

160. The masked cytokine of embodiment 159, wherein the amino acid sequence is produced by introducing one of the following amino acid substitutions into any one of SEQ ID NOs: 1-8, 160, 243-251, 260, 775-792, and 813-822: C125S, C125A, and C125G.

161. The masked cytokine of any one of embodiments 153-158, wherein the amino acid sequence is produced by further introducing one or more amino acid substitutions that stabilize the IL-2 polypeptide or functional fragment thereof.

162. The masked cytokine of embodiment 161, wherein the one or more amino acid substitutions that stabilize the IL-2 polypeptide or functional fragment thereof is the amino acid substitution C125S, C125A, or C125G.

163. The masked cytokine of any one of embodiments 151-162, wherein the masking moiety comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 9, 10, 161-165, 187-218, 221-229, 231, 261, 826 and 827.

164. The masked cytokine of embodiment 149 or embodiment 150, wherein the cytokine or functional fragment thereof is an IL-15 polypeptide or functional fragment thereof.

165. The masked cytokine of embodiment 164, wherein the IL-15 polypeptide or functional fragment thereof comprises the amino acid sequence of SEQ ID NO: 167.

166. The masked cytokine of embodiment 164 or embodiment 165, wherein the masking moiety comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 10, 161-165, 219-229, 232-234, 261, and 823-827.

167. The masked cytokine of embodiment 164 or embodiment 165, wherein the masking moiety comprises an amino acid sequence produced by introducing one or more of the following amino acid substitutions into the amino acid sequence of any one of SEQ ID NOs: 232-234, and 823-825: R24A, R26A, K34A, S40A, L42A, and P67A.

168. The masked cytokine of any one of embodiment 149-167, wherein the first half-life extension domain is a first antibody or fragment thereof, and the second half-life extension domain is a second antibody or fragment thereof.

169. The masked cytokine of embodiment 168, wherein:

a) the first antibody or fragment thereof comprises a first heavy chain polypeptide, and the second antibody or fragment thereof comprises a second light chain polypeptide; or

b) the first antibody or fragment thereof comprises a first light chain polypeptide, and the second antibody or fragment thereof comprises a second heavy chain polypeptide.

170. The masked cytokine of embodiment 169, wherein the first heavy chain polypeptide or the second heavy chain polypeptide comprises one or more amino acid substitutions altering effector function.

171. The masked cytokine of embodiment 170, wherein the first heavy chain polypeptide or the second heavy chain polypeptide:

a) is an IgG1 isotype and comprises the amino substitution(s):

i) N297A, N297G, or N297Q;

ii) L234A and L235A;

iii) C220S, C226S, C229S, and P238S;

iv) C226S, C229S, E233P, L234V, and L235A;

v) L234F, L235E, and P331S;

vi) S267E and L328F;

vii) D265A;

viii) L234A, L235A, and P329G;

b) is an IgG2 isotype and comprises the amino acid substitution(s):

i) V234A and G237A;

ii) H268Q, V309L, A330S, and A331S; or

iii) V234A, G237A, P238S, H268A, V309L, A330S, and P331S; or

e) is an IgG4 isotype and comprises the amino acid substitution(s):

i) L235A, G237A, and E318A;

ii) S228P, L234A, and L235A;

iii) H268Q, V309L, A330S, and P331S; or

iv) S228P and L235A, numbered according to the Kabat EU numbering system.

172. The masked cytokine of embodiment 170, wherein the first heavy chain polypeptide or the second heavy chain polypeptide comprises one or more amino acid substitutions enhancing effector function.

173. The masked cytokine of embodiment 172, wherein the first heavy chain polypeptide or the second heavy chain polypeptide is an IgG1 heavy chain polypeptide and comprises the amino acid substitution(s):

a) S298A, E333A, and K334A;

b) S239D and I332E;

c) S239D, A330L, and I332E;

d) P247I and A339D or A339Q;

e) D280H and K290S;

f) D280H, K290S, and either S298D or S298V;

g) F243L, R292P, and Y300L;

h) F243L, R292P, Y300L, and P396L;

i) F243L, R292P, Y300L, V305I, and P396L;

j) G236A, S239D, and I332E;

k) K326A and E333A;

l) K326W and E333S;

m) K290E, S298G, and T299A;

n) K290E, S298G, T299A, and K326E;

o) K290N, S298G, and T299A;

p) K290N, S298G, T299A, and K326E;

q) K334V;

r) L235S, S239D, and K334V;

s) K334V and Q331M, S239D, F243V, E294L, or S298T;

t) E233L, Q311M, and K334V;

u) L234I, Q311M, and K334V;

v) K334V and S298T, A330M, or A330F;

w) K334V, Q311M, and either A330M or A330F;

x) K334V, S298T, and either A330M or A330F;

y) K334V, S239D, and either A330M or S298T;

z) L234Y, Y296W, and K290Y, F243V, or E294L;

aa) Y296W and either L234Y or K290Y;

ab) S239D, A330S, and I332E,

ac) V264I;

ad) F243L and V264I;

ae) L328M;

af) I332E;

ag) L328M and I332E;

ah) V264I and I332E;

ai) S239E and I332E;

aj) S239Q and I332E;

ak) S239E;

al) A330Y;

am) I332D;

an) L328I and I332E;

ao) L328Q and I332E;

ap) V264T;

aq) V240I;

ar) V266I;

as) S239D;

at) S239D and I332D;

au) S239D and I332N;

av) S239D and I332Q;

aw) S239E and I332D;

ax) S239E and I332N;

ay) S239E and I332Q;

az) S239N and I332D;

ba) S239N and I332E;

bb) S239Q and I332D;

bc) A330Y and I332E;

bd) V264I, A330Y, and I332E;

be) A330L and I332E;

bf) V264I, A330L, and I332E;

bg) L234E, L234Y, or L234I;

bh) L235D, L235S, L235Y, or L235I;

bi) S239T;

bj) V240M;

bk) V264Y;

bl) A330I;

bm) N325T;

bn) I332E and L328D, L328V, L328T, or L328I;

bo) V264I, I332E, and either S239E or S239Q;

bp) S239E, V264I, A330Y, and I332E;

bq) A330Y, I332E, and either S239D or S239N;

br) A330L, I332E, and either S239D or S239N;

bs) V264I, S298A, and I332E;

bt) S298A, I332E, and either S239D or S239N;

bu) S239D, V264I, and I332E;

bv) S239D, V264I, S298A, and I332E;

bw) S239D, V264I, A330L, and I332E;

bx) S239D, I332E, and A330I;

by) P230A;

bz) P230A, E233D, and I332E;

ca) E272Y;

cb) K274T, K274E, K274R, K274L, or K274Y;

cd) F275W;

ce) N276L;

cf) Y278T;

cg) V302I;

ch) E318R;

ci) S324D, S324I or S324V;

cj) K326I or K326T;

ck) T335D, T335R, or T335Y;

cl) V240I and V266I;

cm) S239D, A330Y, I332E, and L234I;

cn) S239D, A330Y, I332E, and L235D;

co) S239D, A330Y, I332E, and V240I;

cp) S239D, A330Y, I332E, and V264T; or

cq) S239D, A330Y, I332E, and either K326E or K326T, numbered according to the Kabat EU numbering system.

174. The masked cytokine of embodiment 169, wherein the first heavy chain polypeptide comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 158, 168, and 169, and the second heavy chain polypeptide comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 158, 168, and 169.

175. The masked cytokine of embodiment 169, wherein the first light chain polypeptide comprises the amino acid sequence of SEQ ID NO: 157 or 170, and the second light chain polypeptide comprises the amino acid sequence of SEQ ID NO: 157 or 170.

176. The masked cytokine of embodiment 168, wherein the first antibody or fragment thereof is a first Fragment crystallizable domain (Fc domain) or fragment thereof, and the second antibody or fragment thereof is a second Fc domain or fragment thereof.

177. The masked cytokine of embodiment 176, wherein the first Fc domain or fragment thereof, and/or the second Fc domain or fragment thereof comprises one or more amino acid substitutions altering effector function.

178. The masked cytokine of embodiment 177, wherein the first Fc domain or fragment thereof and/or the second Fc domain or fragment thereof:

a) is an IgG1 Fc domain or fragment thereof and comprises the amino substitution(s):

i) N297A, N297G, or N297Q;

ii) L234A and L235A;

iii) C220S, C226S, C229S, and P238S;

iv) C226S, C229S, E233P, L234V, and L235A;

v) L234F, L235E, and P331S;

vi) S267E and L328F;

vii) D265A;

viii) L234A, L235A, and P329G;

b) is an IgG2 Fc domain or fragment thereof and comprises the amino acid substitution(s):

i) V234A and G237A;

ii) H268Q, V309L, A330S, and A331S; or

iii) V234A, G237A, P238S, H268A, V309L, A330S, and P331S; or

e) is an IgG4 Fc domain or fragment thereof and comprises the amino acid substitution(s):

i) L235A, G237A, and E318A;

ii) S228P, L234A, and L235A;

iii) H268Q, V309L, A330S, and P331S; or

iv) S228P and L235A, numbered according to the Kabat EU numbering system.

179. The masked cytokine of embodiment 177, wherein the first Fc domain or fragment thereof, and/or the second Fc domain or fragment thereof comprises one or more amino acid substitutions enhancing effector function.

180. The masked cytokine of embodiment 179, wherein the first Fc domain or fragment thereof and/or the second Fc domain or fragment thereof is an IgG1 Fc domain or fragment thereof and comprises the amino acid substitution(s):

a) S298A, E333A, and K334A;

b) S239D and I332E;

c) S239D, A330L, and I332E;

d) P247I and A339D or A339Q;

e) D280H and K290S;

f) D280H, K290S, and either S298D or S298V;

g) F243L, R292P, and Y300L;

h) F243L, R292P, Y300L, and P396L;

i) F243L, R292P, Y300L, V305I, and P396L;

j) G236A, S239D, and I332E;

k) K326A and E333A;

l) K326W and E333S;

m) K290E, S298G, and T299A;

n) K290E, S298G, T299A, and K326E;

o) K290N, S298G, and T299A;

p) K290N, S298G, T299A, and K326E;

q) K334V;

r) L235S, S239D, and K334V;

s) K334V and Q331M, S239D, F243V, E294L, or S298T;

t) E233L, Q311M, and K334V;

u) L234I, Q311M, and K334V;

v) K334V and S298T, A330M, or A330F;

w) K334V, Q311M, and either A330M or A330F;

x) K334V, S298T, and either A330M or A330F;

y) K334V, S239D, and either A330M or S298T;

z) L234Y, Y296W, and K290Y, F243V, or E294L;

aa) Y296W and either L234Y or K290Y;

ab) S239D, A330S, and I332E,

ac) V264I;

ad) F243L and V264I;

ae) L328M;

af) I332E;

ag) L328M and I332E;

ah) V264I and I332E;

ai) S239E and I332E;

aj) S239Q and I332E;

ak) S239E;

al) A330Y;

am) I332D;

an) L328I and I332E;

ao) L328Q and I332E;

ap) V264T;

aq) V240I;

ar) V266I;

as) S239D;

at) S239D and I332D;

au) S239D and I332N;

av) S239D and I332Q;

aw) S239E and I332D;

ax) S239E and I332N;

ay) S239E and I332Q;

az) S239N and I332D;

ba) S239N and I332E;

bb) S239Q and I332D;

bc) A330Y and I332E;

bd) V264I, A330Y, and I332E;

be) A330L and I332E;

bf) V264I, A330L, and I332E;

bg) L234E, L234Y, or L234I;

bh) L235D, L235S, L235Y, or L235I;

bi) S239T;

bj) V240M;

bk) V264Y;

bl) A330I;

bm) N325T;

bn) I332E and L328D, L328V, L328T, or L328I;

bo) V264I, I332E, and either S239E or S239Q;

bp) S239E, V264I, A330Y, and I332E;

bq) A330Y, I332E, and either S239D or S239N;

br) A330L, I332E, and either S239D or S239N;

bs) V264I, S298A, and I332E;

bt) S298A, I332E, and either S239D or S239N;

bu) S239D, V264I, and I332E;

bv) S239D, V264I, S298A, and I332E;

bw) S239D, V264I, A330L, and I332E;

bx) S239D, I332E, and A330I;

by) P230A;

bz) P230A, E233D, and I332E;

ca) E272Y;

cb) K274T, K274E, K274R, K274L, or K274Y;

cd) F275W;

ce) N276L;

cf) Y278T;

cg) V302I;

ch) E318R;

ci) S324D, S324I or S324V;

cj) K326I or K326T;

ck) T335D, T335R, or T335Y;

cl) V240I and V266I;

cm) S239D, A330Y, I332E, and L234I;

cn) S239D, A330Y, I332E, and L235D;

co) S239D, A330Y, I332E, and V240I;

cp) S239D, A330Y, I332E, and V264T; or

cq) S239D, A330Y, I332E, and either K326E or K326T, numbered according to the Kabat EU numbering system.

181. The masked cytokine of embodiment 176, wherein:

a) the first Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 155, and the second Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 156;

b) the first Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 156, and the second Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 155;

c) the first Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 154, and the second Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 154;

d) the first Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 265, and the second Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 156;

e) the first Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 156, and the second Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 265;

f) the first Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 155, and the second Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 616;

g) the first Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 616, and the second Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 155;

h) the first Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 157, and the second Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 158;

i) the first Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 158, and the second Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 157;

j) the first Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 796, and the second Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 774;

k) the first Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 774, and the second Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 796;

l) the first Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 721, and the second Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 619;

m) the first Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 619, and the second Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 721;

n) the first Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 721, and the second Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 772;

o) the first Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 772, and the second Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 721;

p) the first Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 793, and the second Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 622;

q) the first Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 622, and the second Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 793;

r) the first Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 793, and the second Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 773;

s) the first Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 773, and the second Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 793;

t) the first Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 796, and the second Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 625;

u) the first Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 625, and the second Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 796;

v) the first Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 156, and the second Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 156;

w) the first Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 796, and the second Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 625; or

x) the first Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 625, and the second Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 796.

182. The masked cytokine of any one of embodiments 149-167, wherein the first half-life extension domain is a first scFv or fragment thereof, and the second half-life extension domain is a second scFv or fragment thereof.

183. The masked cytokine of any one of embodiments 149-167, wherein the first half-life extension domain is a first Fc domain or fragment thereof, and the second half-life extension domain is a second Fc domain or fragment thereof, and wherein the first Fc domain or fragment thereof is linked to the second Fc domain or fragment thereof.

184. The masked cytokine of embodiment 183, wherein the first Fc domain or fragment thereof is linked to the second Fc domain or fragment thereof via a third linker.

185. The masked cytokine of any one of embodiments 149-167, wherein:

a) the first half-life extension domain is an scFv or fragment thereof, and the second half-life extension domain is an antibody or fragment thereof; or

b) the first half-life extension domain is an antibody or fragment thereof, and the second half-life extension domain is an scFv or fragment thereof.

186. The masked cytokine of any one of embodiments 168-181, wherein the modifications promoting the association of the first and the second half-life extension domain comprise:

a) introducing S354C and T366W mutations in the first antibody or fragment thereof, and introducing Y349C, T366S, L368A, and Y407V mutations in the second antibody or fragment thereof, numbered according to the Kabat EU numbering system;

b) introducing S354C and T366W mutations in the second antibody or fragment thereof, and introducing Y349C, T366S, L368A, and Y407V mutations in the first antibody or fragment thereof, numbered according to the Kabat EU numbering system;

c) introducing K392D and K409D mutations in the first antibody or fragment thereof, and introducing D399K and E356K mutations in the second antibody or fragment thereof, numbered according to the Kabat EU numbering system;

d) introducing K392D and K409D mutations in the second antibody or fragment thereof, and introducing D399K and E356K mutations in the first antibody or fragment thereof, numbered according to the Kabat EU numbering system;

e) introducing S364H and F405A mutations in the first antibody or fragment thereof, and introducing Y349T and T394F mutations in the second antibody or fragment thereof, numbered according to the Kabat EU numbering system; or

f) introducing S364H and F405A mutations in the second antibody or fragment thereof, and introducing Y349T and T394F mutations in the first antibody or fragment thereof, numbered according to the Kabat EU numbering system.

187. The masked cytokine of any one of embodiments 168-181, wherein the amino acid sequence of the first antibody or fragment thereof and the amino acid sequence of the second antibody or fragment thereof are produced by:

a) introducing S354C and T366W mutations in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing Y349C, T366S, L368A, and Y407V mutations in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

b) introducing S354C and T366W mutations in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing Y349C, T366S, L368A, and Y407V mutations in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

c) introducing K392D and K409D mutations in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing D399K and E356K mutations in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

d) introducing K392D and K409D mutations in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing D399K and E356K mutations in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

e) introducing S364H and F405A mutations in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing Y349T and T394F mutations in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system; or

f) introducing S364H and F405A mutations in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing Y349T and T394F mutations in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system.

188. The masked cytokine of any one of embodiments 168-181, wherein the modifications promoting the association of the first and the second half-life extension domain comprise:

a) introducing a Y407T mutation in the first antibody or fragment thereof, and introducing a T366Y mutation in the second antibody or fragment thereof, numbered according to the Kabat EU numbering system;

b) introducing a Y407A mutation in the first antibody or fragment thereof, and introducing a T366W mutation in the second antibody or fragment thereof, numbered according to the Kabat EU numbering system;

c) introducing a F405A mutation in the first antibody or fragment thereof, and introducing a T394W mutation in the second antibody or fragment thereof, numbered according to the Kabat EU numbering system;

d) introducing a F405W mutation in the first antibody or fragment thereof, and introducing a T394S mutation in the second antibody or fragment thereof, numbered according to the Kabat EU numbering system;

e) introducing a Y407T mutation in the first antibody or fragment thereof, and introducing a T366Y mutation in the second antibody or fragment thereof, numbered according to the Kabat EU numbering system;

f) introducing T366Y and F405A mutations in the first antibody or fragment thereof, and introducing T394W and Y407T mutations in the second antibody or fragment thereof, numbered according to the Kabat EU numbering system;

g) introducing T366W and F405W mutations in the first antibody or fragment thereof, and introducing T394S and Y407A mutations in the second antibody or fragment thereof, numbered according to the Kabat EU numbering system;

h) introducing F405W and Y407A mutations in the first antibody or fragment thereof, and introducing T366W and T394S mutations in the second antibody or fragment thereof, numbered according to the Kabat EU numbering system;

i) introducing a T366W mutation in the first antibody or fragment thereof, and introducing T366S, L368A, and Y407V mutations in the second antibody or fragment thereof, numbered according to the Kabat EU numbering system;

j) introducing a Y407T mutation in the second antibody or fragment thereof, and introducing a T366Y mutation in the first antibody or fragment thereof, numbered according to the Kabat EU numbering system;

k) introducing a Y407A mutation in the second antibody or fragment thereof, and introducing a T366W mutation in the first antibody or fragment thereof, numbered according to the Kabat EU numbering system;

l) introducing a F405A mutation in the second antibody or fragment thereof, and introducing a T394W mutation in the first antibody or fragment thereof, numbered according to the Kabat EU numbering system;

m) introducing a F405W mutation in the second antibody or fragment thereof, and introducing a T394S mutation in the first antibody or fragment thereof, numbered according to the Kabat EU numbering system;

n) introducing a Y407T mutation in the second antibody or fragment thereof, and introducing a T366Y mutation in the first antibody or fragment thereof, numbered according to the Kabat EU numbering system;

o) introducing T366Y and F405A mutations in the second antibody or fragment thereof, and introducing T394W and Y407T mutations in the first antibody or fragment thereof, numbered according to the Kabat EU numbering system;

p) introducing T366W and F405W mutations in the second antibody or fragment thereof, and introducing T394S and Y407A mutations in the first antibody or fragment thereof, numbered according to the Kabat EU numbering system;

q) introducing F405W and Y407A mutations in the second antibody or fragment thereof, and introducing T366W and T394S mutations in the first antibody or fragment thereof, numbered according to the Kabat EU numbering system; or

r) introducing a T366W mutation in the second antibody or fragment thereof, and introducing T366S, L368A, and Y407V mutations in the first antibody or fragment thereof, numbered according to the Kabat EU numbering system.

189. The masked cytokine of any one of embodiments 168-181, wherein the amino acid sequence of the first antibody or fragment thereof and the amino acid sequence of the second antibody or fragment thereof are produced by:

a) introducing a Y407T mutation in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing a T366Y mutation in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

b) introducing a Y407A mutation in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing a T366W mutation in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

ı F405A mutation in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing a T394W mutation in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

d) introducing a F405W mutation in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing a T394S mutation in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

e) introducing a Y407T mutation in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing a T366Y mutation in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

f) introducing T366Y and F405A mutations in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing T394W and Y407T mutations in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

g) introducing T366W and F405W mutations in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing T394S and Y407A mutations in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

h) introducing F405W and Y407A mutations in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing T366W and T394S mutations in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

i) introducing a T366W mutation in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing T366S, L368A, and Y407V mutations in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

j) introducing a Y407T mutation in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing a T366Y mutation in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

k) introducing a Y407A mutation in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing a T366W mutation in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

l) introducing a F405A mutation in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing a T394W mutation in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

m) introducing a F405W mutation in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing a T394S mutation in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

n) introducing a Y407T mutation in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing a T366Y mutation in the amino acid sequence of SEQ ID NO: 154 or 169, respectively,

ırding to the Kabat EU numbering system;

T366Y and F405A mutations in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing T394W and Y407T mutations in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

p) introducing T366W and F405W mutations in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing T394S and Y407A mutations in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

q) introducing F405W and Y407A mutations in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing T366W and T394S mutations in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system; or

r) introducing a T366W mutation in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing T366S, L368A, and Y407V mutations in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system.

190. The masked cytokine of any one of embodiments 168-181, wherein the modifications promoting the association of the first and the second half-life extension domain comprise:

a) introducing a K409E mutation in the first antibody or fragment thereof, and introducing a D399K mutation in the second antibody or fragment thereof, numbered according to the Kabat EU numbering system;

b) introducing a K409E mutation in the first antibody or fragment thereof, and introducing a D399R mutation in the second antibody or fragment thereof, numbered according to the Kabat EU numbering system;

c) introducing a K409D mutation in the first antibody or fragment thereof, and introducing a D399K mutation in the second antibody or fragment thereof, numbered according to the Kabat EU numbering system;

d) introducing a K409D mutation in the first antibody or fragment thereof, and introducing a D399R mutation in the second antibody or fragment thereof, numbered according to the Kabat EU numbering system;

e) introducing a K392E mutation in the first antibody or fragment thereof, and introducing a D399R mutation in the second antibody or fragment thereof, numbered according to the Kabat EU numbering system;

f) introducing a K392E mutation in the first antibody or fragment thereof, and introducing a D399K mutation in the second antibody or fragment thereof, numbered according to the Kabat EU numbering system;

g) introducing a K392D mutation in the first antibody or fragment thereof, and introducing a D399R mutation in the second antibody or fragment thereof, numbered according to the Kabat EU

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a K392D mutation in the first antibody or fragment thereof, and introducing a D399K mutation in the second antibody or fragment thereof, numbered according to the Kabat EU numbering system;

i) introducing K409D and K360D mutations in the first antibody or fragment thereof, and introducing D399K and E356K mutations in the second antibody or fragment thereof, numbered according to the Kabat EU numbering system;

j) introducing K409D and K370D mutations in the first antibody or fragment thereof, and introducing D399K and E357K mutations in the second antibody or fragment thereof, numbered according to the Kabat EU numbering system;

k) introducing K409D and K392D mutations in the first antibody or fragment thereof, and introducing D399K, E356K, and E357K mutations in the second antibody or fragment thereof, numbered according to the Kabat EU numbering system;

l) introducing K409D and K392D mutations in the first antibody or fragment thereof, and introducing a D399K mutation in the second antibody or fragment thereof, numbered according to the Kabat EU numbering system;

m) introducing K409D and K392D mutations in the first antibody or fragment thereof, and introducing D399K and E356K mutations in the second antibody or fragment thereof, numbered according to the Kabat EU numbering system;

n) introducing K409D and K392D mutations in the first antibody or fragment thereof, and introducing D399K and E357K mutations in the second antibody or fragment thereof, numbered according to the Kabat EU numbering system;

o) introducing K409D and K370D mutations in the first antibody or fragment thereof, and introducing D399K and E357K mutations in the second antibody or fragment thereof, numbered according to the Kabat EU numbering system;

p) introducing a D399K mutation in the first antibody or fragment thereof, and introducing K409D and K360D mutations in the second antibody or fragment thereof, numbered according to the Kabat EU numbering system;

q) introducing K409D and K439D mutations in the first antibody or fragment thereof, and introducing D399K and E356K mutations in the second antibody or fragment thereof, numbered according to the Kabat EU numbering system;

r) introducing a K409E mutation in the second antibody or fragment thereof, and introducing a D399K mutation in the first antibody or fragment thereof, numbered according to the Kabat EU numbering system;

s) introducing a K409E mutation in the second antibody or fragment thereof, and introducing a D399R mutation in the first antibody or fragment thereof, numbered according to the Kabat EU

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. K409D mutation in the second antibody or fragment thereof, and introducing a D399K mutation in the first antibody or fragment thereof, numbered according to the Kabat EU numbering system;

u) introducing a K409D mutation in the second antibody or fragment thereof, and introducing a D399R mutation in the first antibody or fragment thereof, numbered according to the Kabat EU numbering system;

v) introducing a K392E mutation in the second antibody or fragment thereof, and introducing a D399R mutation in the first antibody or fragment thereof, numbered according to the Kabat EU numbering system;

w) introducing a K392E mutation in the second antibody or fragment thereof, and introducing a D399K mutation in the first antibody or fragment thereof, numbered according to the Kabat EU numbering system;

x) introducing a K392D mutation in the second antibody or fragment thereof, and introducing a D399R mutation in the first antibody or fragment thereof, numbered according to the Kabat EU numbering system;

y) introducing a K392D mutation in the second antibody or fragment thereof, and introducing a D399K mutation in the first antibody or fragment thereof, numbered according to the Kabat EU numbering system;

z) introducing K409D and K360D mutations in the second antibody or fragment thereof, and introducing D399K and E356K mutations in the first antibody or fragment thereof, numbered according to the Kabat EU numbering system;

aa) introducing K409D and K370D mutations in the second antibody or fragment thereof, and introducing D399K and E357K mutations in the first antibody or fragment thereof, numbered according to the Kabat EU numbering system;

ab) introducing K409D and K392D mutations in the second antibody or fragment thereof, and introducing D399K, E356K, and E357K mutations in the first antibody or fragment thereof, numbered according to the Kabat EU numbering system;

ac) introducing K409D and K392D mutations in the second antibody or fragment thereof, and introducing a D399K mutation in the first antibody or fragment thereof, numbered according to the Kabat EU numbering system;

ad) introducing K409D and K392D mutations in the second antibody or fragment thereof, and introducing D399K and E356K mutations in the first antibody or fragment thereof, numbered according to the Kabat EU numbering system;

ae) introducing K409D and K392D mutations in the second antibody or fragment thereof, and introducing D399K and E357K mutations in the first antibody or fragment thereof, numbered according

J numbering system;

K409D and K370D mutations in the second antibody or fragment thereof, and introducing D399K and E357K mutations in the first antibody or fragment thereof, numbered according to the Kabat EU numbering system;

ag) introducing a D399K mutation in the second antibody or fragment thereof, and introducing K409D and K360D mutations in the first antibody or fragment thereof, numbered according to the Kabat EU numbering system; or

ah) introducing K409D and K439D mutations in the second antibody or fragment thereof, and introducing D399K and E356K mutations in the first antibody or fragment thereof, numbered according to the Kabat EU numbering system.

191. The masked cytokine of any one of embodiments 168-181, wherein the amino acid sequence of the first antibody or fragment thereof and the amino acid sequence of the second antibody or fragment thereof are produced by:

a) introducing a K409E mutation in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing a D399K mutation in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

b) introducing a K409E mutation in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing a D399R mutation in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

c) introducing a K409D mutation in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing a D399K mutation in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

d) introducing a K409D mutation in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing a D399R mutation in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

e) introducing a K392E mutation in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing a D399R mutation in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

f) introducing a K392E mutation in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing a D399K mutation in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

g) introducing a K392D mutation in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing a D399R mutation in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

a K392D mutation in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing a D399K mutation in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

i) introducing K409D and K360D mutations in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing D399K and E356K mutations in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

j) introducing K409D and K370D mutations in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing D399K and E357K mutations in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

k) introducing K409D and K392D mutations in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing D399K, E356K, and E357K mutations in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

l) introducing K409D and K392D mutations in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing a D399K mutation in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

m) introducing K409D and K392D mutations in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing D399K and E356K mutations in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

n) introducing K409D and K392D mutations in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing D399K and E357K mutations in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

o) introducing K409D and K370D mutations in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing D399K and E357K mutations in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

p) introducing a D399K mutation in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing K409D and K360D mutations in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

q) introducing K409D and K439D mutations in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing D399K and E356K mutations in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

r) introducing a K409E mutation in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing a D399K mutation in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

s) introducing a K409E mutation in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing a D399R mutation in the amino acid sequence of SEQ ID NO: 154 or 169, respectively,

rding to the Kabat EU numbering system;

. K409D mutation in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing a D399K mutation in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

u) introducing a K409D mutation in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing a D399R mutation in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

v) introducing a K392E mutation in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing a D399R mutation in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

w) introducing a K392E mutation in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing a D399K mutation in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

x) introducing a K392D mutation in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing a D399R mutation in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

y) introducing a K392D mutation in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing a D399K mutation in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

z) introducing K409D and K360D mutations in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing D399K and E356K mutations in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

aa) introducing K409D and K370D mutations in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing D399K and E357K mutations in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

ab) introducing K409D and K392D mutations in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing D399K, E356K, and E357K mutations in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

ac) introducing K409D and K392D mutations in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing a D399K mutation in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

ad) introducing K409D and K392D mutations in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing D399K and E356K mutations in the amino acid sequence of SEQ ID NO: 154 or 169, numbered according to the Kabat EU numbering system;

ae) introducing K409D and K392D mutations in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing D399K and E357K mutations in the amino acid sequence of SEQ ID NO: 154 or

ly, numbered according to the Kabat EU numbering system;

K409D and K370D mutations in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing D399K and E357K mutations in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

ag) introducing a D399K mutation in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing K409D and K360D mutations in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system; or

ah) introducing K409D and K439D mutations in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing D399K and E356K mutations in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system.

192. The masked cytokine of any one of embodiments 150-191, wherein the first linker comprises a first cleavable peptide; and/or wherein the second linker comprises a second cleavable peptide.

193. The masked cytokine of any one of embodiments 150-192, wherein the first linker comprises a first N-terminal spacer domain, and/or a first C-terminal spacer domain.

194. The masked cytokine of embodiment 193, wherein the first linker comprises:

a) the first N-terminal spacer domain, the first cleavable peptide, and the first C-terminal spacer domain;

b) the first N-terminal spacer domain and the first cleavable peptide;

c) the first N-terminal spacer domain and the first C-terminal spacer domain;

d) the first cleavable peptide and the first C-terminal spacer domain;

e) the first N-terminal spacer domain; or

f) the first C-terminal spacer domain.

195. The masked cytokine of any one of embodiments 150-194, wherein the second linker comprises a second N-terminal spacer domain, and/or a second C-terminal spacer domain.

196. The masked cytokine of embodiment 195, wherein the second linker comprises:

a) the second N-terminal spacer domain, the second cleavable peptide, and the second C-terminal spacer domain;

b) the second N-terminal spacer domain and the second cleavable peptide;

c) the second N-terminal spacer domain and the second C-terminal spacer domain;

d) the second cleavable peptide and the second C-terminal spacer domain;

econd N-terminal spacer domain; or

-terminal spacer domain.

197. The masked cytokine of any one of embodiments 192-196, wherein the first cleavable peptide comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 96-153, 236-242, 264, 270-302, 306-317, 342-347, 356-415, 420-491, 494-501, 504-535, and 538-555; and/or wherein the second cleavable peptide comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 96-153, 236-242, 264, 270-302, 306-317, 342-347, 356-415, 420-491, 494-501, 504-535, and 538-555.

198. The masked cytokine of any one of embodiments 193-197, wherein the first N-terminal spacer domain comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 20-95 235, 263, 268, 269, 727, 794, 799, and 857-878, and/or the first C-terminal spacer domain comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 20-95, 235, 268, 269, 303-305, 323-338, 340, 341, 727, 794, and 799.

199. The masked cytokine of any one of embodiments 192-196, wherein the first cleavable peptide comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 96-153, 264, 270-302, 306-317, 342-347, 356-415, 420-491, 494-501, 504-535, and 538-555, and an amino acid sequence selected from the group consisting of SEQ ID NOs: 236-242.

200. The masked cytokine of embodiment 199, wherein the amino acid sequence selected from the group consisting of SEQ ID NOs: 96-153, 264, 270-302, 306-317, 342-347, 356-415, 420-491, 494-501, 504-535, and 538-555 comprises an N-terminus and a C-terminus, and the amino acid sequence selected from the group consisting of SEQ ID NOs: 236-242 is linked to the N-terminus or the C-terminus of the amino acid sequence selected from the group consisting of SEQ ID NOs: 96-153, 264, 270-302, 306-317, 342-347, 356-415, 420-491, 494-501, 504-535, and 538-555.

201. The masked cytokine of any one of embodiments 195-200, wherein the second N-terminal spacer domain comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 20-95, 235, 268, 269, 303-305, 323-338, 340, 341, 727, 794, and 799, and/or the second C-terminal spacer domain comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 20-95, 235, 268, 269, 303-305, 323-338, 340, 341, 727, 794, and 799.

202. The masked cytokine of any one of embodiments 192-201, wherein the second cleavable peptide comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 96-153,

342-347, 356-415, 420-491, 494-501, 504-535, and 538-555, and an amino acid sequence selected from the group consisting of SEQ ID NOs: 236-242.

203. The masked cytokine of embodiment 202, wherein the amino acid sequence selected from the group consisting of SEQ ID NOs: 96-153, 264, 270-302, 306-317, 342-347, 356-415, 420-491, 494-501, 504-535, and 538-555 comprises an N-terminus and a C-terminus, and the amino acid sequence selected from the group consisting of SEQ ID NOs: 236-242 is linked to the N-terminus or the C-terminus of the amino acid sequence selected from the group consisting of SEQ ID NOs: 96-153, 264, 270-302, 306-317, 342-347, 356-415, 420-491, 494-501, 504-535, and 538-555.

204. The masked cytokine of any one of embodiments 150-203, wherein the first linker comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 11-153, 235-242, 262-264, 268-320, 323-338, 340-354, 356-555, 668, 691, 724, 725, 727, 762-771, 794, and 797-812, and/or the second linker comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 11-153, 235-242, 262-264, 268-320, 323-338, 340-354, 356-555, 668, 691, 724, 725, 727, 762-771, 794, and 797-812.

205. The masked cytokine of any one of embodiments 184-204, wherein the third linker comprises a third N-terminal spacer domain, and/or a third C-terminal spacer domain.

206. The masked cytokine of embodiment 205, wherein the third N-terminal spacer domain comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 20-95, 235, 268, 269, 303-305, 323-338, 340, 341, 727, 794, and 799, and/or the third C-terminal spacer domain comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 20-95, 235, 268, 269, 303-305, 323-338, 340, 341, 727, 794, and 799.

207. The masked cytokine of any one of embodiments 192-206, wherein the first cleavable peptide and/or the second cleavable peptide is a substrate for a protease that is co-localized in a region or a tissue expressing a cytokine receptor.

208. The masked cytokine of embodiment 207, wherein the cytokine receptor is an IL-2 cytokine receptor or an IL-15 cytokine receptor.

209. The masked cytokine of any one of embodiments 184-208, wherein the first cleavable peptide and/or the second cleavable peptide is cleaved by one or more enzyme selected from the group ABHD12, ADAM12, ABHD12B, ABHD13, ABHD17A, ADAM19, ADAM20,

ADAM30, ADAM33, ADAM8, ABHD17A, ADAMDEC1, ADAMTS1, ADAMTS10, ADAMTS12, ADAMTS13, ADAMTS14, ADAMTS15, ADAMTS16, ADAMTS17, ADAMTS18, ADAMTS19, ADAMTS2, ADAMTS20, ADAMTS3, ADAMTS4, ABHD17B, ADAMTS5, ADAMTS6, ADAMTS7, ADAMTS8, ADAMTS9, ADAMTSL1, ADAMTSL2, ADAMTSL3, ABHD17C, ADAMTSL5, ASTL, BMP1, CELA1, CELA2A, CELA2B, CELA3A, CELA3B, ADAM10, ADAM15, ADAM17, ADAM9, ADAMTS4, CTSE, CTSF, ADAMTSL4, CMA1, CTRB1, CTRC, CTSO, CTRl, CTSA, CTSW, CTSB, CTSC, CTSD, ESP1, CTSG, CTSH, GZMA, GZMB, GZMH, CTSK, GZMM, CTSL, CTSS, CTSV, CTSZ, HTRA4, KLK10, KLK11, KLK13, KLK14, KLK2, KLK4, DPP4, KLK6, KLK7, KLKB1, ECE1, ECE2, ECEL1, MASP2, MEP1A, MEP1B, ELANE, FAP, GZMA, MMP11, GZMK, HGFAC, HPN, HTRA1, MMP11, MMP16, MMP17, MMP19, HTRA2, MMP20, MMP21, HTRA3, HTRA4, KEL, MMP23B, MMP24, MMP25, MMP26, MMP27, MMP28, KLK5, MMP3, MMP7, MMP8, MMP9, LGMN, LNPEP, MASP1, PAPPA, PAPPA2, PCSK1, NAPSA, PCSK5, PCSK6, MME, MMP1, MMP10, PLAT, PLAU, PLG, PRSS1, PRSS12, PRSS2, PRSS21, PRSS3, PRSS33, PRSS4, PRSS55, PRSS57, MMP12, PRSS8, PRSS9, PRTN3, MMP13, MMP14, ST14, TMPRSS10, TMPRSS11A, TMPRSS11D, TMPRSS11E, TMPRSS11F, TMPRSS12, TMPRSS13, MMP15, TMPRSS15, MMP2, TMPRSS2, TMPRSS3, TMPRSS4, TMPRSS5, TMPRSS6, TMPRSS7, TMPRSS9, NRDC, OVCH1, PAMR1, PCSK3, PHEX, TINAG, TPSAB1, TPSD1, and TPSG1.

210. The masked cytokine of any one of embodiments 149-209, wherein the first half-life extension domain and/or the second half-life extension domain is conjugated to an agent.

211. The masked cytokine of embodiment 210, wherein the agent is an inhibitor of tubulin polymerization, a DNA damaging agent, or a DNA synthesis inhibitor.

212. The masked cytokine of embodiment 211, wherein the agent is a maytansinoid, an auristatin, a pyrrolobenzodiazepine (PBD) dimer, a calicheamicin, a duocarmycin, a indo-linobenzodiazepine dimer or exatecan derivative Dxd.

213. The masked cytokine of embodiment 210, wherein the agent is an immune stimulant.

214. The masked cytokine of embodiment 213, wherein the immune stimulant is a stimulator of interferon genes (STING) agonist or a toll-like receptor (TLR) agonist.

215. The masked cytokine of embodiment 214, wherein the STING agonist is a cyclic DN).

216. The masked cytokine of embodiment 215, wherein the CDN is selected from the group consisting of cGAMP, c-di-AMP, c-di-GMP, cAIMP, c-di-IMP, 4-(2-chloro-6-fluorobenzyl)-N-(furan-2-ylmethyl)-3-oxo-3,4-dihydro-2H-benzo[b][1,4]thiazine-6-carboxamide.

217. The masked cytokine of embodiment 214, wherein the TLR agonist is an agonist of a TLR selected from the group consisting of TLR1, TLR2, TLR3, TLR4, TLR5, TLR6, TLR7, TLR8, TLR9, and TLR10.

218. A masked cytokine comprising:

a) a first half-life extension domain and a second half-life extension domain;

b) a first masking moiety and a second masking moiety; and

c) a cytokine or functional fragment thereof,

wherein the first masking moiety is linked to the first half-life extension domain,

wherein the second masking moiety is linked to the cytokine or functional fragment thereof,

wherein either the second masking moiety or the cytokine or functional fragment thereof is linked to the second half-life extension domain, and

wherein the first half-life extension domain and the second half-life extension domain contain modifications promoting the association of the first and the second half-life extension domain.

219. The masked cytokine of embodiment 218, wherein:

a) the first masking moiety is linked to the first half-life extension domain via a first linker; and/or

b) either the second masking moiety or the cytokine or functional fragment thereof is linked to the second half-life extension domain via a second linker.

220. The masked cytokine of embodiment 218 or embodiment 219, wherein the second masking moiety is linked to the cytokine or functional fragment thereof via a third linker.

221. The masked cytokine of any one of embodiments 218-220, wherein the cytokine or functional fragment thereof is an IL-2 polypeptide or functional fragment thereof.

222. The masked cytokine of embodiment 221, wherein the IL-2 polypeptide or functional fragment thereof comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 1-8, 160, 243-251, 230, 243-251, 260, 775-792, and 813-822.

ısked cytokine of embodiment 221, wherein the IL-2 polypeptide or functional fragment thereof comprises an amino acid sequence produced by introducing one or more amino acid substitutions into the amino acid sequence of the IL-2 polypeptide or functional fragment thereof that reduces the affinity of the IL-2 polypeptide or functional fragment thereof for CD25 (IL-2Rα).

224. The masked cytokine of embodiment 223, wherein the amino acid sequence is produced by introducing one or more of the following amino acid substitutions into any one of SEQ ID NOs: 1-8, 160, 243-251, 260, 775-792, and 813-822: R38A, F42A, F42K, F42E, K43A, Y45A, Y45N, Y45R, E62A, E62R, E62S, and L72G.

225. The masked cytokine of embodiment 221, wherein the IL-2 polypeptide or functional fragment thereof comprises an amino acid sequence produced by introducing one or more amino acid substitutions into the amino acid sequence of the IL-2 polypeptide or functional fragment thereof that increases the affinity of the IL-2 polypeptide or functional fragment thereof for IL-2Rβ or IL-2Rγ.

226. The masked cytokine of embodiment 225, wherein the amino acid sequence is produced by introducing one or more of the following amino acid substitutions into any one of SEQ ID NOs: 1-8, 160, 243-251, 260, 775-792, and 813-822: H16I, L18C, D20A, D20L, D20F, N29L, L80F, R81D, L85V, I86V, and I92F.

227. The masked cytokine of embodiment 223 or embodiment 224, wherein the amino acid sequence is produced by further introducing one or more amino acid substitutions that increase the affinity of the IL-2 polypeptide or functional fragment thereof for IL-2Rβ or IL-2Rγ.

228. The masked cytokine of embodiment 227, wherein the one or more amino acid substitutions that increase the affinity of the IL-2 polypeptide or functional fragment thereof for IL-2Rβ or IL-2Rγ is selected from the group consisting of H16I, L18C, D20A, D20L, D20F, N29L, L80F, R81D, L85V, I86V, and I92F.

229. The masked cytokine of embodiment 221, wherein the IL-2 polypeptide or functional fragment thereof comprises an amino acid sequence produced by introducing one or more amino acid substitutions into the amino acid sequence of the IL-2 polypeptide or functional fragment thereof that stabilizes the IL-2 polypeptide or functional fragment thereof.

ısked cytokine of embodiment 229, wherein the amino acid sequence is produced by introducing one of the following amino acid substitutions into any one of SEQ ID NOs: 1-8, 160, 243-251, 260, 775-792, and 813-822: C125S, C125A, and C125G.

231. The masked cytokine of any one of embodiments 223-228, wherein the amino acid sequence is produced by further introducing one or more amino acid substitutions that stabilize the IL-2 polypeptide or functional fragment thereof.

232. The masked cytokine of embodiment 231, wherein the one or more amino acid substitutions that stabilize the IL-2 polypeptide or functional fragment thereof is the amino acid substitution C125S, C125A, or C125G.

233. The masked cytokine of any one of embodiments 221-232, wherein the first masking moiety comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 9, 10, 161-165, 187-218, 221-229, 231, 261, 826 and 827 and the second masking moiety comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 9, 10, 161-165, 187-218, 221-229, 231, 261, 826 and 827 and wherein the amino acid sequence of the first masking moiety and the second masking moiety are different.

234. The masked cytokine of any one of embodiments 221-233, wherein:

a) the first masking moiety comprises the amino acid sequence of SEQ ID NO: 9 or 231, and the second masking moiety comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 10, 161-165, 187-218, 221-226, 261, 826 and 827; or

b) the first masking moiety comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 10, 161-165, 187-218, 221-226, 261, 826 and 827, and the second masking moiety comprises the amino acid sequence of SEQ ID NO: 9 or 231.

235. The masked cytokine of any one of embodiments 218-220, wherein the cytokine or functional fragment thereof is an IL-15 polypeptide or functional fragment thereof.

236. The masked cytokine of embodiment 235, wherein the IL-15 polypeptide or functional fragment thereof comprises the amino acid sequence of SEQ ID NO: 167.

237. The masked cytokine of embodiment 235 or embodiment 236, wherein

king moiety comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 232-234, and 823-825, and the second masking moiety comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 10, 161-165, 219-229, 261, 826 and 827;

b) the first masking moiety comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 10, 161-165, 219-229, 261, 826 and 827, and the second masking moiety comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 232-234, and 823-825;

c) the first masking moiety comprises an amino acid sequence produced by introducing one or more of the following amino acid substitutions into the amino acid sequence of any one of SEQ ID NOs: 232-234, and 823-825: R24A, R26A, K34A, S40A, L42A, and P67A, and the second masking moiety comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 10, 161-165, 219-229, 261, 826 and 827; or

d) the first masking moiety comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 10, 161-165, 219-229, 261, 826 and 827, and the second masking moiety comprises an amino acid sequence produced by introducing one or more of the following amino acid substitutions into the amino acid sequence of any one of SEQ ID NOs: 232-234, and 823-825: R24A, R26A, K34A, S40A, L42A, and P67A.

238. The masked cytokine of any one of embodiments 218-237, wherein the first half-life extension domain is a first antibody or fragment thereof, and the second half-life extension domain is a second antibody or fragment thereof.

239. The masked cytokine of embodiment 238, wherein:

a) the first antibody or fragment thereof comprises a first heavy chain polypeptide, and the second antibody or fragment thereof comprises a second light chain polypeptide; or

b) the first antibody or fragment thereof comprises a first light chain polypeptide, and the second antibody or fragment thereof comprises a second heavy chain polypeptide.

240. The masked cytokine of embodiment 239, wherein the first heavy chain polypeptide, or the second heavy chain polypeptide comprises one or more amino acid substitutions altering effector function.

241. The masked cytokine of embodiment 240, wherein the first heavy chain polypeptide or the second heavy chain polypeptide:

a) is an IgG1 isotype and comprises the amino substitution(s):

i) N297A, N297G, or N297Q;

ii) L234A and L235A;

C220S, C226S, C229S, and P238S;

iv) C226S, C229S, E233P, L234V, and L235A;

v) L234F, L235E, and P331S;

vi) S267E and L328F;

vii) D265A;

viii) L234A, L235A, and P329G;

b) is an IgG2 isotype and comprises the amino acid substitution(s):

i) V234A and G237A;

ii) H268Q, V309L, A330S, and A331S; or

iii) V234A, G237A, P238S, H268A, V309L, A330S, and P331S; or

e) is an IgG4 isotype and comprises the amino acid substitution(s):

i) L235A, G237A, and E318A;

ii) S228P, L234A, and L235A;

iii) H268Q, V309L, A330S, and P331S; or

iv) S228P and L235A, numbered according to the Kabat EU numbering system.

242. The masked cytokine of embodiment 240, wherein the first heavy chain polypeptide or the second heavy chain polypeptide comprises one or more amino acid substitutions enhancing effector function.

243. The masked cytokine of embodiment 242, wherein the first heavy chain polypeptide or the second heavy chain polypeptide is an IgG1 heavy chain polypeptide and comprises the amino acid substitution(s):

a) S298A, E333A, and K334A;

b) S239D and I332E;

c) S239D, A330L, and I332E;

d) P247I and A339D or A339Q;

e) D280H and K290S;

f) D280H, K290S, and either S298D or S298V;

g) F243L, R292P, and Y300L;

h) F243L, R292P, Y300L, and P396L;

i) F243L, R292P, Y300L, V305I, and P396L;

j) G236A, S239D, and I332E;

k) K326A and E333A;

l) K326W and E333S;

K290E, S298G, and T299A;

, S298G, T299A, and K326E;

o) K290N, S298G, and T299A;

p) K290N, S298G, T299A, and K326E;

q) K334V;

r) L235S, S239D, and K334V;

s) K334V and Q331M, S239D, F243V, E294L, or S298T;

t) E233L, Q311M, and K334V;

u) L234I, Q311M, and K334V;

v) K334V and S298T, A330M, or A330F;

w) K334V, Q311M, and either A330M or A330F;

x) K334V, S298T, and either A330M or A330F;

y) K334V, S239D, and either A330M or S298T;

z) L234Y, Y296W, and K290Y, F243V, or E294L;

aa) Y296W and either L234Y or K290Y;

ab) S239D, A330S, and I332E,

ac) V264I;

ad) F243L and V264I;

ae) L328M;

af) I332E;

ag) L328M and I332E;

ah) V264I and I332E;

ai) S239E and I332E;

aj) S239Q and I332E;

ak) S239E;

al) A330Y;

am) I332D;

an) L328I and I332E;

ao) L328Q and I332E;

ap) V264T;

aq) V240I;

ar) V266I;

as) S239D;

at) S239D and I332D;

au) S239D and I332N;

av) S239D and I332Q;

S239E and I332D;

and I332N;

ay) S239E and I332Q;

az) S239N and I332D;

ba) S239N and I332E;

bb) S239Q and I332D;

bc) A330Y and I332E;

bd) V264I, A330Y, and I332E;

be) A330L and I332E;

bf) V264I, A330L, and I332E;

bg) L234E, L234Y, or L234I;

bh) L235D, L235S, L235Y, or L235I;

bi) S239T;

bj) V240M;

bk) V264Y;

bl) A330I;

bm) N325T;

bn) I332E and L328D, L328V, L328T, or L328I;

bo) V264I, I332E, and either S239E or S239Q;

bp) S239E, V264I, A330Y, and I332E;

bq) A330Y, I332E, and either S239D or S239N;

br) A330L, I332E, and either S239D or S239N;

bs) V264I, S298A, and I332E;

bt) S298A, I332E, and either S239D or S239N;

bu) S239D, V264I, and I332E;

bv) S239D, V264I, S298A, and I332E;

bw) S239D, V264I, A330L, and I332E;

bx) S239D, I332E, and A330I;

by) P230A;

bz) P230A, E233D, and I332E;

ca) E272Y;

cb) K274T, K274E, K274R, K274L, or K274Y;

cd) F275W;

ce) N276L;

cf) Y278T;

cg) V302I;

E318R;

, S324I or S324V;

cj) K326I or K326T;

ck) T335D, T335R, or T335Y;

cl) V240I and V266I;

cm) S239D, A330Y, I332E, and L234I;

cn) S239D, A330Y, I332E, and L235D;

co) S239D, A330Y, I332E, and V240I;

cp) S239D, A330Y, I332E, and V264T; or

cq) S239D, A330Y, I332E, and either K326E or K326T, numbered according to the Kabat EU numbering system.

244. The masked cytokine of embodiment 239, wherein the first heavy chain polypeptide comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 158, 168, and 169, and the second heavy chain polypeptide comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 158, 168, and 169.

245. The masked cytokine of embodiment 239, wherein the first light chain polypeptide comprises the amino acid sequence of SEQ ID NO: 157 or 170, and the second light chain polypeptide comprises the amino acid sequence of SEQ ID NO: 157 or 170.

246. The masked cytokine of embodiment 238, wherein the first antibody or fragment thereof is a first Fragment crystallizable domain (Fc domain) or fragment thereof, and the second antibody or fragment thereof is a second Fc domain or fragment thereof.

247. The masked cytokine of embodiment 246, wherein the first Fc domain or fragment thereof, and/or the second Fc domain or fragment thereof comprises one or more amino acid substitutions altering effector function.

248. The masked cytokine of embodiment 247, wherein the first Fc domain or fragment thereof and/or the second Fc domain or fragment thereof:

a) is an IgG1 Fc domain or fragment thereof and comprises the amino substitution(s):

i) N297A, N297G, or N297Q;

ii) L234A and L235A;

iii) C220S, C226S, C229S, and P238S;

iv) C226S, C229S, E233P, L234V, and L235A;

v) L234F, L235E, and P331S;

S267E and L328F;

vii) D265A;

viii) L234A, L235A, and P329G;

b) is an IgG2 Fc domain or fragment thereof and comprises the amino acid substitution(s):

i) V234A and G237A;

ii) H268Q, V309L, A330S, and A331S; or

iii) V234A, G237A, P238S, H268A, V309L, A330S, and P331S; or

e) is an IgG4 Fc domain or fragment thereof and comprises the amino acid substitution(s):

i) L235A, G237A, and E318A;

ii) S228P, L234A, and L235A;

iii) H268Q, V309L, A330S, and P331S; or

iv) S228P and L235A, numbered according to the Kabat EU numbering system.

249. The masked cytokine of embodiment 247, wherein first Fc domain or fragment thereof, and/or the second Fc domain or fragment thereof comprises one or more amino acid substitutions enhancing effector function.

250. The masked cytokine of embodiment 249, wherein the first Fc domain or fragment thereof, and/or the second Fc domain or fragment thereof is an IgG1 Fc domain or fragment thereof and comprises the amino acid substitution(s):

a) S298A, E333A, and K334A;

b) S239D and I332E;

c) S239D, A330L, and I332E;

d) P247I and A339D or A339Q;

e) D280H and K290S;

f) D280H, K290S, and either S298D or S298V;

g) F243L, R292P, and Y300L;

h) F243L, R292P, Y300L, and P396L;

i) F243L, R292P, Y300L, V305I, and P396L;

j) G236A, S239D, and I332E;

k) K326A and E333A;

l) K326W and E333S;

m) K290E, S298G, and T299A;

n) K290E, S298G, T299A, and K326E;

o) K290N, S298G, and T299A;

K290N, S298G, T299A, and K326E;

;

r) L235S, S239D, and K334V;

s) K334V and Q331M, S239D, F243V, E294L, or S298T;

t) E233L, Q311M, and K334V;

u) L234I, Q311M, and K334V;

v) K334V and S298T, A330M, or A330F;

w) K334V, Q311M, and either A330M or A330F;

x) K334V, S298T, and either A330M or A330F;

y) K334V, S239D, and either A330M or S298T;

z) L234Y, Y296W, and K290Y, F243V, or E294L;

aa) Y296W and either L234Y or K290Y;

ab) S239D, A330S, and I332E,

ac) V264I;

ad) F243L and V264I;

ae) L328M;

af) I332E;

ag) L328M and I332E;

ah) V264I and I332E;

ai) S239E and I332E;

aj) S239Q and I332E;

ak) S239E;

al) A330Y;

am) I332D;

an) L328I and I332E;

ao) L328Q and I332E;

ap) V264T;

aq) V240I;

ar) V266I;

as) S239D;

at) S239D and I332D;

au) S239D and I332N;

av) S239D and I332Q;

aw) S239E and I332D;

ax) S239E and I332N;

ay) S239E and I332Q;

S239N and I332D;

and I332E;

bb) S239Q and I332D;

bc) A330Y and I332E;

bd) V264I, A330Y, and I332E;

be) A330L and I332E;

bf) V264I, A330L, and I332E;

bg) L234E, L234Y, or L234I;

bh) L235D, L235S, L235Y, or L235I;

bi) S239T;

bj) V240M;

bk) V264Y;

bl) A330I;

bm) N325T;

bn) I332E and L328D, L328V, L328T, or L328I;

bo) V264I, I332E, and either S239E or S239Q;

bp) S239E, V264I, A330Y, and I332E;

bq) A330Y, I332E, and either S239D or S239N;

br) A330L, I332E, and either S239D or S239N;

bs) V264I, S298A, and I332E;

bt) S298A, I332E, and either S239D or S239N;

bu) S239D, V264I, and I332E;

bv) S239D, V264I, S298A, and I332E;

bw) S239D, V264I, A330L, and I332E;

bx) S239D, I332E, and A330I;

by) P230A;

bz) P230A, E233D, and I332E;

ca) E272Y;

cb) K274T, K274E, K274R, K274L, or K274Y;

cd) F275W;

ce) N276L;

cf) Y278T;

cg) V302I;

ch) E318R;

ci) S324D, S324I or S324V;

cj) K326I or K326T;

T335D, T335R, or T335Y;

and V266I;

cm) S239D, A330Y, I332E, and L234I;

cn) S239D, A330Y, I332E, and L235D;

co) S239D, A330Y, I332E, and V240I;

cp) S239D, A330Y, I332E, and V264T; or

cq) S239D, A330Y, I332E, and either K326E or K326T, numbered according to the Kabat EU numbering system.

251. The masked cytokine of embodiment 246, wherein:

a) the first Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 155, and the second Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 156;

b) the first Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 156, and the second Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 155;

c) the first Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 154, and the second Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 154;

d) the first Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 265, and the second Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 156;

e) the first Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 156, and the second Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 265;

f) the first Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 155, and the second Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 616;

g) the first Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 616, and the second Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 155;

h) the first Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 157, and the second Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 158;

i) the first Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 158, and the second Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO:

omain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 796, and the second Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 774;

k) the first Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 774, and the second Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 796;

l) the first Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 721, and the second Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 619;

m) the first Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 619, and the second Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 721;

n) the first Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 721, and the second Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 772;

o) the first Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 772, and the second Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 721;

p) the first Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 793, and the second Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 622;

q) the first Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 622, and the second Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 793;

r) the first Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 793, and the second Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 773;

s) the first Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 773, and the second Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 793;

t) the first Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 796, and the second Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 625;

u) the first Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 625, and the second Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO:

omain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 156, and the second Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 156;

w) the first Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 796, and the second Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 625; or

x) the first Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 625, and the second Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 796.

252. The masked cytokine of any one of embodiments 218-237, wherein the first half-life extension domain is a first scFv or fragment thereof, and the second half-life extension domain is a second scFv or fragment thereof.

253. The masked cytokine of any one of embodiments 218-237, wherein the first half-life extension domain is a first Fc domain or fragment thereof, and the second half-life extension domain is a second Fc domain or fragment thereof, and wherein the first Fc domain or fragment thereof is linked to the second Fc domain or fragment thereof.

254. The masked cytokine of embodiment 253, wherein the first Fc domain or fragment thereof is linked to the second Fc domain or fragment thereof via a fourth linker.

255. The masked cytokine of any one of embodiments 218-237, wherein:

a) the first half-life extension domain is an scFv or fragment thereof, and the second half-life extension domain is an antibody or fragment thereof; or

a) the first half-life extension domain is an antibody or fragment thereof, and the second half-life extension domain is an scFv or fragment thereof.

256. The masked cytokine of any one of embodiments 238-251, wherein the modifications promoting the association of the first and the second half-life extension domain comprise:

a) introducing S354C and T366W mutations in the first antibody or fragment thereof, and introducing Y349C, T366S, L368A, and Y407V mutations in the second antibody or fragment thereof, numbered according to the Kabat EU numbering system;

b) introducing S354C and T366W mutations in the second antibody or fragment thereof, and introducing Y349C, T366S, L368A, and Y407V mutations in the first antibody or fragment thereof,

rding to the Kabat EU numbering system;

K392D and K409D mutations in the first antibody or fragment thereof, and introducing D399K and E356K mutations in the second antibody or fragment thereof, numbered according to the Kabat EU numbering system;

d) introducing K392D and K409D mutations in the second antibody or fragment thereof, and introducing D399K and E356K mutations in the first antibody or fragment thereof, numbered according to the Kabat EU numbering system;

e) introducing S364H and F405A mutations in the first antibody or fragment thereof, and introducing Y349T and T394F mutations in the second antibody or fragment thereof, numbered according to the Kabat EU numbering system; or

f) introducing S364H and F405A mutations in the second antibody or fragment thereof, and introducing Y349T and T394F mutations in the first antibody or fragment thereof, numbered according to the Kabat EU numbering system.

257. The masked cytokine of any one of embodiments 238-251, wherein the amino acid sequence of the first antibody or fragment thereof and the amino acid sequence of the second antibody or fragment thereof are produced by:

a) introducing S354C and T366W mutations in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing Y349C, T366S, L368A, and Y407V mutations in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

b) introducing S354C and T366W mutations in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing Y349C, T366S, L368A, and Y407V mutations in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

c) introducing K392D and K409D mutations in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing D399K and E356K mutations in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

d) introducing K392D and K409D mutations in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing D399K and E356K mutations in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

e) introducing S364H and F405A mutations in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing Y349T and T394F mutations in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system; or

f) introducing S364H and F405A mutations in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing Y349T and T394F mutations in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system.

ısked cytokine of any one of embodiments 238-251, wherein the modifications promoting the association of the first and the second half-life extension domain comprise:

a) introducing a Y407T mutation in the first antibody or fragment thereof, and introducing a T366Y mutation in the second antibody or fragment thereof, numbered according to the Kabat EU numbering system;

b) introducing a Y407A mutation in the first antibody or fragment thereof, and introducing a T366W mutation in the second antibody or fragment thereof, numbered according to the Kabat EU numbering system;

c) introducing a F405A mutation in the first antibody or fragment thereof, and introducing a T394W mutation in the second antibody or fragment thereof, numbered according to the Kabat EU numbering system;

d) introducing a F405W mutation in the first antibody or fragment thereof, and introducing a T394S mutation in the second antibody or fragment thereof, numbered according to the Kabat EU numbering system;

e) introducing a Y407T mutation in the first antibody or fragment thereof, and introducing a T366Y mutation in the second antibody or fragment thereof, numbered according to the Kabat EU numbering system;

f) introducing T366Y and F405A mutations in the first antibody or fragment thereof, and introducing T394W and Y407T mutations in the second antibody or fragment thereof, numbered according to the Kabat EU numbering system;

g) introducing T366W and F405W mutations in the first antibody or fragment thereof, and introducing T394S and Y407A mutations in the second antibody or fragment thereof, numbered according to the Kabat EU numbering system;

h) introducing F405W and Y407A mutations in the first antibody or fragment thereof, and introducing T366W and T394S mutations in the second antibody or fragment thereof, numbered according to the Kabat EU numbering system;

i) introducing a T366W mutation in the first antibody or fragment thereof, and introducing T366S, L368A, and Y407V mutations in the second antibody or fragment thereof, numbered according to the Kabat EU numbering system;

j) introducing a Y407T mutation in the second antibody or fragment thereof, and introducing a T366Y mutation in the first antibody or fragment thereof, numbered according to the Kabat EU numbering system;

k) introducing a Y407A mutation in the second antibody or fragment thereof, and introducing a T366W mutation in the first antibody or fragment thereof, numbered according to the Kabat EU numbering system;

F405A mutation in the second antibody or fragment thereof, and introducing a T394W mutation in the first antibody or fragment thereof, numbered according to the Kabat EU numbering system;

m) introducing a F405W mutation in the second antibody or fragment thereof, and introducing a T394S mutation in the first antibody or fragment thereof, numbered according to the Kabat EU numbering system;

n) introducing a Y407T mutation in the second antibody or fragment thereof, and introducing a T366Y mutation in the first antibody or fragment thereof, numbered according to the Kabat EU numbering system;

o) introducing T366Y and F405A mutations in the second antibody or fragment thereof, and introducing T394W and Y407T mutations in the first antibody or fragment thereof, numbered according to the Kabat EU numbering system;

p) introducing T366W and F405W mutations in the second antibody or fragment thereof, and introducing T394S and Y407A mutations in the first antibody or fragment thereof, numbered according to the Kabat EU numbering system;

q) introducing F405W and Y407A mutations in the second antibody or fragment thereof, and introducing T366W and T394S mutations in the first antibody or fragment thereof, numbered according to the Kabat EU numbering system; or

r) introducing a T366W mutation in the second antibody or fragment thereof, and introducing T366S, L368A, and Y407V mutations in the first antibody or fragment thereof, numbered according to the Kabat EU numbering system.

259. The masked cytokine of any one of embodiments 238-251, wherein the amino acid sequence of the first antibody or fragment thereof and the amino acid sequence of the second antibody or fragment thereof are produced by:

a) introducing a Y407T mutation in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing a T366Y mutation in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

b) introducing a Y407A mutation in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing a T366W mutation in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

c) introducing a F405A mutation in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing a T394W mutation in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

a F405W mutation in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing a T394S mutation in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

e) introducing a Y407T mutation in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing a T366Y mutation in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

f) introducing T366Y and F405A mutations in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing T394W and Y407T mutations in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

g) introducing T366W and F405W mutations in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing T394S and Y407A mutations in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

h) introducing F405W and Y407A mutations in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing T366W and T394S mutations in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

i) introducing a T366W mutation in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing T366S, L368A, and Y407V mutations in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

j) introducing a Y407T mutation in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing a T366Y mutation in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

k) introducing a Y407A mutation in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing a T366W mutation in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

l) introducing a F405A mutation in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing a T394W mutation in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

m) introducing a F405W mutation in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing a T394S mutation in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

n) introducing a Y407T mutation in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing a T366Y mutation in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

o) introducing T366Y and F405A mutations in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing T394W and Y407T mutations in the amino acid sequence of SEQ ID NO: 154 or

ly, numbered according to the Kabat EU numbering system;

T366W and F405W mutations in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing T394S and Y407A mutations in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

q) introducing F405W and Y407A mutations in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing T366W and T394S mutations in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system; or

r) introducing a T366W mutation in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing T366S, L368A, and Y407V mutations in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system.

260. The masked cytokine of any one of embodiments 238-251, wherein the modifications promoting the association of the first and the second half-life extension domain comprise:

a) introducing a K409E mutation in the first antibody or fragment thereof, and introducing a D399K mutation in the second antibody or fragment thereof, numbered according to the Kabat EU numbering system;

b) introducing a K409E mutation in the first antibody or fragment thereof, and introducing a D399R mutation in the second antibody or fragment thereof, numbered according to the Kabat EU numbering system;

c) introducing a K409D mutation in the first antibody or fragment thereof, and introducing a D399K mutation in the second antibody or fragment thereof, numbered according to the Kabat EU numbering system;

d) introducing a K409D mutation in the first antibody or fragment thereof, and introducing a D399R mutation in the second antibody or fragment thereof, numbered according to the Kabat EU numbering system;

e) introducing a K392E mutation in the first antibody or fragment thereof, and introducing a D399R mutation in the second antibody or fragment thereof, numbered according to the Kabat EU numbering system;

f) introducing a K392E mutation in the first antibody or fragment thereof, and introducing a D399K mutation in the second antibody or fragment thereof, numbered according to the Kabat EU numbering system;

g) introducing a K392D mutation in the first antibody or fragment thereof, and introducing a D399R mutation in the second antibody or fragment thereof, numbered according to the Kabat EU numbering system;

h) introducing a K392D mutation in the first antibody or fragment thereof, and introducing a D399K mutation in the second antibody or fragment thereof, numbered according to the Kabat EU

em;

K409D and K360D mutations in the first antibody or fragment thereof, and introducing D399K and E356K mutations in the second antibody or fragment thereof, numbered according to the Kabat EU numbering system;

j) introducing K409D and K370D mutations in the first antibody or fragment thereof, and introducing D399K and E357K mutations in the second antibody or fragment thereof, numbered according to the Kabat EU numbering system;

k) introducing K409D and K392D mutations in the first antibody or fragment thereof, and introducing D399K, E356K, and E357K mutations in the second antibody or fragment thereof, numbered according to the Kabat EU numbering system;

l) introducing K409D and K392D mutations in the first antibody or fragment thereof, and introducing a D399K mutation in the second antibody or fragment thereof, numbered according to the Kabat EU numbering system;

m) introducing K409D and K392D mutations in the first antibody or fragment thereof, and introducing D399K and E356K mutations in the second antibody or fragment thereof, numbered according to the Kabat EU numbering system;

n) introducing K409D and K392D mutations in the first antibody or fragment thereof, and introducing D399K and E357K mutations in the second antibody or fragment thereof, numbered according to the Kabat EU numbering system;

o) introducing K409D and K370D mutations in the first antibody or fragment thereof, and introducing D399K and E357K mutations in the second antibody or fragment thereof, numbered according to the Kabat EU numbering system;

p) introducing a D399K mutation in the first antibody or fragment thereof, and introducing K409D and K360D mutations in the second antibody or fragment thereof, numbered according to the Kabat EU numbering system;

q) introducing K409D and K439D mutations in the first antibody or fragment thereof, and introducing D399K and E356K mutations in the second antibody or fragment thereof, numbered according to the Kabat EU numbering system;

r) introducing a K409E mutation in the second antibody or fragment thereof, and introducing a D399K mutation in the first antibody or fragment thereof, numbered according to the Kabat EU numbering system;

s) introducing a K409E mutation in the second antibody or fragment thereof, and introducing a D399R mutation in the first antibody or fragment thereof, numbered according to the Kabat EU numbering system;

t) introducing a K409D mutation in the second antibody or fragment thereof, and introducing a D399K mutation in the first antibody or fragment thereof, numbered according to the Kabat EU

em;

a K409D mutation in the second antibody or fragment thereof, and introducing a D399R mutation in the first antibody or fragment thereof, numbered according to the Kabat EU numbering system;

v) introducing a K392E mutation in the second antibody or fragment thereof, and introducing a D399R mutation in the first antibody or fragment thereof, numbered according to the Kabat EU numbering system;

w) introducing a K392E mutation in the second antibody or fragment thereof, and introducing a D399K mutation in the first antibody or fragment thereof, numbered according to the Kabat EU numbering system;

x) introducing a K392D mutation in the second antibody or fragment thereof, and introducing a D399R mutation in the first antibody or fragment thereof, numbered according to the Kabat EU numbering system;

y) introducing a K392D mutation in the second antibody or fragment thereof, and introducing a D399K mutation in the first antibody or fragment thereof, numbered according to the Kabat EU numbering system;

z) introducing K409D and K360D mutations in the second antibody or fragment thereof, and introducing D399K and E356K mutations in the first antibody or fragment thereof, numbered according to the Kabat EU numbering system;

aa) introducing K409D and K370D mutations in the second antibody or fragment thereof, and introducing D399K and E357K mutations in the first antibody or fragment thereof, numbered according to the Kabat EU numbering system;

ab) introducing K409D and K392D mutations in the second antibody or fragment thereof, and introducing D399K, E356K, and E357K mutations in the first antibody or fragment thereof, numbered according to the Kabat EU numbering system;

ac) introducing K409D and K392D mutations in the second antibody or fragment thereof, and introducing a D399K mutation in the first antibody or fragment thereof, numbered according to the Kabat EU numbering system;

ad) introducing K409D and K392D mutations in the second antibody or fragment thereof, and introducing D399K and E356K mutations in the first antibody or fragment thereof, numbered according to the Kabat EU numbering system;

ae) introducing K409D and K392D mutations in the second antibody or fragment thereof, and introducing D399K and E357K mutations in the first antibody or fragment thereof, numbered according to the Kabat EU numbering system;

af) introducing K409D and K370D mutations in the second antibody or fragment thereof, and introducing D399K and E357K mutations in the first antibody or fragment thereof, numbered according to the Kabat EU numbering system;

a D399K mutation in the second antibody or fragment thereof, and introducing K409D and K360D mutations in the first antibody or fragment thereof, numbered according to the Kabat EU numbering system; or

ah) introducing K409D and K439D mutations in the second antibody or fragment thereof, and introducing D399K and E356K mutations in the first antibody or fragment thereof, numbered according to the Kabat EU numbering system.

261. The masked cytokine of any one of embodiments 238-251, wherein the amino acid sequence of the first antibody or fragment thereof and the amino acid sequence of the second antibody or fragment thereof are produced by:

a) introducing a K409E mutation in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing a D399K mutation in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

b) introducing a K409E mutation in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing a D399R mutation in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

c) introducing a K409D mutation in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing a D399K mutation in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

d) introducing a K409D mutation in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing a D399R mutation in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

e) introducing a K392E mutation in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing a D399R mutation in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

f) introducing a K392E mutation in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing a D399K mutation in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

g) introducing a K392D mutation in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing a D399R mutation in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

h) introducing a K392D mutation in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing a D399K mutation in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

K409D and K360D mutations in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing D399K and E356K mutations in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

j) introducing K409D and K370D mutations in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing D399K and E357K mutations in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

k) introducing K409D and K392D mutations in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing D399K, E356K, and E357K mutations in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

l) introducing K409D and K392D mutations in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing a D399K mutation in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

m) introducing K409D and K392D mutations in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing D399K and E356K mutations in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

n) introducing K409D and K392D mutations in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing D399K and E357K mutations in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

o) introducing K409D and K370D mutations in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing D399K and E357K mutations in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

p) introducing a D399K mutation in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing K409D and K360D mutations in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

q) introducing K409D and K439D mutations in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing D399K and E356K mutations in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

r) introducing a K409E mutation in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing a D399K mutation in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

s) introducing a K409E mutation in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing a D399R mutation in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

t) introducing a K409D mutation in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing a D399K mutation in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, rding to the Kabat EU numbering system;

a K409D mutation in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing a D399R mutation in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

v) introducing a K392E mutation in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing a D399R mutation in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

w) introducing a K392E mutation in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing a D399K mutation in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

x) introducing a K392D mutation in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing a D399R mutation in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

y) introducing a K392D mutation in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing a D399K mutation in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

z) introducing K409D and K360D mutations in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing D399K and E356K mutations in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

aa) introducing K409D and K370D mutations in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing D399K and E357K mutations in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

ab) introducing K409D and K392D mutations in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing D399K, E356K, and E357K mutations in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

ac) introducing K409D and K392D mutations in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing a D399K mutation in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

ad) introducing K409D and K392D mutations in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing D399K and E356K mutations in the amino acid sequence of SEQ ID NO: 154 or 169, numbered according to the Kabat EU numbering system;

ae) introducing K409D and K392D mutations in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing D399K and E357K mutations in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

af) introducing K409D and K370D mutations in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing D399K and E357K mutations in the amino acid sequence of SEQ ID NO: 154 or

ly, numbered according to the Kabat EU numbering system;

a D399K mutation in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing K409D and K360D mutations in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system; or

ah) introducing K409D and K439D mutations in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing D399K and E356K mutations in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system.

262. The masked cytokine of any one of embodiments 219-261, wherein the first linker comprises a first cleavable peptide; and/or wherein the second linker comprises a second cleavable peptide.

263. The masked cytokine of any one of embodiments 219-262, wherein the first linker comprises a first N-terminal spacer domain, and/or a first C-terminal spacer domain.

264. The masked cytokine of embodiment 263, wherein the first linker comprises:

a) the first N-terminal spacer domain, the first cleavable peptide, and the first C-terminal spacer domain;

b) the first N-terminal spacer domain and the first cleavable peptide;

c) the first N-terminal spacer domain and the first C-terminal spacer domain;

d) the first cleavable peptide and the first C-terminal spacer domain;

e) the first N-terminal spacer domain; or

f) the first C-terminal spacer domain.

265. The masked cytokine of any one of embodiments 219-264, wherein the second linker comprises a second N-terminal spacer domain, and/or a second C-terminal spacer domain.

266. The masked cytokine of embodiment 265, wherein the second linker comprises:

a) the second N-terminal spacer domain, the second cleavable peptide, and the second C-terminal spacer domain;

b) the second N-terminal spacer domain and the second cleavable peptide;

c) the second N-terminal spacer domain and the second C-terminal spacer domain;

d) the second cleavable peptide and the second C-terminal spacer domain;

e) the second N-terminal spacer domain; or

f) the second C-terminal spacer domain.

ısked cytokine of any one of embodiments 262-266, wherein the first cleavable peptide comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 96-153, 236-242, 264, 270-302, 306-317, 342-347, 356-415, 420-491, 494-501, 504-535, and 538-555; and/or wherein the second cleavable peptide comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 96-153, 236-242, 264, 270-302, 306-317, 342-347, 356-415, 420-491, 494-501, 504-535, and 538-555.

268. The masked cytokine of any one of embodiments 263-267, wherein the first N-terminal spacer domain comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 20-95, 235, 268, 269, 303-305, 323-338, 340, 341, 727, 794, and 799, and/or the first C-terminal spacer domain comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 20-95, 235, 268, 269, 303-305, 323-338, 340, 341, 727, 794, and 799.

269. The masked cytokine of any one of embodiments 262-266, wherein the first cleavable peptide comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 96-153, 264, 270-302, 306-317, 342-347, 356-415, 420-491, 494-501, 504-535, and 538-555, and an amino acid sequence selected from the group consisting of SEQ ID NOs: 236-242.

270. The masked cytokine of embodiment 269, wherein the amino acid sequence selected from the group consisting of SEQ ID NOs: 96-153, 264, 270-302, 306-317, 342-347, 356-415, 420-491, 494-501, 504-535, and 538-555 comprises an N-terminus and a C-terminus, and the amino acid sequence selected from the group consisting of SEQ ID NOs: 236-242 is linked to the N-terminus or the C-terminus of the amino acid sequence selected from the group consisting of SEQ ID NOs: 96-153, 264, 270-302, 306-317, 342-347, 356-415, 420-491, 494-501, 504-535, and 538-555.

271. The masked cytokine of any one of embodiments 265-270, wherein the second N-terminal spacer domain comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 20-95, 235, 268, 269, 303-305, 323-338, 340, 341, 727, 794, and 799, and/or the second C-terminal spacer domain comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 20-95, 235, 268, 269, 303-305, 323-338, 340, 341, 727, 794, and 799.

272. The masked cytokine of any one of embodiments 262-271, wherein the second cleavable peptide comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 96-153, 264, 270-302, 306-317, 342-347, 356-415, 420-491, 494-501, 504-535, and 538-555, and an amino acid sequence selected from the group consisting of SEQ ID NOs: 236-242.

ısked cytokine of embodiment 272, wherein the amino acid sequence selected from the group consisting of SEQ ID NOs: 96-153, 264, 270-302, 306-317, 342-347, 356-415, 420-491, 494-501, 504-535, and 538-555 comprises an N-terminus and a C-terminus, and the amino acid sequence selected from the group consisting of SEQ ID NOs: 236-242 is linked to the N-terminus or the C-terminus of the amino acid sequence selected from the group consisting of SEQ ID NOs: 96-153, 264, 270-302, 306-317, 342-347, 356-415, 420-491, 494-501, 504-535, and 538-555.

274. The masked cytokine of any one of embodiments 218-273, wherein the first linker comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 11-153, 235-242, 262-264, 268-320, 323-338, 340-354, 356-555, 668, 691, 724, 725, 727, 762-771, 794, and 797-812, and/or the second linker comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 11-153, 235-242, 262-264, 268-320, 323-338, 340-354, 356-555, 668, 691, 724, 725, 727, 762-771, 794, and 797-812.

275. The masked cytokine of any one of embodiments 219-274, wherein the third linker comprises a cleavable peptide.

276. The masked cytokine of any one of embodiments 219-275, wherein the third linker comprises a third N-terminal spacer domain, and/or a third C-terminal spacer domain.

277. The masked cytokine of embodiment 276, wherein the third linker comprises:

a) the third N-terminal spacer domain, the third cleavable peptide, and the third C-terminal spacer domain;

b) the third N-terminal spacer domain and the third cleavable peptide;

c) the third N-terminal spacer domain and the third C-terminal spacer domain;

d) the third cleavable peptide and the third C-terminal spacer domain;

e) the third N-terminal spacer domain; or

f) the third C-terminal spacer domain.

278. The masked cytokine of any one of embodiments 275-277, wherein the third cleavable peptide comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 96-153, 236-242, 264, 270-302, 306-317, 342-347, 356-415, 420-491, 494-501, 504-535, and 538-555; and/or wherein the third cleavable peptide comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 96-153, 236-242, 264, 270-302, 306-317, 342-347, 356-415, 420-491, 494-501, 504-535, and 538-555.

ısked cytokine of any one of embodiments 276-278, wherein the third N-terminal spacer domain comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 20-95, 235, 268, 269, 303-305, 323-338, 340, 341, 727, 794, and 799, and/or the third C-terminal spacer domain comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 20-95, 235, 268, 269, 303-305, 323-338, 340, 341, 727, 794, and 799.

280. The masked cytokine of any one of embodiments 275-279, wherein the third cleavable peptide comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 96-153, 264, 270-302, 306-317, 342-347, 356-415, 420-491, 494-501, 504-535, and 538-555, and an amino acid sequence selected from the group consisting of SEQ ID NOs: 236-242.

281. The masked cytokine of embodiment 280, wherein the amino acid sequence selected from the group consisting of SEQ ID NOs: 96-153, 264, 270-302, 306-317, 342-347, 356-415, 420-491, 494-501, 504-535, and 538-555 comprises an N-terminus and a C-terminus, and the amino acid sequence selected from the group consisting of SEQ ID NOs: 236-242 is linked to the N-terminus or the C-terminus of the amino acid sequence selected from the group consisting of SEQ ID NOs: 96-153, 264, 270-302, 306-317, 342-347, 356-415, 420-491, 494-501, 504-535, and 538-555.

282. The masked cytokine of any one of embodiments 219-281, wherein the third linker comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 11-153, 235-242, 262-264, 268-320, 323-338, 340-354, 356-555, 668, 691, 724, 725, 727, 762-771, 794, and 797-812, and/or the third linker comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 11-153, 235-242, 262-264, 268-320, 323-338, 340-354, 356-555, 668, 691, 724, 725, 727, 762-771, 794, and 797-812.

283. The masked cytokine of any one of embodiments 254-282, wherein the fourth linker comprises a fourth N-terminal spacer domain, and/or a fourth C-terminal spacer domain.

284. The masked cytokine of embodiment 283, wherein the fourth N-terminal spacer domain comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 20-95, 235, 268, 269, 303-305, 323-338, 340, 341, 727, 794, and 799, and/or the fourth C-terminal spacer domain comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 20-95, 235, 268, 269, 303-305, 323-338, 340, 341, 727, 794, and 799.

ısked cytokine of any one of embodiments 262-284, wherein the first cleavable peptide, the second cleavable peptide, and/or the third cleavable peptide is a substrate for a protease that is co-localized in a region or a tissue expressing a cytokine receptor.

286. The masked cytokine of embodiment 285, wherein the cytokine receptor is an IL-2 cytokine receptor or an IL-15 cytokine receptor.

287. The masked cytokine of any one of embodiments 262-286, wherein the first cleavable peptide, the second cleavable peptide, and/or the third cleavable peptide is cleaved by one or more enzyme selected from the group consisting of: ABHD12, ADAM12, ABHD12B, ABHD13, ABHD17A, ADAM19, ADAM20, ADAM21, ADAM28, ADAM30, ADAM33, ADAM8, ABHD17A, ADAMDEC1, ADAMTS1, ADAMTS10, ADAMTS12, ADAMTS13, ADAMTS14, ADAMTS15, ADAMTS16, ADAMTS17, ADAMTS18, ADAMTS19, ADAMTS2, ADAMTS20, ADAMTS3, ADAMTS4, ABHD17B, ADAMTS5, ADAMTS6, ADAMTS7, ADAMTS8, ADAMTS9, ADAMTSL1, ADAMTSL2, ADAMTSL3, ABHD17C, ADAMTSL5, ASTL, BMP1, CELA1, CELA2A, CELA2B, CELA3A, CELA3B, ADAM10, ADAM15, ADAM17, ADAM9, ADAMTS4, CTSE, CTSF, ADAMTSL4, CMA1, CTRB1, CTRC, CTSO, CTRl, CTSA, CTSW, CTSB, CTSC, CTSD, ESP1, CTSG, CTSH, GZMA, GZMB, GZMH, CTSK, GZMM, CTSL, CTSS, CTSV, CTSZ, HTRA4, KLK10, KLK11, KLK13, KLK14, KLK2, KLK4, DPP4, KLK6, KLK7, KLKB1, ECE1, ECE2, ECEL1, MASP2, MEP1A, MEP1B, ELANE, FAP, GZMA, MMP11, GZMK, HGFAC, HPN, HTRA1, MMP11, MMP16, MMP17, MMP19, HTRA2, MMP20, MMP21, HTRA3, HTRA4, KEL, MMP23B, MMP24, MMP25, MMP26, MMP27, MMP28, KLK5, MMP3, MMP7, MMP8, MMP9, LGMN, LNPEP, MASP1, PAPPA, PAPPA2, PCSK1, NAPSA, PCSK5, PCSK6, MME, MMP1, MMP10, PLAT, PLAU, PLG, PRSS1, PRSS12, PRSS2, PRSS21, PRSS3, PRSS33, PRSS4, PRSS55, PRSS57, MMP12, PRSS8, PRSS9, PRTN3, MMP13, MMP14, ST14, TMPRSS10, TMPRSS11A, TMPRSS11D, TMPRSS11E, TMPRSS11F, TMPRSS12, TMPRSS13, MMP15, TMPRSS15, MMP2, TMPRSS2, TMPRSS3, TMPRSS4, TMPRSS5, TMPRSS6, TMPRSS7, TMPRSS9, NRDC, OVCH1, PAMR1, PCSK3, PHEX, TINAG, TPSAB1, TPSD1, and TPSG1.

288. The masked cytokine of any one of embodiments 218-287, wherein the first half-life extension domain and/or the second half-life extension domain is conjugated to an agent.

289. The masked cytokine of embodiment 288, wherein the agent is an inhibitor of tubulin polymerization, a DNA damaging agent, or a DNA synthesis inhibitor.

ısked cytokine of embodiment 289, wherein the agent is a maytansinoid, an auristatin, a pyrrolobenzodiazepine (PBD) dimer, a calicheamicin, a duocarmycin, a indolinobenzodiazepine dimer or exatecan derivative Dxd.

291. The masked cytokine of embodiment 288, wherein the agent is an immune stimulant.

292. The masked cytokine of embodiment 291, wherein the immune stimulant is a stimulator of interferon genes (STING) agonist or a toll-like receptor (TLR) agonist.

293. The masked cytokine of embodiment 292, wherein the STING agonist is a cyclic dinucleotide (CDN).

294. The masked cytokine of embodiment 293, wherein the CDN is selected from the group consisting of cGAMP, c-di-AMP, c-di-GMP, cAIMP, c-di-IMP, 4-(2-chloro-6-fluorobenzyl)-N-(furan-2-ylmethyl)-3-oxo-3,4-dihydro-2H-benzo[b][1,4]thiazine-6-carboxamide.

295. The masked cytokine of embodiment 292, wherein the TLR agonist is an agonist of a TLR selected from the group consisting of TLR1, TLR2, TLR3, TLR4, TLR5, TLR6, TLR7, TLR8, TLR9, and TLR10.

296. A nucleic acid encoding the masked cytokine of any one of embodiments 1-295 and 320-409.

297. A vector comprising the nucleic acid of embodiment 296.

298. The vector of embodiment 297, which is an expression vector.

299. A host cell comprising the nucleic acid of embodiment 296.

300. A method of producing a masked cytokine comprising culturing the host cell of embodiment 299 under a condition that produces the masked cytokine.

301. The method of embodiment 300, further comprising recovering the masked cytokine produced by the host cell.

302. A masked cytokine produced by the method of embodiment 300 or embodiment 301.

position comprising the masked cytokine of any one of embodiments 1-295 and 320-409.

304. A composition comprising the masked cytokine of embodiment 302.

305. The composition of embodiment 303 or embodiment 304, further comprising an anti-inflammatory agent or an anti-cancer agent.

306. The composition of embodiment 305, wherein the anti-cancer agent is selected from the group consisting of a PD-1 inhibitor, an EGFR inhibitor, a HER2 inhibitor , a VEGFR inhibitor, a CTLA-4 inhibitor, a BTLA inhibitor, a B7H4 inhibitor, a B7H3 inhibitor, a CSFIR inhibitor, an HVEM inhibitor, a CD27 inhibitor, a KIR inhibitor, an NKG2A inhibitor, an NKG2D agonist, a TWEAK inhibitor, an ALK inhibitor, a CD52 targeting antibody, a CCR4 targeting antibody, a PD-L1 inhibitor, a KIT inhibitor, a PDGFR inhibitor, a BAFF inhibitor, an HDAC inhibitor, a VEGF ligand inhibitor, a CD19 targeting molecule, a FOLR1 targeting molecule, a DLL3 targeting molecule, a DKK1 targeting molecule, a MUC1 targeting molecule, a MUC16 targeting molecule, a PSMA targeting molecule, an MSLN targeting molecule, an NY-ES0-1 targeting molecule, a B7H3 targeting molecule, a B7H4 targeting molecule, a BCMA targeting molecule, a CD29 targeting molecule, a CD151targeting molecule, a CD123 targeting molecule, a CD33 targeting molecule, a CD37 targeting molecule, a CDH19 targeting molecule, a CEA targeting molecule, a Claudin 18.2 targeting molecule, a CLEC12A targeting molecule, an EGFRVIII targeting molecule, an EPCAM targeting molecule, an EPHA2 targeting molecule, an FCRH5 targeting molecule, an FLT3 targeting molecule, a GD2 targeting molecule, a glypican 3 targeting molecule, a gpA33 targeting molecule, a GPRC5D targeting molecule, an IL-23R targeting molecule, an IL-1RAP targeting molecule, a MCSP targeting molecule, a RON targeting molecule, a ROR1 targeting molecule, a STEAP2 targeting molecule, a TfR targeting molecule, a CD166 targeting molecule, a TPBG targeting molecule, a TROP2 targeting molecule, a proteasome inhibitor, an ABL inhibitor, a CD30 inhibitor, a FLT3 inhibitor, a MET inhibitor, a RET inhibitor, an IL-1β inhibitor, a MEK inhibitor, a ROS1 inhibitor, a BRAF inhibitor, a CD38 inhibitor, a RANKL inhibitor, a B4GALNT1 inhibitor, a SLAMF7 inhibitor, an IDH2 inhibitor, an mTOR inhibitor, a CD20 targeting antibody, a BTK inhibitor, a PI3K inhibitor, a FLT3 inhibitor, a PARP inhibitor, a CDK4 inhibitor, a CDK6 inhibitor, an FGFR inhibitor, a RAF inhibitor, a JAK1 inhibitor, a JAK2 inhibitor, a JAK3 inhibitor, an IL-6 inhibitor, a IL-17 inhibitor, a Smoothened inhibitor, an IL-6R inhibitor, a BCL2 inhibitor, a PTCH inhibitor, a PIGF inhibitor, a TGFB inhibitor, a CD28 agonist, a CD3 agonist, CD40 agonist, a GITR agonist, a OX40 agonist, a VISTA agonist, a CD137 agonist, a LAG3 inhibitor, a TIM3 inhibitor, a TIGIT inhibitor, and an IL-2R inhibitor.

mposition of embodiment 305, wherein the anti-inflammatory agent is a cyclooxygenase (COX) inhibitor or an NF-κB inhibitor.

308. The composition of embodiment 307, wherein the COX inhibitor is a COX-1 and/or COX-2 inhibitor.

309. The composition of embodiment 307 or embodiment 308, wherein the COX inhibitor is selected from the group consisting of SC-560, FR122047, P6, mofezolac, TFAP, flurbiprofen, ketoprofen, celecoxib, rofecoxib, meloxicam, piroxicam, deracoxib, parecoxib, valdecoxib, etoricoxib, a chromene derivative, a chroman derivative, N-(2-cyclohexyloxynitrophenyl) methane sulfonamide, parecoxib, lumiracoxib, RS 57067, T-614, BMS-347070, JTE-522, S-2474, SVT- 2016, CT-3, ABT-963, SC-58125, nimesulide, flosulide, NS-398, L- 745337, RWJ-63556, L-784512, darbufelone, CS-502, LAS-34475, LAS- 34555, S-33516, diclofenac, mefenamic acid, SD-8381, ibuprofen, naproxen, ketorolac, indomethacin, aspirin, naproxen, tolmetin, piroxicam, and meclofenamate.

310. The composition of embodiment 307, wherein the NF-κB inhibitor is selected from the group consisting of an IKK complex inhibitor, an IκB degradation inhibitor, an NF-κB nuclear translocation inhibitor, a p65 acetylation inhibitor, an NF-κB DNA binding inhibitor, an NF-κB transactivation inhibitor, and a p53 induction inhibitor.

311. The composition of embodiment 307 or embodiment 308, wherein the NF-κB inhibitor is selected from the group consisting of TPCA-1, NF-κB Activation Inhibitor VI (BOT-64), BMS-345541, amlexanox, SC-514 (GK-01140), IMD-0354, IKK-16, BAY-11-7082, MG-115, MG-132, lactacystin, epoxomicin, parthenolide, carfilzomib, MLN-4924 (pevonedistat), JSH-23 rolipram, gallic acid, anacardic acid, GYY-4137, p-XSC, CV-3988, prostaglandin E2 (PGE2), LY-294002, wortmannin, mesalamine, quinacrine, and flavopiridol.

312. A pharmaceutical composition comprising the masked cytokine of any one of embodiments 1-295 and 320-409, and a pharmaceutically acceptable carrier.

313. A pharmaceutical composition comprising the masked cytokine of embodiment 302, and a pharmaceutically acceptable carrier.

314. A kit comprising the masked cytokine of any one of embodiments 1-295 and 320-409, or the composition of any one of embodiments 303-311, or the pharmaceutical composition of embodiment 312 or 313.

ıod of treating or preventing a neoplastic disease in a subject, the method comprising administering to the subject an effective amount of the masked cytokine of any one of embodiments 1-295 and 320-409, or the composition of any one of embodiments 303-311.

316. The method of embodiment 315, wherein the neoplastic disease is a cancer.

317. The method of embodiment 316, wherein the cancer is leukemia, lymphoma, head and neck cancer, colorectal cancer, prostate cancer, pancreatic cancer, melanoma, breast cancer, neuroblastoma, lung cancer, ovarian cancer, osteosarcoma, bladder cancer, cervical cancer, liver cancer, kidney cancer, skin cancer or testicular cancer.

318. A method of treating or preventing an inflammatory or autoimmune disease in a subject, the method comprising administering to the subject an effective amount of the masked cytokine of any one of embodiments 1-295 and 320-409, or the composition of any one of embodiments 303-311.

319. The method of embodiment 318, wherein the inflammatory or autoimmune disease is selected from the group consisting of atherosclerosis, obesity, inflammatory bowel disease (IBD), rheumatoid arthritis, allergic encephalitis, psoriasis, atopic skin disease, osteoporosis, peritonitis, hepatitis, lupus, celiac disease, Sjogren′s syndrome, polymyalgia rheumatica, multiple sclerosis (MS), ankylosing spondylitis, type 1 diabetes mellitus, alopecia areata, vasculitis, and temporal arteritis, graft versus host disease (GVHD), asthma, COPD, a paraneoplastic autoimmune disease, cartilage inflammation, juvenile arthritis, juvenile rheumatoid arthritis, pauciarticular juvenile rheumatoid arthritis, polyarticular juvenile rheumatoid arthritis, systemic onset juvenile rheumatoid arthritis, juvenile ankylosing spondylitis, juvenile enteropathic arthritis, juvenile reactive arthritis, juvenile Reiter's Syndrome, SEA Syndrome (Seronegativity, Enthesopathy, Arthropathy Syndrome), juvenile dermatomyositis , juvenile psoriatic arthritis, juvenile Scleroderma, juvenile systemic lupus erythematosus, juvenile vasculitis, pauciarticular rheumatoid arthritis, systemic onset rheumatoid arthritis, enteropathic arthritis, reactive arthritis, Reiter's Syndrome, dermatomyositis, psoriatic arthritis, Scleroderma, vasculitis, myolitis, polymyolitis, dermatomyolitis, polyarteritis nodossa, Wegener's granulomatosis, arteritis, ploymyalgia rheumatica, sarcoidosis, Sclerosis, primary biliary Sclerosis, Sclerosing cholangitis, psoriasis, plaque psoriasis, guttate psoriasis, inverse psoriasis, pustular psoriasis, erythrodermic psoriasis, dermatitis, atopic dermatitis, atherosclerosis, Still's disease, Systemic Lupus Erythematosus (SLE), myasthenia gravis, Crohn's disease, ulcerative colitis, celiac disease, rhinosinusitis, rhinosinusitis with polyps, eosinophilic esophogitis, eosinophilic bronchitis, Guillain-Barre disease, thyroiditis (e.g., Graves' disease), Addison's disease, Raynaud's phenomenon, autoimmune hepatitis, transplantation rejection, kidney damage, hepatitis C-induced vasculitis, and spontaneous loss

ɛed cytokine comprising:

a) a first half-life extension domain comprising the amino acid sequence of SEQ ID NO: 155, and a second half-life extension domain comprising the amino acid sequence of SEQ ID NO: 156;

b) a masking moiety comprising the amino acid sequence of SEQ ID NO: 261; and

c) a cytokine or functional fragment thereof comprising the amino acid sequence of SEQ ID NO: 3,

wherein the masking moiety is linked to the first half-life extension domain,

wherein the cytokine or functional fragment thereof is linked to the second half-life extension domain, and

wherein the first half-life extension domain and the second half-life extension domain contain modifications promoting the association of the first and the second half-life extension domain.

321. The masked cytokine of embodiment 320, wherein the masking moiety is linked to the first half-life extension domain via a first linker, and wherein the cytokine or functional fragment thereof is linked to the second half-life extension domain via a second linker.

322. The masked cytokine of embodiment 321, wherein the first linker comprises the amino acid sequence of SEQ ID NO: 28.

323. The masked cytokine of embodiment 321 or embodiment 322, wherein the second linker comprises a cleavable peptide comprising the amino acid sequence of SEQ ID NO: 264.

324. The masked cytokine of any one of embodiments 321-323, wherein the second linker comprises the amino acid sequence of SEQ ID NO: 811.

325. The masked cytokine of any one of embodiments 320-324, wherein the masked cytokine comprises the amino acid sequence of SEQ ID NO: 266.

326. The masked cytokine of any one of embodiments 320-325, wherein the masked cytokine comprises the amino acid sequence of SEQ ID NO: 267.

327. The masked cytokine of any one of embodiments 320-326, wherein the masked cytokine comprises the amino acid sequences of SEQ ID NOs: 266 and 267.

ısked cytokine of embodiment 1, wherein the masked cytokine comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 585-597, 602, 610-614, 627-636, 642, and 643.

329. The masked cytokine of embodiment 70, wherein the masked cytokine comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 567 and 598-601.

330. The masked cytokine of embodiment 149, wherein the masked cytokine comprises the amino acid sequences of: SEQ ID NOs: 562 and 563; or SEQ ID NOs: 608 and 603; or SEQ ID NOs: 604 and 603; or SEQ ID NOs: 605 and 603; or SEQ ID NOs: 606 and 603; or SEQ ID NOs: 615 and 617; or SEQ ID NOs: 266 and 267; or SEQ ID NOs: 618 and 620; or SEQ ID NOs: 621 and 623; or SEQ ID NOs: 624 and 626; or SEQ ID NOs: 608 and 267; or SEQ ID NOs: 663 and 664; or SEQ ID NOs: 665 and 666; or SEQ ID NOs: 667 and 267; or SEQ ID NOs: 669 and 267; or SEQ ID NOs: 670 and 671; or SEQ ID NOs: 670 and 671; or SEQ ID NOs: 672 and 267; or SEQ ID NOs: 673 and 267; or SEQ ID NOs: 674 and 267; or SEQ ID NOs: 675 and 267; or SEQ ID NOs: 676 and 267; or SEQ ID NOs: 677 and 267; or SEQ ID NOs: 678 and 267; or SEQ ID NOs: 679 and 267; or SEQ ID NOs: 680 and 267; or SEQ ID NOs: 681 and 267; or SEQ ID NOs: 682 and 267; or SEQ ID NOs: 683 and 267; or SEQ ID NOs: 684 and 267; or SEQ ID NOs: 685 and 267; or SEQ ID NOs: 686 and 267; SEQ ID NOs: 687 and 267; or SEQ ID NOs: 688 and 267; or SEQ ID NOs: 689 and 267; or SEQ ID NOs: 690 and 267; or SEQ ID NOs: 692 and 267; or SEQ ID NOs: 693 and 267; or SEQ ID NOs: 694 and 267; or SEQ ID NOs: 695 and 267; or SEQ ID NOs: 696 and 267; or SEQ ID NOs: 697 and 267; or SEQ ID NOs: 698 and 267; or SEQ ID NOs: 699 and 267; or SEQ ID NOs: 700 and 267; or SEQ ID NOs: 701 and 267; or SEQ ID NOs: 702 and 267; or SEQ ID NOs: 703 and 267; or SEQ ID NOs: 704 and 267; or SEQ ID NOs: 705 and 267; or SEQ ID NOs: 706 and 267; or SEQ ID NOs: 707 and 267; or SEQ ID NOs: 708 and 267; or SEQ ID NOs: 709 and 267; or SEQ ID NOs: 710 and 267; or SEQ ID NOs: 711 and 267; or SEQ ID NOs: 712 and 667; or SEQ ID NOs: 713 and 267; or SEQ ID NOs: 714 and 267; or SEQ ID NOs: 716 and 699; or SEQ ID NOs: 717 and 267; or SEQ ID NOs: 718 and 267; or SEQ ID NOs: 719 and 267; or SEQ ID NOs: 720 and 267; or SEQ ID NOs: 722 and 267; or SEQ ID NOs: 723 and 267; or SEQ ID NOs: 720 and 267; or SEQ ID NOs: 728 and 267; or SEQ ID NOs: 729 and 267; or SEQ ID NOs: 730 and 267; or SEQ ID NOs: 731 and 267; or SEQ ID NOs: 732 and 267; or SEQ ID NOs: 733 and 267; or SEQ ID NOs: 734 and 267; or SEQ ID NOs: 735 and 267; or SEQ ID NOs: 736 and 267; or SEQ ID NOs: 737 and 267; or SEQ ID NOs: 738 and 267; or SEQ ID NOs: 739 and 267; or SEQ ID NOs: 740 and 267; or SEQ ID NOs: 741 and 267; or SEQ ID NOs: 742 and 267; or SEQ ID NOs: 743 and 267; or SEQ ID NOs: 744 and 267; or SEQ ID NOs: 745 and 267; or SEQ ID NOs: 746 and 267; or SEQ ID NOs: 674 and 828; or SEQ ID NOs: 674 and 829; or SEQ ID NOs: 726 and 830; or SEQ ID NOs: 726

Q ID NOs: 747 and 671; or SEQ ID NOs: 715 and 267; or SEQ ID NOs: 715 and 671; or

571; or SEQ ID NOs: 749 and 671; or SEQ ID NOs: 750 and 671; or SEQ ID NOs: 751 and 671; or SEQ ID NOs: 752 and 671; or SEQ ID NOs: 753 and 671; or SEQ ID NOs: 754 and 671; or SEQ ID NOs: 758 and 671; or SEQ ID NOs: 759 and 671; or SEQ ID NOs: 760 and 671; or SEQ ID NOs: 761 and 671.

331. The masked cytokine of embodiment 218, wherein the masked cytokine comprises the amino acid sequences of: SEQ ID NOs: 755 and 616; or SEQ ID NOs: 756 and 616; or SEQ ID NOs: 757 and 616.

332. A masked cytokine comprising:

a) a first half-life extension domain and a second half-life extension domain;

b) a first masking moiety and a second masking moiety; and

c) a cytokine or functional fragment thereof,

wherein the first masking moiety is linked to the first half-life extension domain,

wherein the second masking moiety is linked to the first masking moiety,

wherein the cytokine or functional fragment thereof is linked to the second half-life extension domain, and

wherein the first half-life extension domain and the second half-life extension domain contain modifications promoting the association of the first and the second half-life extension domain.

333. The masked cytokine of embodiment 332, wherein:

a) the first masking moiety is linked to the first half-life extension domain via a first linker; and/or

b) the second masking moiety is linked to the first masking moiety via a second linker.

334. The masked cytokine of embodiment 332 or 333, wherein the cytokine or functional fragment thereof is linked to the second half-life extension domain via a third linker.

335. The masked cytokine of any one of embodiments 332-334, wherein the cytokine or functional fragment thereof is an IL-2 polypeptide or functional fragment thereof.

336. The masked cytokine of embodiment 335, wherein the IL-2 polypeptide or functional fragment thereof comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 1-8, 160, 243-251, 230, 243-251, 260, 775-792, and 813-822.

ısked cytokine of embodiment 335, wherein the IL-2 polypeptide or functional fragment thereof comprises an amino acid sequence produced by introducing one or more amino acid substitutions into the amino acid sequence of the IL-2 polypeptide or functional fragment thereof that reduces the affinity of the IL-2 polypeptide or functional fragment thereof for CD25 (IL-2Rα).

338. The masked cytokine of embodiment 337, wherein the amino acid sequence is produced by introducing one or more of the following amino acid substitutions into any one of SEQ ID NOs: 1-8, 160, 243-251, 260, 775-792, and 813-822: R38A, F42A, F42K, F42E, K43A, Y45A, Y45N, Y45R, E62A, E62R, E62S, and L72G.

339. The masked cytokine of embodiment 335, wherein the IL-2 polypeptide or functional fragment thereof comprises an amino acid sequence produced by introducing one or more amino acid substitutions into the amino acid sequence of the IL-2 polypeptide or functional fragment thereof that increases the affinity of the IL-2 polypeptide or functional fragment thereof for IL-2Rβ or IL-2Rγ.

340. The masked cytokine of embodiment 339, wherein the amino acid sequence is produced by introducing one or more of the following amino acid substitutions into any one of SEQ ID NOs: 1-8, 160, 243-251, 260, 775-792, and 813-822: H16I, L18C, D20A, D20L, D20F, N29L, L80F, R81D, L85V, I86V, and I92F.

341. The masked cytokine of embodiment 337 or embodiment 338, wherein the amino acid sequence is produced by further introducing one or more amino acid substitutions that increase the affinity of the IL-2 polypeptide or functional fragment thereof for IL-2Rβ or IL-2Rγ.

342. The masked cytokine of embodiment 341, wherein the one or more amino acid substitutions that increase the affinity of the IL-2 polypeptide or functional fragment thereof for IL-2Rβ or IL-2Rγ is selected from the group consisting of H16I, L18C, D20A, D20L, D20F, N29L, L80F, R81D, L85V, I86V, and I92F.

343. The masked cytokine of embodiment 335, wherein the IL-2 polypeptide or functional fragment thereof comprises an amino acid sequence produced by introducing one or more amino acid substitutions into the amino acid sequence of the IL-2 polypeptide or functional fragment thereof that stabilizes the IL-2 polypeptide or functional fragment thereof.

ısked cytokine of embodiment 343, wherein the amino acid sequence is produced by introducing one of the following amino acid substitutions into any one of SEQ ID NOs: 1-8, 160, 243-251, 260, 775-792, and 813-822: C125S, C125A, and C125G.

345. The masked cytokine of any one of embodiments 337-342, wherein the amino acid sequence is produced by further introducing one or more amino acid substitutions that stabilize the IL-2 polypeptide or functional fragment thereof.

346. The masked cytokine of embodiment 345, wherein the one or more amino acid substitutions that stabilize the IL-2 polypeptide or functional fragment thereof is the amino acid substitution C125S, C125A, or C125G.

347. The masked cytokine of any one of embodiments 335-346, wherein the first masking moiety comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 9, 10, 161-165, 187-218, 221-229, 231, 261, 826 and 827 and the second masking moiety comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 9, 10, 161-165, 187-218, 221-229, 231, 261, 826 and 827 and wherein the amino acid sequence of the first masking moiety and the second masking moiety are different.

348. The masked cytokine of any one of embodiments 335-347, wherein:

a) the first masking moiety comprises the amino acid sequence of SEQ ID NO: 9 or 231, and the second masking moiety comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 10, 161-165, 187-218, 221-226, 261, 826 and 827; or

b) the first masking moiety comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 10, 161-165, 187-218, 221-226, 261, 826 and 827, and the second masking moiety comprises the amino acid sequence of SEQ ID NO: 9 or 231.

349. The masked cytokine of any one of embodiments 332-334, wherein the cytokine or functional fragment thereof is an IL-15 polypeptide or functional fragment thereof.

350. The masked cytokine of embodiment 349, wherein the IL-15 polypeptide or functional fragment thereof comprises the amino acid sequence of SEQ ID NO: 167.

351. The masked cytokine of embodiment 349 or embodiment 350, wherein

king moiety comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 232-234, and 823-825, and the second masking moiety comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 10, 161-165, 219-229, 261, 826 and 827;

b) the first masking moiety comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 10, 161-165, 219-229, 261, 826 and 827, and the second masking moiety comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 232-234, and 823-825;

c) the first masking moiety comprises an amino acid sequence produced by introducing one or more of the following amino acid substitutions into the amino acid sequence of any one of SEQ ID NOs: 232-234, and 823-825: R24A, R26A, K34A, S40A, L42A, and P67A, and the second masking moiety comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 10, 161-165, 219-229, 261, 826 and 827; or

d) the first masking moiety comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 10, 161-165, 219-229, 261, 826 and 827, and the second masking moiety comprises an amino acid sequence produced by introducing one or more of the following amino acid substitutions into the amino acid sequence of any one of SEQ ID NOs: 232-234, and 823-825: R24A, R26A, K34A, S40A, L42A, and P67A.

352. The masked cytokine of any one of embodiments 332-351, wherein the first half-life extension domain is a first antibody or fragment thereof, and the second half-life extension domain is a second antibody or fragment thereof.

353. The masked cytokine of embodiment 352, wherein:

a) the first antibody or fragment thereof comprises a first heavy chain polypeptide, and the second antibody or fragment thereof comprises a second light chain polypeptide; or

b) the first antibody or fragment thereof comprises a first light chain polypeptide, and the second antibody or fragment thereof comprises a second heavy chain polypeptide.

354. The masked cytokine of embodiment 353, wherein the first heavy chain polypeptide, or the second heavy chain polypeptide comprises one or more amino acid substitutions altering effector function.

355. The masked cytokine of embodiment 354, wherein the first heavy chain polypeptide or the second heavy chain polypeptide:

a) is an IgG1 isotype and comprises the amino substitution(s):

i) N297A, N297G, or N297Q;

ii) L234A and L235A;

C220S, C226S, C229S, and P238S;

iv) C226S, C229S, E233P, L234V, and L235A;

v) L234F, L235E, and P331S;

vi) S267E and L328F;

vii) D265A;

viii) L234A, L235A, and P329G;

b) is an IgG2 isotype and comprises the amino acid substitution(s):

i) V234A and G237A;

ii) H268Q, V309L, A330S, and A331S; or

iii) V234A, G237A, P238S, H268A, V309L, A330S, and P331S; or

e) is an IgG4 isotype and comprises the amino acid substitution(s):

i) L235A, G237A, and E318A;

ii) S228P, L234A, and L235A;

iii) H268Q, V309L, A330S, and P331S; or

iv) S228P and L235A, numbered according to the Kabat EU numbering system.

356. The masked cytokine of embodiment 353, wherein the first heavy chain polypeptide or the second heavy chain polypeptide comprises one or more amino acid substitutions enhancing effector function.

357. The masked cytokine of embodiment 356, wherein the first heavy chain polypeptide or the second heavy chain polypeptide is an IgG1 heavy chain polypeptide and comprises the amino acid substitution(s):

a) S298A, E333A, and K334A;

b) S239D and I332E;

c) S239D, A330L, and I332E;

d) P247I and A339D or A339Q;

e) D280H and K290S;

f) D280H, K290S, and either S298D or S298V;

g) F243L, R292P, and Y300L;

h) F243L, R292P, Y300L, and P396L;

i) F243L, R292P, Y300L, V305I, and P396L;

j) G236A, S239D, and I332E;

k) K326A and E333A;

l) K326W and E333S;

K290E, S298G, and T299A;

, S298G, T299A, and K326E;

o) K290N, S298G, and T299A;

p) K290N, S298G, T299A, and K326E;

q) K334V;

r) L235S, S239D, and K334V;

s) K334V and Q331M, S239D, F243V, E294L, or S298T;

t) E233L, Q311M, and K334V;

u) L234I, Q311M, and K334V;

v) K334V and S298T, A330M, or A330F;

w) K334V, Q311M, and either A330M or A330F;

x) K334V, S298T, and either A330M or A330F;

y) K334V, S239D, and either A330M or S298T;

z) L234Y, Y296W, and K290Y, F243V, or E294L;

aa) Y296W and either L234Y or K290Y;

ab) S239D, A330S, and I332E,

ac) V264I;

ad) F243L and V264I;

ae) L328M;

af) I332E;

ag) L328M and I332E;

ah) V264I and I332E;

ai) S239E and I332E;

aj) S239Q and I332E;

ak) S239E;

al) A330Y;

am) I332D;

an) L328I and I332E;

ao) L328Q and I332E;

ap) V264T;

aq) V240I;

ar) V266I;

as) S239D;

at) S239D and I332D;

au) S239D and I332N;

av) S239D and I332Q;

S239E and I332D;

and I332N;

ay) S239E and I332Q;

az) S239N and I332D;

ba) S239N and I332E;

bb) S239Q and I332D;

bc) A330Y and I332E;

bd) V264I, A330Y, and I332E;

be) A330L and I332E;

bf) V264I, A330L, and I332E;

bg) L234E, L234Y, or L234I;

bh) L235D, L235S, L235Y, or L235I;

bi) S239T;

bj) V240M;

bk) V264Y;

bl) A330I;

bm) N325T;

bn) I332E and L328D, L328V, L328T, or L328I;

bo) V264I, I332E, and either S239E or S239Q;

bp) S239E, V264I, A330Y, and I332E;

bq) A330Y, I332E, and either S239D or S239N;

br) A330L, I332E, and either S239D or S239N;

bs) V264I, S298A, and I332E;

bt) S298A, I332E, and either S239D or S239N;

bu) S239D, V264I, and I332E;

bv) S239D, V264I, S298A, and I332E;

bw) S239D, V264I, A330L, and I332E;

bx) S239D, I332E, and A330I;

by) P230A;

bz) P230A, E233D, and I332E;

ca) E272Y;

cb) K274T, K274E, K274R, K274L, or K274Y;

cd) F275W;

ce) N276L;

cf) Y278T;

cg) V302I;

E318R;

, S324I or S324V;

cj) K326I or K326T;

ck) T335D, T335R, or T335Y;

cl) V240I and V266I;

cm) S239D, A330Y, I332E, and L234I;

cn) S239D, A330Y, I332E, and L235D;

co) S239D, A330Y, I332E, and V240I;

cp) S239D, A330Y, I332E, and V264T; or

cq) S239D, A330Y, I332E, and either K326E or K326T, numbered according to the Kabat EU numbering system.

358. The masked cytokine of embodiment 353, wherein the first heavy chain polypeptide comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 158, 168, and 169, and the second heavy chain polypeptide comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 158, 168, and 169.

359. The masked cytokine of embodiment 353, wherein the first light chain polypeptide comprises the amino acid sequence of SEQ ID NO: 157 or 170, and the second light chain polypeptide comprises the amino acid sequence of SEQ ID NO: 157 or 170.

360. The masked cytokine of embodiment 352, wherein the first antibody or fragment thereof is a first Fragment crystallizable domain (Fc domain) or fragment thereof, and the second antibody or fragment thereof is a second Fc domain or fragment thereof.

361. The masked cytokine of embodiment 360, wherein the first Fc domain or fragment thereof, and/or the second Fc domain or fragment thereof comprises one or more amino acid substitutions altering effector function.

362. The masked cytokine of embodiment 361, wherein the first Fc domain or fragment thereof and/or the second Fc domain or fragment thereof:

a) is an IgG1 Fc domain or fragment thereof and comprises the amino substitution(s):

i) N297A, N297G, or N297Q;

ii) L234A and L235A;

iii) C220S, C226S, C229S, and P238S;

iv) C226S, C229S, E233P, L234V, and L235A;

v) L234F, L235E, and P331S;

S267E and L328F;

vii) D265A;

viii) L234A, L235A, and P329G;

b) is an IgG2 Fc domain or fragment thereof and comprises the amino acid substitution(s):

i) V234A and G237A;

ii) H268Q, V309L, A330S, and A331S; or

iii) V234A, G237A, P238S, H268A, V309L, A330S, and P331S; or

e) is an IgG4 Fc domain or fragment thereof and comprises the amino acid substitution(s):

i) L235A, G237A, and E318A;

ii) S228P, L234A, and L235A;

iii) H268Q, V309L, A330S, and P331S; or

iv) S228P and L235A, numbered according to the Kabat EU numbering system.

363. The masked cytokine of embodiment 361, wherein the first Fc domain or fragment thereof and/or the second Fc domain or fragment thereof comprises one or more amino acid substitutions enhancing effector function.

364. The masked cytokine of embodiment 363, wherein the first Fc domain or fragment thereof and/or the second Fc domain or fragment thereof is an IgG1 Fc domain or fragment thereof and comprises the amino acid substitution(s):

a) S298A, E333A, and K334A;

b) S239D and I332E;

c) S239D, A330L, and I332E;

d) P247I and A339D or A339Q;

e) D280H and K290S;

f) D280H, K290S, and either S298D or S298V;

g) F243L, R292P, and Y300L;

h) F243L, R292P, Y300L, and P396L;

i) F243L, R292P, Y300L, V305I, and P396L;

j) G236A, S239D, and I332E;

k) K326A and E333A;

l) K326W and E333S;

m) K290E, S298G, and T299A;

n) K290E, S298G, T299A, and K326E;

o) K290N, S298G, and T299A;

K290N, S298G, T299A, and K326E;

;

r) L235S, S239D, and K334V;

s) K334V and Q331M, S239D, F243V, E294L, or S298T;

t) E233L, Q311M, and K334V;

u) L234I, Q311M, and K334V;

v) K334V and S298T, A330M, or A330F;

w) K334V, Q311M, and either A330M or A330F;

x) K334V, S298T, and either A330M or A330F;

y) K334V, S239D, and either A330M or S298T;

z) L234Y, Y296W, and K290Y, F243V, or E294L;

aa) Y296W and either L234Y or K290Y;

ab) S239D, A330S, and I332E,

ac) V264I;

ad) F243L and V264I;

ae) L328M;

af) I332E;

ag) L328M and I332E;

ah) V264I and I332E;

ai) S239E and I332E;

aj) S239Q and I332E;

ak) S239E;

al) A330Y;

am) I332D;

an) L328I and I332E;

ao) L328Q and I332E;

ap) V264T;

aq) V240I;

ar) V266I;

as) S239D;

at) S239D and I332D;

au) S239D and I332N;

av) S239D and I332Q;

aw) S239E and I332D;

ax) S239E and I332N;

ay) S239E and I332Q;

S239N and I332D;

and I332E;

bb) S239Q and I332D;

bc) A330Y and I332E;

bd) V264I, A330Y, and I332E;

be) A330L and I332E;

bf) V264I, A330L, and I332E;

bg) L234E, L234Y, or L234I;

bh) L235D, L235S, L235Y, or L235I;

bi) S239T;

bj) V240M;

bk) V264Y;

bl) A330I;

bm) N325T;

bn) I332E and L328D, L328V, L328T, or L328I;

bo) V264I, I332E, and either S239E or S239Q;

bp) S239E, V264I, A330Y, and I332E;

bq) A330Y, I332E, and either S239D or S239N;

br) A330L, I332E, and either S239D or S239N;

bs) V264I, S298A, and I332E;

bt) S298A, I332E, and either S239D or S239N;

bu) S239D, V264I, and I332E;

bv) S239D, V264I, S298A, and I332E;

bw) S239D, V264I, A330L, and I332E;

bx) S239D, I332E, and A330I;

by) P230A;

bz) P230A, E233D, and I332E;

ca) E272Y;

cb) K274T, K274E, K274R, K274L, or K274Y;

cd) F275W;

ce) N276L;

cf) Y278T;

cg) V302I;

ch) E318R;

ci) S324D, S324I or S324V;

cj) K326I or K326T;

T335D, T335R, or T335Y;

and V266I;

cm) S239D, A330Y, I332E, and L234I;

cn) S239D, A330Y, I332E, and L235D;

co) S239D, A330Y, I332E, and V240I;

cp) S239D, A330Y, I332E, and V264T; or

cq) S239D, A330Y, I332E, and either K326E or K326T, numbered according to the Kabat EU numbering system.

365. The masked cytokine of embodiment 360, wherein:

a) the first Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 155, and the second Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 156;

b) the first Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 156, and the second Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 155;

c) the first Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 154, and the second Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 154;

d) the first Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 265, and the second Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 156;

e) the first Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 156, and the second Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 265;

f) the first Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 155, and the second Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 616;

g) the first Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 616, and the second Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 155;

h) the first Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 157, and the second Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 158;

i) the first Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 158, and the second Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO:

omain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 796, and the second Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 774;

k) the first Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 774, and the second Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 796;

l) the first Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 721, and the second Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 619;

m) the first Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 619, and the second Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 721;

n) the first Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 721, and the second Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 772;

o) the first Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 772, and the second Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 721;

p) the first Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 793, and the second Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 622;

q) the first Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 622, and the second Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 793;

r) the first Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 793, and the second Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 773;

s) the first Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 773, and the second Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 793;

t) the first Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 796, and the second Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 625;

u) the first Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 625, and the second Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO:

omain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 156, and the second Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 156;

w) the first Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 796, and the second Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 625; or

x) the first Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 625, and the second Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 796.

366. The masked cytokine of any one of embodiments 332-351, wherein the first half-life extension domain is a first scFv or fragment thereof, and the second half-life extension domain is a second scFv or fragment thereof.

367. The masked cytokine of any one of embodiments 332-351, wherein the first half-life extension domain is a first Fc domain or fragment thereof, and the second half-life extension domain is a second Fc domain or fragment thereof, and wherein the first Fc domain or fragment thereof is linked to the second Fc domain or fragment thereof.

368. The masked cytokine of embodiment 367, wherein the first Fc domain or fragment thereof is linked to the second Fc domain or fragment thereof via a fourth linker.

369. The masked cytokine of any one of embodiments 232-351, wherein:

a) the first half-life extension domain is an scFv or fragment thereof, and the second half-life extension domain is an antibody or fragment thereof; or

a) the first half-life extension domain is an antibody or fragment thereof, and the second half-life extension domain is an scFv or fragment thereof.

370. The masked cytokine of any one of embodiments 352-365, wherein the modifications promoting the association of the first and the second half-life extension domain comprise:

a) introducing S354C and T366W mutations in the first antibody or fragment thereof, and introducing Y349C, T366S, L368A, and Y407V mutations in the second antibody or fragment thereof, numbered according to the Kabat EU numbering system;

b) introducing S354C and T366W mutations in the second antibody or fragment thereof, and introducing Y349C, T366S, L368A, and Y407V mutations in the first antibody or fragment thereof,

rding to the Kabat EU numbering system;

K392D and K409D mutations in the first antibody or fragment thereof, and introducing D399K and E356K mutations in the second antibody or fragment thereof, numbered according to the Kabat EU numbering system;

d) introducing K392D and K409D mutations in the second antibody or fragment thereof, and introducing D399K and E356K mutations in the first antibody or fragment thereof, numbered according to the Kabat EU numbering system;

e) introducing S364H and F405A mutations in the first antibody or fragment thereof, and introducing Y349T and T394F mutations in the second antibody or fragment thereof, numbered according to the Kabat EU numbering system; or

f) introducing S364H and F405A mutations in the second antibody or fragment thereof, and introducing Y349T and T394F mutations in the first antibody or fragment thereof, numbered according to the Kabat EU numbering system.

371. The masked cytokine of any one of embodiments 352-365, wherein the amino acid sequence of the first antibody or fragment thereof and the amino acid sequence of the second antibody or fragment thereof are produced by:

a) introducing S354C and T366W mutations in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing Y349C, T366S, L368A, and Y407V mutations in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

b) introducing S354C and T366W mutations in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing Y349C, T366S, L368A, and Y407V mutations in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

c) introducing K392D and K409D mutations in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing D399K and E356K mutations in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

d) introducing K392D and K409D mutations in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing D399K and E356K mutations in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

e) introducing S364H and F405A mutations in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing Y349T and T394F mutations in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system; or

f) introducing S364H and F405A mutations in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing Y349T and T394F mutations in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system.

ısked cytokine of any one of embodiments 352-365, wherein the modifications promoting the association of the first and the second half-life extension domain comprise:

a) introducing a Y407T mutation in the first antibody or fragment thereof, and introducing a T366Y mutation in the second antibody or fragment thereof, numbered according to the Kabat EU numbering system;

b) introducing a Y407A mutation in the first antibody or fragment thereof, and introducing a T366W mutation in the second antibody or fragment thereof, numbered according to the Kabat EU numbering system;

c) introducing a F405A mutation in the first antibody or fragment thereof, and introducing a T394W mutation in the second antibody or fragment thereof, numbered according to the Kabat EU numbering system;

d) introducing a F405W mutation in the first antibody or fragment thereof, and introducing a T394S mutation in the second antibody or fragment thereof, numbered according to the Kabat EU numbering system;

e) introducing a Y407T mutation in the first antibody or fragment thereof, and introducing a T366Y mutation in the second antibody or fragment thereof, numbered according to the Kabat EU numbering system;

f) introducing T366Y and F405A mutations in the first antibody or fragment thereof, and introducing T394W and Y407T mutations in the second antibody or fragment thereof, numbered according to the Kabat EU numbering system;

g) introducing T366W and F405W mutations in the first antibody or fragment thereof, and introducing T394S and Y407A mutations in the second antibody or fragment thereof, numbered according to the Kabat EU numbering system;

h) introducing F405W and Y407A mutations in the first antibody or fragment thereof, and introducing T366W and T394S mutations in the second antibody or fragment thereof, numbered according to the Kabat EU numbering system;

i) introducing a T366W mutation in the first antibody or fragment thereof, and introducing T366S, L368A, and Y407V mutations in the second antibody or fragment thereof, numbered according to the Kabat EU numbering system;

j) introducing a Y407T mutation in the second antibody or fragment thereof, and introducing a T366Y mutation in the first antibody or fragment thereof, numbered according to the Kabat EU numbering system;

k) introducing a Y407A mutation in the second antibody or fragment thereof, and introducing a T366W mutation in the first antibody or fragment thereof, numbered according to the Kabat EU numbering system;

F405A mutation in the second antibody or fragment thereof, and introducing a T394W mutation in the first antibody or fragment thereof, numbered according to the Kabat EU numbering system;

m) introducing a F405W mutation in the second antibody or fragment thereof, and introducing a T394S mutation in the first antibody or fragment thereof, numbered according to the Kabat EU numbering system;

n) introducing a Y407T mutation in the second antibody or fragment thereof, and introducing a T366Y mutation in the first antibody or fragment thereof, numbered according to the Kabat EU numbering system;

o) introducing T366Y and F405A mutations in the second antibody or fragment thereof, and introducing T394W and Y407T mutations in the first antibody or fragment thereof, numbered according to the Kabat EU numbering system;

p) introducing T366W and F405W mutations in the second antibody or fragment thereof, and introducing T394S and Y407A mutations in the first antibody or fragment thereof, numbered according to the Kabat EU numbering system;

q) introducing F405W and Y407A mutations in the second antibody or fragment thereof, and introducing T366W and T394S mutations in the first antibody or fragment thereof, numbered according to the Kabat EU numbering system; or

r) introducing a T366W mutation in the second antibody or fragment thereof, and introducing T366S, L368A, and Y407V mutations in the first antibody or fragment thereof, numbered according to the Kabat EU numbering system.

373. The masked cytokine of any one of embodiments 352-365, wherein the amino acid sequence of the first antibody or fragment thereof and the amino acid sequence of the second antibody or fragment thereof are produced by:

a) introducing a Y407T mutation in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing a T366Y mutation in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

b) introducing a Y407A mutation in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing a T366W mutation in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

c) introducing a F405A mutation in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing a T394W mutation in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

a F405W mutation in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing a T394S mutation in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

e) introducing a Y407T mutation in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing a T366Y mutation in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

f) introducing T366Y and F405A mutations in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing T394W and Y407T mutations in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

g) introducing T366W and F405W mutations in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing T394S and Y407A mutations in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

h) introducing F405W and Y407A mutations in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing T366W and T394S mutations in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

i) introducing a T366W mutation in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing T366S, L368A, and Y407V mutations in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

j) introducing a Y407T mutation in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing a T366Y mutation in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

k) introducing a Y407A mutation in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing a T366W mutation in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

l) introducing a F405A mutation in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing a T394W mutation in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

m) introducing a F405W mutation in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing a T394S mutation in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

n) introducing a Y407T mutation in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing a T366Y mutation in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

o) introducing T366Y and F405A mutations in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing T394W and Y407T mutations in the amino acid sequence of SEQ ID NO: 154 or

ly, numbered according to the Kabat EU numbering system;

T366W and F405W mutations in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing T394S and Y407A mutations in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

q) introducing F405W and Y407A mutations in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing T366W and T394S mutations in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system; or

r) introducing a T366W mutation in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing T366S, L368A, and Y407V mutations in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system.

374. The masked cytokine of any one of embodiments 352-365, wherein the modifications promoting the association of the first and the second half-life extension domain comprise:

a) introducing a K409E mutation in the first antibody or fragment thereof, and introducing a D399K mutation in the second antibody or fragment thereof, numbered according to the Kabat EU numbering system;

b) introducing a K409E mutation in the first antibody or fragment thereof, and introducing a D399R mutation in the second antibody or fragment thereof, numbered according to the Kabat EU numbering system;

c) introducing a K409D mutation in the first antibody or fragment thereof, and introducing a D399K mutation in the second antibody or fragment thereof, numbered according to the Kabat EU numbering system;

d) introducing a K409D mutation in the first antibody or fragment thereof, and introducing a D399R mutation in the second antibody or fragment thereof, numbered according to the Kabat EU numbering system;

e) introducing a K392E mutation in the first antibody or fragment thereof, and introducing a D399R mutation in the second antibody or fragment thereof, numbered according to the Kabat EU numbering system;

f) introducing a K392E mutation in the first antibody or fragment thereof, and introducing a D399K mutation in the second antibody or fragment thereof, numbered according to the Kabat EU numbering system;

g) introducing a K392D mutation in the first antibody or fragment thereof, and introducing a D399R mutation in the second antibody or fragment thereof, numbered according to the Kabat EU numbering system;

h) introducing a K392D mutation in the first antibody or fragment thereof, and introducing a D399K mutation in the second antibody or fragment thereof, numbered according to the Kabat EU

em;

K409D and K360D mutations in the first antibody or fragment thereof, and introducing D399K and E356K mutations in the second antibody or fragment thereof, numbered according to the Kabat EU numbering system;

j) introducing K409D and K370D mutations in the first antibody or fragment thereof, and introducing D399K and E357K mutations in the second antibody or fragment thereof, numbered according to the Kabat EU numbering system;

k) introducing K409D and K392D mutations in the first antibody or fragment thereof, and introducing D399K, E356K, and E357K mutations in the second antibody or fragment thereof, numbered according to the Kabat EU numbering system;

l) introducing K409D and K392D mutations in the first antibody or fragment thereof, and introducing a D399K mutation in the second antibody or fragment thereof, numbered according to the Kabat EU numbering system;

m) introducing K409D and K392D mutations in the first antibody or fragment thereof, and introducing D399K and E356K mutations in the second antibody or fragment thereof, numbered according to the Kabat EU numbering system;

n) introducing K409D and K392D mutations in the first antibody or fragment thereof, and introducing D399K and E357K mutations in the second antibody or fragment thereof, numbered according to the Kabat EU numbering system;

o) introducing K409D and K370D mutations in the first antibody or fragment thereof, and introducing D399K and E357K mutations in the second antibody or fragment thereof, numbered according to the Kabat EU numbering system;

p) introducing a D399K mutation in the first antibody or fragment thereof, and introducing K409D and K360D mutations in the second antibody or fragment thereof, numbered according to the Kabat EU numbering system;

q) introducing K409D and K439D mutations in the first antibody or fragment thereof, and introducing D399K and E356K mutations in the second antibody or fragment thereof, numbered according to the Kabat EU numbering system;

r) introducing a K409E mutation in the second antibody or fragment thereof, and introducing a D399K mutation in the first antibody or fragment thereof, numbered according to the Kabat EU numbering system;

s) introducing a K409E mutation in the second antibody or fragment thereof, and introducing a D399R mutation in the first antibody or fragment thereof, numbered according to the Kabat EU numbering system;

t) introducing a K409D mutation in the second antibody or fragment thereof, and introducing a D399K mutation in the first antibody or fragment thereof, numbered according to the Kabat EU

em;

a K409D mutation in the second antibody or fragment thereof, and introducing a D399R mutation in the first antibody or fragment thereof, numbered according to the Kabat EU numbering system;

v) introducing a K392E mutation in the second antibody or fragment thereof, and introducing a D399R mutation in the first antibody or fragment thereof, numbered according to the Kabat EU numbering system;

w) introducing a K392E mutation in the second antibody or fragment thereof, and introducing a D399K mutation in the first antibody or fragment thereof, numbered according to the Kabat EU numbering system;

x) introducing a K392D mutation in the second antibody or fragment thereof, and introducing a D399R mutation in the first antibody or fragment thereof, numbered according to the Kabat EU numbering system;

y) introducing a K392D mutation in the second antibody or fragment thereof, and introducing a D399K mutation in the first antibody or fragment thereof, numbered according to the Kabat EU numbering system;

z) introducing K409D and K360D mutations in the second antibody or fragment thereof, and introducing D399K and E356K mutations in the first antibody or fragment thereof, numbered according to the Kabat EU numbering system;

aa) introducing K409D and K370D mutations in the second antibody or fragment thereof, and introducing D399K and E357K mutations in the first antibody or fragment thereof, numbered according to the Kabat EU numbering system;

ab) introducing K409D and K392D mutations in the second antibody or fragment thereof, and introducing D399K, E356K, and E357K mutations in the first antibody or fragment thereof, numbered according to the Kabat EU numbering system;

ac) introducing K409D and K392D mutations in the second antibody or fragment thereof, and introducing a D399K mutation in the first antibody or fragment thereof, numbered according to the Kabat EU numbering system;

ad) introducing K409D and K392D mutations in the second antibody or fragment thereof, and introducing D399K and E356K mutations in the first antibody or fragment thereof, numbered according to the Kabat EU numbering system;

ae) introducing K409D and K392D mutations in the second antibody or fragment thereof, and introducing D399K and E357K mutations in the first antibody or fragment thereof, numbered according to the Kabat EU numbering system;

af) introducing K409D and K370D mutations in the second antibody or fragment thereof, and introducing D399K and E357K mutations in the first antibody or fragment thereof, numbered according to the Kabat EU numbering system;

a D399K mutation in the second antibody or fragment thereof, and introducing K409D and K360D mutations in the first antibody or fragment thereof, numbered according to the Kabat EU numbering system; or

ah) introducing K409D and K439D mutations in the second antibody or fragment thereof, and introducing D399K and E356K mutations in the first antibody or fragment thereof, numbered according to the Kabat EU numbering system.

375. The masked cytokine of any one of embodiments 352-365, wherein the amino acid sequence of the first antibody or fragment thereof and the amino acid sequence of the second antibody or fragment thereof are produced by:

a) introducing a K409E mutation in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing a D399K mutation in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

b) introducing a K409E mutation in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing a D399R mutation in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

c) introducing a K409D mutation in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing a D399K mutation in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

d) introducing a K409D mutation in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing a D399R mutation in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

e) introducing a K392E mutation in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing a D399R mutation in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

f) introducing a K392E mutation in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing a D399K mutation in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

g) introducing a K392D mutation in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing a D399R mutation in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

h) introducing a K392D mutation in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing a D399K mutation in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

K409D and K360D mutations in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing D399K and E356K mutations in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

j) introducing K409D and K370D mutations in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing D399K and E357K mutations in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

k) introducing K409D and K392D mutations in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing D399K, E356K, and E357K mutations in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

l) introducing K409D and K392D mutations in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing a D399K mutation in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

m) introducing K409D and K392D mutations in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing D399K and E356K mutations in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

n) introducing K409D and K392D mutations in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing D399K and E357K mutations in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

o) introducing K409D and K370D mutations in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing D399K and E357K mutations in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

p) introducing a D399K mutation in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing K409D and K360D mutations in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

q) introducing K409D and K439D mutations in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing D399K and E356K mutations in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

r) introducing a K409E mutation in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing a D399K mutation in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

s) introducing a K409E mutation in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing a D399R mutation in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

t) introducing a K409D mutation in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing a D399K mutation in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, rding to the Kabat EU numbering system;

a K409D mutation in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing a D399R mutation in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

v) introducing a K392E mutation in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing a D399R mutation in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

w) introducing a K392E mutation in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing a D399K mutation in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

x) introducing a K392D mutation in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing a D399R mutation in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

y) introducing a K392D mutation in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing a D399K mutation in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

z) introducing K409D and K360D mutations in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing D399K and E356K mutations in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

aa) introducing K409D and K370D mutations in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing D399K and E357K mutations in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

ab) introducing K409D and K392D mutations in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing D399K, E356K, and E357K mutations in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

ac) introducing K409D and K392D mutations in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing a D399K mutation in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

ad) introducing K409D and K392D mutations in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing D399K and E356K mutations in the amino acid sequence of SEQ ID NO: 154 or 169, numbered according to the Kabat EU numbering system;

ae) introducing K409D and K392D mutations in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing D399K and E357K mutations in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system;

af) introducing K409D and K370D mutations in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing D399K and E357K mutations in the amino acid sequence of SEQ ID NO: 154 or

ly, numbered according to the Kabat EU numbering system;

a D399K mutation in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing K409D and K360D mutations in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system; or

ah) introducing K409D and K439D mutations in the amino acid sequence of SEQ ID NO: 154 or 169, and introducing D399K and E356K mutations in the amino acid sequence of SEQ ID NO: 154 or 169, respectively, numbered according to the Kabat EU numbering system.

376. The masked cytokine of any one of embodiments 333-375, wherein the first linker comprises a first cleavable peptide; and/or wherein the second linker comprises a second cleavable peptide.

377. The masked cytokine of any one of embodiments 333-376, wherein the first linker comprises a first N-terminal spacer domain, and/or a first C-terminal spacer domain.

378. The masked cytokine of embodiment 377, wherein the first linker comprises:

a) the first N-terminal spacer domain, the first cleavable peptide, and the first C-terminal spacer domain;

b) the first N-terminal spacer domain and the first cleavable peptide;

c) the first N-terminal spacer domain and the first C-terminal spacer domain;

d) the first cleavable peptide and the first C-terminal spacer domain;

e) the first N-terminal spacer domain; or

f) the first C-terminal spacer domain.

379. The masked cytokine of any one of embodiments 333-378, wherein the second linker comprises a second N-terminal spacer domain, and/or a second C-terminal spacer domain.

380. The masked cytokine of embodiment 379, wherein the second linker comprises:

a) the second N-terminal spacer domain, the second cleavable peptide, and the second C-terminal spacer domain;

b) the second N-terminal spacer domain and the second cleavable peptide;

c) the second N-terminal spacer domain and the second C-terminal spacer domain;

d) the second cleavable peptide and the second C-terminal spacer domain;

e) the second N-terminal spacer domain; or

f) the second C-terminal spacer domain.

ısked cytokine of any one of embodiments 376-380, wherein the first cleavable peptide comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 96-153, 236-242, 264, 270-302, 306-317, 342-347, 356-415, 420-491, 494-501, 504-535, and 538-555; and/or wherein the second cleavable peptide comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 96-153, 236-242, 264, 270-302, 306-317, 342-347, 356-415, 420-491, 494-501, 504-535, and 538-555.

382. The masked cytokine of any one of embodiments 377-381, wherein the first N-terminal spacer domain comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 20-95, 235, 268, 269, 303-305, 323-338, 340, 341, 727, 794, and 799, and/or the first C-terminal spacer domain comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 20-95, 235, 268, 269, 303-305, 323-338, 340, 341, 727, 794, and 799.

383. The masked cytokine of any one of embodiments 376-380, wherein the first cleavable peptide comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 96-153, 264, 270-302, 306-317, 342-347, 356-415, 420-491, 494-501, 504-535, and 538-555, and an amino acid sequence selected from the group consisting of SEQ ID NOs: 236-242.

384. The masked cytokine of embodiment 383, wherein the amino acid sequence selected from the group consisting of SEQ ID NOs: 96-153, 264, 270-302, 306-317, 342-347, 356-415, 420-491, 494-501, 504-535, and 538-555 comprises an N-terminus and a C-terminus, and the amino acid sequence selected from the group consisting of SEQ ID NOs: 236-242 is linked to the N-terminus or the C-terminus of the amino acid sequence selected from the group consisting of SEQ ID NOs: 96-153, 264, 270-302, 306-317, 342-347, 356-415, 420-491, 494-501, 504-535, and 538-555.

385. The masked cytokine of any one of embodiments 379-384, wherein the second N-terminal spacer domain comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 20-95, 235, 268, 269, 303-305, 323-338, 340, 341, 727, 794, and 799, and/or the second C-terminal spacer domain comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 20-95, 235, 268, 269, 303-305, 323-338, 340, 341, 727, 794, and 799.

386. The masked cytokine of any one of embodiments 376-385, wherein the second cleavable peptide comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 96-153, 264, 270-302, 306-317, 342-347, 356-415, 420-491, 494-501, 504-535, and 538-555, and an amino acid sequence selected from the group consisting of SEQ ID NOs: 236-242.

ısked cytokine of embodiment 386, wherein the amino acid sequence selected from the group consisting of SEQ ID NOs: 96-153, 264, 270-302, 306-317, 342-347, 356-415, 420-491, 494-501, 504-535, and 538-555 comprises an N-terminus and a C-terminus, and the amino acid sequence selected from the group consisting of SEQ ID NOs: 236-242 is linked to the N-terminus or the C-terminus of the amino acid sequence selected from the group consisting of SEQ ID NOs: 96-153, 264, 270-302, 306-317, 342-347, 356-415, 420-491, 494-501, 504-535, and 538-555.

388. The masked cytokine of any one of embodiments 333-387, wherein the first linker comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 11-153, 235-242, 262-264, 268-320, 323-338, 340-354, 356-555, 668, 691, 724, 725, 727, 762-771, 794, and 797-812, and/or the second linker comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 11-153, 235-242, 262-264, 268-320, 323-338, 340-354, 356-555, 668, 691, 724, 725, 727, 762-771, 794, and 797-812.

389. The masked cytokine of any one of embodiments 334-388, wherein the third linker comprises a third cleavable peptide.

390. The masked cytokine of any one of embodiments 334-389, wherein the third linker comprises a third N-terminal spacer domain, and/or a third C-terminal spacer domain.

391. The masked cytokine of embodiment 390, wherein the third linker comprises:

a) the third N-terminal spacer domain, the third cleavable peptide, and the third C-terminal spacer domain;

b) the third N-terminal spacer domain and the third cleavable peptide;

c) the third N-terminal spacer domain and the third C-terminal spacer domain;

d) the third cleavable peptide and the third C-terminal spacer domain;

e) the third N-terminal spacer domain; or

f) the third C-terminal spacer domain.

392. The masked cytokine of any one of embodiments 389-391, wherein the third cleavable peptide comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 96-153, 236-242, 264, 270-302, 306-317, 342-347, 356-415, 420-491, 494-501, 504-535, and 538-555; and/or wherein the third cleavable peptide comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 96-153, 236-242, 264, 270-302, 306-317, 342-347, 356-415, 420-491, 494-501, 504-535, and 538-555.

ısked cytokine of any one of embodiments 390-392, wherein the third N-terminal spacer domain comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 20-95, 235, 268, 269, 303-305, 323-338, 340, 341, 727, 794, and 799, and/or the third C-terminal spacer domain comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 20-95, 235, 268, 269, 303-305, 323-338, 340, 341, 727, 794, and 799.

394. The masked cytokine of any one of embodiments 389-393, wherein the third cleavable peptide comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 96-153, 264, 270-302, 306-317, 342-347, 356-415, 420-491, 494-501, 504-535, and 538-555, and an amino acid sequence selected from the group consisting of SEQ ID NOs: 236-242.

395. The masked cytokine of embodiment 394, wherein the amino acid sequence selected from the group consisting of SEQ ID NOs: 96-153, 264, 270-302, 306-317, 342-347, 356-415, 420-491, 494-501, 504-535, and 538-555 comprises an N-terminus and a C-terminus, and the amino acid sequence selected from the group consisting of SEQ ID NOs: 236-242 is linked to the N-terminus or the C-terminus of the amino acid sequence selected from the group consisting of SEQ ID NOs: 96-153, 264, 270-302, 306-317, 342-347, 356-415, 420-491, 494-501, 504-535, and 538-555.

396. The masked cytokine of any one of embodiments 334-395, wherein the third linker comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 11-153, 235-242, 262-264, 268-320, 323-338, 340-354, 356-555, 668, 691, 724, 725, 727, 762-771, 794, and 797-812, and/or the third linker comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 11-153, 235-242, 262-264, 268-320, 323-338, 340-354, 356-555, 668, 691, 724, 725, 727, 762-771, 794, and 797-812.

397. The masked cytokine of any one of embodiments 368-396, wherein the fourth linker comprises a fourth N-terminal spacer domain, and/or a fourth C-terminal spacer domain.

398. The masked cytokine of embodiment 397, wherein the fourth N-terminal spacer domain comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 20-95, 235, 268, 269, 303-305, 323-338, 340, 341, 727, 794, and 799, and/or the fourth C-terminal spacer domain comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 20-95, 235, 268, 269, 303-305, 323-338, 340, 341, 727, 794, and 799.

ısked cytokine of any one of embodiments 376-398, wherein the first cleavable peptide, the second cleavable peptide, and/or the third cleavable peptide is a substrate for a protease that is co-localized in a region or a tissue expressing a cytokine receptor.

400. The masked cytokine of embodiment 399, wherein the cytokine receptor is an IL-2 cytokine receptor or an IL-15 cytokine receptor.

401. The masked cytokine of any one of embodiments 376-400, wherein the first cleavable peptide, the second cleavable peptide, and/or the third cleavable peptide is cleaved by one or more enzyme selected from the group consisting of: ABHD12, ADAM12, ABHD12B, ABHD13, ABHD17A, ADAM19, ADAM20, ADAM21, ADAM28, ADAM30, ADAM33, ADAM8, ABHD17A, ADAMDEC1, ADAMTS1, ADAMTS10, ADAMTS12, ADAMTS13, ADAMTS14, ADAMTS15, ADAMTS16, ADAMTS17, ADAMTS18, ADAMTS19, ADAMTS2, ADAMTS20, ADAMTS3, ADAMTS4, ABHD17B, ADAMTS5, ADAMTS6, ADAMTS7, ADAMTS8, ADAMTS9, ADAMTSL1, ADAMTSL2, ADAMTSL3, ABHD17C, ADAMTSL5, ASTL, BMP1, CELA1, CELA2A, CELA2B, CELA3A, CELA3B, ADAM10, ADAM15, ADAM17, ADAM9, ADAMTS4, CTSE, CTSF, ADAMTSL4, CMA1, CTRB1, CTRC, CTSO, CTRl, CTSA, CTSW, CTSB, CTSC, CTSD, ESP1, CTSG, CTSH, GZMA, GZMB, GZMH, CTSK, GZMM, CTSL, CTSS, CTSV, CTSZ, HTRA4, KLK10, KLK11, KLK13, KLK14, KLK2, KLK4, DPP4, KLK6, KLK7, KLKB1, ECE1, ECE2, ECEL1, MASP2, MEP1A, MEP1B, ELANE, FAP, GZMA, MMP11, GZMK, HGFAC, HPN, HTRA1, MMP11, MMP16, MMP17, MMP19, HTRA2, MMP20, MMP21, HTRA3, HTRA4, KEL, MMP23B, MMP24, MMP25, MMP26, MMP27, MMP28, KLK5, MMP3, MMP7, MMP8, MMP9, LGMN, LNPEP, MASP1, PAPPA, PAPPA2, PCSK1, NAPSA, PCSK5, PCSK6, MME, MMP1, MMP10, PLAT, PLAU, PLG, PRSS1, PRSS12, PRSS2, PRSS21, PRSS3, PRSS33, PRSS4, PRSS55, PRSS57, MMP12, PRSS8, PRSS9, PRTN3, MMP13, MMP14, ST14, TMPRSS10, TMPRSS11A, TMPRSS11D, TMPRSS11E, TMPRSS11F, TMPRSS12, TMPRSS13, MMP15, TMPRSS15, MMP2, TMPRSS2, TMPRSS3, TMPRSS4, TMPRSS5, TMPRSS6, TMPRSS7, TMPRSS9, NRDC, OVCH1, PAMR1, PCSK3, PHEX, TINAG, TPSAB1, TPSD1, and TPSG1.

402. The masked cytokine of any one of embodiments 332-401, wherein the first half-life extension domain and/or the second half-life extension domain is conjugated to an agent.

403. The masked cytokine of embodiment 402, wherein the agent is an inhibitor of tubulin polymerization, a DNA damaging agent, or a DNA synthesis inhibitor.

ısked cytokine of embodiment 403, wherein the agent is a maytansinoid, an auristatin, a pyrrolobenzodiazepine (PBD) dimer, a calicheamicin, a duocarmycin, a indolinobenzodiazepine dimer or exatecan derivative Dxd.

405. The masked cytokine of embodiment 402, wherein the agent is an immune stimulant.

406. The masked cytokine of embodiment 405, wherein the immune stimulant is a stimulator of interferon genes (STING) agonist or a toll-like receptor (TLR) agonist.

407. The masked cytokine of embodiment 406, wherein the STING agonist is a cyclic dinucleotide (CDN).

408. The masked cytokine of embodiment 407, wherein the CDN is selected from the group consisting of cGAMP, c-di-AMP, c-di-GMP, cAIMP, c-di-IMP, 4-(2-chloro-6-fluorobenzyl)-N-(furan-2-ylmethyl)-3-oxo-3,4-dihydro-2H-benzo[b][1,4]thiazine-6-carboxamide.

409. The masked cytokine of embodiment 406, wherein the TLR agonist is an agonist of a TLR selected from the group consisting of TLR1, TLR2, TLR3, TLR4, TLR5, TLR6, TLR7, TLR8, TLR9, and TLR10.

VIII. EXAMPLES

[0589] The invention will be more fully understood by reference to the following examples. They should not, however, be construed as limiting the scope of the invention. It is understood that the examples and embodiments described herein are for illustrative purposes only and that various modifications or changes in light thereof will be suggested to persons skilled in the art and are to be included within the spirit and purview of this application and scope of the appended claims.

[0590] Although some examples describe the engineering, production, and/or testing of "masked" versions of an IL-2 polypeptide construct or IL-15 polypeptide construct, some examples also employ parental "non-masked" versions of the IL-2 polypeptide construct or IL-15 polypeptide construct, such as for comparison, or other constructs that include one or more of the components described herein that are tested as controls for comparison. Accordingly, the description of, for instance, testing done on masked IL-2 polypeptide constructs does not necessarily mean that non-masked versions of the construct were

ering of Masked IL-2 Polypeptides and Masked IL-15 Polypeptides

[0591] Masked IL-2 polypeptide constructs and masked IL-15 polypeptide constructs are generated in accordance with the teachings herein. In the subsequent examples, some experiments involve use of the masked IL-2 and IL-15 polypeptide constructs in monomer form, and some experiments involve use of the masked IL-2 and IL-15 polypeptide constructs in dimer form, such as a dimer formed through disulfide bonds linking two copies of the same masked polypeptide construct (homodimer), or a heterodimer formed by two different polypeptides (*see, e.g.*, Tables 8-11).

[0592] Masked IL-2 polypeptide constructs are generated that include an IL-2 polypeptide or functional fragment thereof, a masking moiety, and a half-life extension domain, such as albumin, an antibody or fragment thereof (e.g., an Fc region, heavy chain, and/or light chain), an albumin-binding peptide, an IgG-binding peptide, or a polyamino acid sequence. Some IL-2 polypeptide constructs are also generated that include an IL-2 polypeptide or functional fragment thereof linked to a half-life extension domain without also including a masking moiety. Some of the constructs also include a linker that comprises a cleavable peptide and links the masking moiety to the IL-2 polypeptide or functional fragment thereof, thereby resulting in an activatable masked IL-2 polypeptide construct. Some of the constructs also include a linker that links the IL-2 polypeptide or functional fragment thereof to the half-life extension domain. Some of the constructs also include a linker that links the IL-2 polypeptide or functional fragment thereof to the masking moiety. The masked IL-2 polypeptide constructs that do not include a cleavable peptide in the linker that links the IL-2 polypeptide or functional fragment thereof to the masking moiety are also referred to as non-activatable masked IL-2 polypeptide constructs or non-activatable IL-2 polypeptide constructs because they do not include a cleavable peptide. The structure and composition of exemplary IL-2 polypeptide constructs are provided in Table 4.

Table 4

Construct #	Cytokine or functional fragment thereof (C)	Linker (L1)	Masking moiety (MM)	Linker (L2)	Half-life extension domain (H)	Structure (N- to C-terminal direction)	Amino Acid Sequence
2001	SEQ ID NO: 1	-	-	-	SEQ ID NO: 154	H-C	
2002	SEQ ID NO: 1	SEQ ID NO: 20	SEQ ID NO: 9	-	SEQ ID NO: 154	H-L1-MM-C	
2003	SEQ ID NO: 1	SEQ ID NO: 21	SEQ ID NO: 9	-	SEQ ID NO: 154	C-L1-MM-H	
2004	SEQ ID NO: 3	-	-	-	SEQ ID NO: 154	H-C	
2005	SEQ ID NO: 4	-	-	-	SEQ ID NO: 154	H-C	
2006	SEQ ID NO: 5	-	-	-	SEQ ID NO: 154	H-C	
2014	SEQ ID NO: 1	-	SEQ ID NO: 10	SEQ ID NO: 15	SEQ ID NO: 154	H-C-L2-MM	
2017	SEQ ID NO: 3	-	SEQ ID NO: 10	SEQ ID NO: 15	SEQ ID NO: 154	H-C-L2-MM	
2018	SEQ ID NO: 4	-	SEQ ID NO: 10	SEQ ID NO: 15	SEQ ID NO: 154	H-C-L2-MM	
2019	SEQ ID NO: 5	-	SEQ ID NO: 10	SEQ ID NO: 15	SEQ ID NO: 154	H-C-L2-MM	
2024	SEQ ID NO: 6	-	-	-	SEQ ID NO: 154	H-C	
2025	SEQ ID NO: 7	-	-	-	SEQ ID NO: 154	H-C	
2026	SEQ ID NO: 8	-	-	-	SEQ ID NO: 154	H-C	
2027	SEQ ID NO: 1	SEQ ID NO: 20	SEQ ID NO: 9	SEQ ID NO: 30	SEQ ID NO: 154	H-L1-MM-L2-C	
2028	SEQ ID NO: 1	SEQ ID NO: 20	SEQ ID NO: 9	SEQ ID NO: 31	SEQ ID NO: 154	H-L1-MM-L2-C	
2029	SEQ ID NO: 1	SEQ ID NO: 20	SEQ ID NO: 9	SEQ ID NO: 32	SEQ ID NO: 154	H-L1-MM-L2-C	
2030	SEQ ID NO: 1	SEQ ID NO: 20	SEQ ID NO: 9	SEQ ID NO: 33	SEQ ID NO: 154	H-L1-MM-L2-C	
2031	SEQ ID NO: 2	SEQ ID NO: 20	SEQ ID NO: 9	SEQ ID NO: 29	SEQ ID NO: 154	H-L1-MM-L2-C	
2032	SEQ ID NO: 2	SEQ ID NO: 20	SEQ ID NO: 9	SEQ ID NO: 30	SEQ ID NO: 154	H-L1-MM-L2-C	
2033	SEQ ID NO: 2	SEQ ID NO: 20	SEQ ID NO: 9	SEQ ID NO: 31	SEQ ID NO: 154	H-L1-MM-L2-C	
2034	SEQ ID NO: 2	SEQ ID NO: 20	SEQ ID NO: 9	SEQ ID NO: 32	SEQ ID NO: 154	H-L1-MM-L2-C	
2035	SEQ ID NO: 2	SEQ ID NO: 20	SEQ ID NO: 9	SEQ ID NO: 33	SEQ ID NO: 154	H-L1-MM-L2-C	
2036	SEQ ID NO: 1	SEQ ID NO: 26	SEQ ID NO: 9	-	SEQ ID NO: 154	C-L1-MM-H	
2037	SEQ ID NO: 1	SEQ ID NO: 27	SEQ ID NO: 9	-	SEQ ID NO: 154	C-L1-MM-H	
2038	SEQ ID NO: 2	SEQ ID NO: 20	SEQ ID NO: 9	-	SEQ ID NO: 154	C-L1-MM-H	
2039	SEQ ID NO: 2	SEQ ID NO: 20	SEQ ID NO: 9	-	SEQ ID NO: 154	C-L1-MM-H	
2040	SEQ ID NO: 2	SEQ ID NO: 20	SEQ ID NO: 9	-	SEQ ID NO: 154	C-L1-MM-H	
2041	SEQ ID NO: 1	-	SEQ ID NO: 10	SEQ ID NO: 16	SEQ ID NO: 154	H-C-L2-MM	
2042	SEQ ID NO: 1	-	SEQ ID NO: 10	SEQ ID NO: 17	SEQ ID NO: 154	H-C-L2-MM	
2043	SEQ ID NO: 1	-	SEQ ID NO: 10	SEQ ID NO: 18	SEQ ID NO: 154	H-C-L2-MM	
2044	SEQ ID NO: 1	-	SEQ ID NO: 10	SEQ ID NO: 19	SEQ ID NO: 154	H-C-L2-MM	

Construct #	Cytokine or functional fragment thereof (C)	Linker (L1)	Masking moiety (MM)	Linker (L2)	Half-life extension domain (H)	Structure (N- to C-terminal direction)	Amino Acid Sequence
2045	SEQ ID NO: 3	-	SEQ ID NO: 10	SEQ ID NO: 16	SEQ ID NO: 154	H-C-L2-MM	
2046	SEQ ID NO: 3	-	SEQ ID NO: 10	SEQ ID NO: 17	SEQ ID NO: 154	H-C-L2-MM	
2047	SEQ ID NO: 3	-	SEQ ID NO: 10	SEQ ID NO: 18	SEQ ID NO: 154	H-C-L2-MM	
2048	SEQ ID NO: 3	-	SEQ ID NO: 10	SEQ ID NO: 19	SEQ ID NO: 154	H-C-L2-MM	
2049	SEQ ID NO: 4	-	SEQ ID NO: 10	SEQ ID NO: 16	SEQ ID NO: 154	H-C-L2-MM	
2050	SEQ ID NO: 4	-	SEQ ID NO: 10	SEQ ID NO: 17	SEQ ID NO: 154	H-C-L2-MM	
2051	SEQ ID NO: 4	-	SEQ ID NO: 10	SEQ ID NO: 18	SEQ ID NO: 154	H-C-L2-MM	
2052	SEQ ID NO: 4	-	SEQ ID NO: 10	SEQ ID NO: 19	SEQ ID NO: 154	H-C-L2-MM	
2053	SEQ ID NO: 5	-	SEQ ID NO: 10	SEQ ID NO: 16	SEQ ID NO: 154	H-C-L2-MM	
2054	SEQ ID NO: 5	-	SEQ ID NO: 10	SEQ ID NO: 17	SEQ ID NO: 154	H-C-L2-MM	
2055	SEQ ID NO: 5	-	SEQ ID NO: 10	SEQ ID NO: 18	SEQ ID NO: 154	H-C-L2-MM	
2056	SEQ ID NO: 5	-	SEQ ID NO: 10	SEQ ID NO: 19	SEQ ID NO: 154	H-C-L2-MM	
2057	SEQ ID NO: 6	-	SEQ ID NO: 10	SEQ ID NO: 15	SEQ ID NO: 154	H-C-L2-MM	
2058	SEQ ID NO: 6	-	SEQ ID NO: 10	SEQ ID NO: 16	SEQ ID NO: 154	H-C-L2-MM	
2059	SEQ ID NO: 6	-	SEQ ID NO: 10	SEQ ID NO: 17	SEQ ID NO: 154	H-C-L2-MM	
2060	SEQ ID NO: 6	-	SEQ ID NO: 10	SEQ ID NO: 18	SEQ ID NO: 154	H-C-L2-MM	
2061	SEQ ID NO: 6	-	SEQ ID NO: 10	SEQ ID NO: 19	SEQ ID NO: 154	H-C-L2-MM	
2062	SEQ ID NO: 7	-	SEQ ID NO: 10	SEQ ID NO: 15	SEQ ID NO: 154	H-C-L2-MM	
2063	SEQ ID NO: 7	-	SEQ ID NO: 10	SEQ ID NO: 16	SEQ ID NO: 154	H-C-L2-MM	
2064	SEQ ID NO: 7	-	SEQ ID NO: 10	SEQ ID NO: 17	SEQ ID NO: 154	H-C-L2-MM	
2065	SEQ ID NO: 7	-	SEQ ID NO: 10	SEQ ID NO: 18	SEQ ID NO: 154	H-C-L2-MM	
2066	SEQ ID NO: 7	-	SEQ ID NO: 10	SEQ ID NO: 19	SEQ ID NO: 154	H-C-L2-MM	
2067	SEQ ID NO: 8	-	SEQ ID NO: 10	SEQ ID NO: 15	SEQ ID NO: 154	H-C-L2-MM	
2068	SEQ ID NO: 8	-	SEQ ID NO: 10	SEQ ID NO: 16	SEQ ID NO: 154	H-C-L2-MM	
2069	SEQ ID NO: 8	-	SEQ ID NO: 10	SEQ ID NO: 17	SEQ ID NO: 154	H-C-L2-MM	
2070	SEQ ID NO: 8	-	SEQ ID NO: 10	SEQ ID NO: 18	SEQ ID NO: 154	H-C-L2-MM	
2071	SEQ ID NO: 8	-	SEQ ID NO: 10	SEQ ID NO: 19	SEQ ID NO: 154	H-C-L2-MM	
2109	SEQ ID NO: 2	-	-	-	SEQ ID NO: 154	H-C	
AK032	SEQ ID NO: 1	-	-	-	SEQ ID NO: 154	H-C	SEQ ID NO: 556
AK033	SEQ ID NO: 1	SEQ ID NO: 20	SEQ ID NO: 9	SEQ ID NO: 29	SEQ ID NO: 154	H-L1-MM-L2-C	SEQ ID NO: 557
AK034	SEQ ID NO: 1	SEQ ID NO: 21	SEQ ID NO: 9	-	SEQ ID NO: 154	C-L1-MM-H	SEQ ID NO: 558
AK035	SEQ ID NO: 3	-	-	-	SEQ ID NO: 154	H-C	SEQ ID NO: 559
AK036	SEQ ID NO: 4	-	-	-	SEQ ID NO: 154	H-C	SEQ ID NO: 560
AK037	SEQ ID NO: 5	-	-	-	SEQ ID NO: 154	H-C	SEQ ID NO: 561

Construct #	Cytokine or functional fragment thereof (C)	Linker (L1)	Masking moiety (MM)	Linker (L2)	Half-life extension domain (H)	Structure (N- to C-terminal direction)	Amino Acid Sequence
AK040	SEQ ID NO: 1	SEQ ID NO: 15	SEQ ID NO: 10	-	SEQ ID NO: 154	H-C-L1-MM	SEQ ID NO: 566
AK042	SEQ ID NO: 6	-	-	-	SEQ ID NO: 154	H-C	SEQ ID NO: 568
AK043	SEQ ID NO: 7	-	-	-	SEQ ID NO: 154	H-C	SEQ ID NO: 569
AK044	SEQ ID NO: 8	-	-	-	SEQ ID NO: 154	H-C	SEQ ID NO: 570
AK045	SEQ ID NO: 1	SEQ ID NO: 20	SEQ ID NO: 9	SEQ ID NO: 30	SEQ ID NO: 154	H-L1-MM-L2-C	SEQ ID NO: 571
AK046	SEQ ID NO: 1	SEQ ID NO: 20	SEQ ID NO: 9	SEQ ID NO: 31	SEQ ID NO: 154	H-L1-MM-L2-C	SEQ ID NO: 572
AK047	SEQ ID NO: 1	SEQ ID NO: 20	SEQ ID NO: 9	SEQ ID NO: 32	SEQ ID NO: 154	H-L1-MM-L2-C	SEQ ID NO: 573
AK048	SEQ ID NO: 1	SEQ ID NO: 20	SEQ ID NO: 9	SEQ ID NO: 33	SEQ ID NO: 154	H-L1-MM-L2-C	SEQ ID NO: 574
AK049	SEQ ID NO: 2	SEQ ID NO: 20	SEQ ID NO: 9	SEQ ID NO: 29	SEQ ID NO: 154	H-L1-MM-L2-C	SEQ ID NO: 575
AK050	SEQ ID NO: 2	SEQ ID NO: 20	SEQ ID NO: 9	SEQ ID NO: 30	SEQ ID NO: 154	H-L1-MM-L2-C	SEQ ID NO: 576
AK051	SEQ ID NO: 2	SEQ ID NO: 20	SEQ ID NO: 9	SEQ ID NO: 31	SEQ ID NO: 154	H-L1-MM-L2-C	SEQ ID NO: 577
AK052	SEQ ID NO: 2	SEQ ID NO: 20	SEQ ID NO: 9	SEQ ID NO: 32	SEQ ID NO: 154	H-L1-MM-L2-C	SEQ ID NO: 578
AK053	SEQ ID NO: 2	SEQ ID NO: 20	SEQ ID NO: 9	SEQ ID NO: 33	SEQ ID NO: 154	H-L1-MM-L2-C	SEQ ID NO: 579
AK054	SEQ ID NO: 1	SEQ ID NO: 26	SEQ ID NO: 9	-	SEQ ID NO: 154	C-L1-MM-H	SEQ ID NO: 580
AK055	SEQ ID NO: 1	SEQ ID NO: 27	SEQ ID NO: 9	-	SEQ ID NO: 154	C-L1-MM-H	SEQ ID NO: 581
AK056	SEQ ID NO: 2	SEQ ID NO: 21	SEQ ID NO: 9	-	SEQ ID NO: 154	C-L1-MM-H	SEQ ID NO: 582
AK057	SEQ ID NO: 2	SEQ ID NO: 26	SEQ ID NO: 9	-	SEQ ID NO: 154	C-L1-MM-H	SEQ ID NO: 583
AK058	SEQ ID NO: 2	SEQ ID NO: 27	SEQ ID NO: 9	-	SEQ ID NO: 154	C-L1-MM-H	SEQ ID NO: 584
AK059	SEQ ID NO: 1	SEQ ID NO: 16	SEQ ID NO: 10	-	SEQ ID NO: 154	H-C-L1-MM	SEQ ID NO: 585
AK060	SEQ ID NO: 1	SEQ ID NO: 17	SEQ ID NO: 10	-	SEQ ID NO: 154	H-C-L1-MM	SEQ ID NO: 586
AK061	SEQ ID NO: 1	SEQ ID NO: 18	SEQ ID NO: 10	-	SEQ ID NO: 154	H-C-L1-MM	SEQ ID NO: 587
AK062	SEQ ID NO: 1	SEQ ID NO: 19	SEQ ID NO: 10	-	SEQ ID NO: 154	H-C-L1-MM	SEQ ID NO: 588
AK063	SEQ ID NO: 3	SEQ ID NO: 16	SEQ ID NO: 10	-	SEQ ID NO: 154	H-C-L1-MM	SEQ ID NO: 589
AK064	SEQ ID NO: 3	SEQ ID NO: 17	SEQ ID NO: 10	-	SEQ ID NO: 154	H-C-L1-MM	SEQ ID NO: 590
AK065	SEQ ID NO: 3	SEQ ID NO: 18	SEQ ID NO: 10	-	SEQ ID NO: 154	H-C-L1-MM	SEQ ID NO: 591
AK066	SEQ ID NO: 3	SEQ ID NO: 19	SEQ ID NO: 10	-	SEQ ID NO: 154	H-C-L1-MM	SEQ ID NO: 592
AK067	SEQ ID NO: 6	SEQ ID NO: 15	SEQ ID NO: 10	-	SEQ ID NO: 154	H-C-L1-MM	SEQ ID NO: 593
AK068	SEQ ID NO: 6	SEQ ID NO: 16	SEQ ID NO: 10	-	SEQ ID NO: 154	H-C-L1-MM	SEQ ID NO: 594
AK069	SEQ ID NO: 6	SEQ ID NO: 17	SEQ ID NO: 10	-	SEQ ID NO: 154	H-C-L1-MM	SEQ ID NO: 595
AK070	SEQ ID NO: 6	SEQ ID NO: 18	SEQ ID NO: 10	-	SEQ ID NO: 154	H-C-L1-MM	SEQ ID NO: 596
AK071	SEQ ID NO: 6	SEQ ID NO: 19	SEQ ID NO: 10	-	SEQ ID NO: 154	H-C-L1-MM	SEQ ID NO: 597
AK112	SEQ ID NO: 1	SEQ ID NO: 15	SEQ ID NO: 261	-	SEQ ID NO: 154	H-C-L1-MM	SEQ ID NO: 602
AK080	SEQ ID NO: 2	-	-	-	SEQ ID NO: 154	H-C	SEQ ID NO: 607
AK082	-	SEQ ID NO: 28	SEQ ID NO: 10	-	SEQ ID NO: 155	H-L1-MM	SEQ ID NO: 609

Construct #	Cytokine or functional fragment thereof (C)	Linker (L1)	Masking moiety (MM)	Linker (L2)	Half-life extension domain (H)	Structure (N- to C-terminal direction)	Amino Acid Sequence
AK083	SEQ ID NO: 1	SEQ ID NO: 15	SEQ ID NO: 226	-	SEQ ID NO: 154	H-C-L1-MM	SEQ ID NO: 610
AK084	SEQ ID NO: 1	SEQ ID NO: 16	SEQ ID NO: 226	-	SEQ ID NO: 154	H-C-L1-MM	SEQ ID NO: 611
AK085	SEQ ID NO: 1	SEQ ID NO: 17	SEQ ID NO: 226	-	SEQ ID NO: 154	H-C-L1-MM	SEQ ID NO: 612
AK086	SEQ ID NO: 1	SEQ ID NO: 18	SEQ ID NO: 226	-	SEQ ID NO: 154	H-C-L1-MM	SEQ ID NO: 613
AK087	SEQ ID NO: 1	SEQ ID NO: 19	SEQ ID NO: 226	-	SEQ ID NO: 154	H-C-L1-MM	SEQ ID NO: 614
AK096	SEQ ID NO: 1	SEQ ID NO: 762	-	-	SEQ ID NO: 154	H-C-L1	SEQ ID NO: 627
AK097	SEQ ID NO: 1	SEQ ID NO: 763	-	-	SEQ ID NO: 154	H-C-L1	SEQ ID NO: 628
AK098	SEQ ID NO: 1	SEQ ID NO: 764	-	-	SEQ ID NO: 154	H-C-L1	SEQ ID NO: 629
AK099	SEQ ID NO: 1	SEQ ID NO: 765	-	-	SEQ ID NO: 154	H-C-L1	SEQ ID NO: 630
AK100	SEQ ID NO: 1	SEQ ID NO: 766	-	-	SEQ ID NO: 154	H-C-L1	SEQ ID NO: 631
AK101	SEQ ID NO: 1	SEQ ID NO: 767	-	-	SEQ ID NO: 154	H-C-L1	SEQ ID NO: 632
AK102	SEQ ID NO: 1	SEQ ID NO: 768	-	-	SEQ ID NO: 154	H-C-L1	SEQ ID NO: 633
AK103	SEQ ID NO: 1	SEQ ID NO: 769	-	-	SEQ ID NO: 154	H-C-L1	SEQ ID NO: 634
AK104	SEQ ID NO: 1	SEQ ID NO: 770	-	-	SEQ ID NO: 154	H-C-L1	SEQ ID NO: 635
AK105	SEQ ID NO: 1	SEQ ID NO: 771	-	-	SEQ ID NO: 154	H-C-L1	SEQ ID NO: 636
AK106	-	SEQ ID NO: 28	SEQ ID NO: 261	-	SEQ ID NO: 154	H-L1-MM	SEQ ID NO: 637
AK112	SEQ ID NO: 1	SEQ ID NO: 15	SEQ ID NO: 261	-	SEQ ID NO: 154	H-C-L1-MM	SEQ ID NO: 602
AK113	SEQ ID NO: 3	SEQ ID NO: 15	SEQ ID NO: 261	-	SEQ ID NO: 154	H-C-L1-MM	SEQ ID NO: 642
AK114	SEQ ID NO: 6	SEQ ID NO: 15	SEQ ID NO: 261	-	SEQ ID NO: 154	H-C-L1-MM	SEQ ID NO: 643
AK115	-	SEQ ID NO: 28	SEQ ID NO: 10	-	SEQ ID NO: 155	H-L1-MM	SEQ ID NO: 644
AK116	SEQ ID NO: 775	-	-	-	SEQ ID NO: 154	H-C	SEQ ID NO: 645
AK117	SEQ ID NO: 776	-	-	-	SEQ ID NO: 154	H-C	SEQ ID NO: 646
AK118	SEQ ID NO: 777	-	-	-	SEQ ID NO: 154	H-C	SEQ ID NO: 647
AK119	SEQ ID NO: 778	-	-	-	SEQ ID NO: 154	H-C	SEQ ID NO: 648
AK120	SEQ ID NO: 779	-	-	-	SEQ ID NO: 154	H-C	SEQ ID NO: 649
AK121	SEQ ID NO: 780	-	-	-	SEQ ID NO: 154	H-C	SEQ ID NO: 650
AK122	SEQ ID NO: 781	-	-	-	SEQ ID NO: 154	H-C	SEQ ID NO: 651
AK123	SEQ ID NO: 782	-	-	-	SEQ ID NO: 154	H-C	SEQ ID NO: 652
AK124	SEQ ID NO: 783	-	-	-	SEQ ID NO: 154	H-C	SEQ ID NO: 653
AK125	SEQ ID NO: 784	-	-	-	SEQ ID NO: 154	H-C	SEQ ID NO: 654
AK126	SEQ ID NO: 785	-	-	-	SEQ ID NO: 154	H-C	SEQ ID NO: 655
AK127	SEQ ID NO: 786	-	-	-	SEQ ID NO: 154	H-C	SEQ ID NO: 656
AK128	SEQ ID NO: 787	-	-	-	SEQ ID NO: 154	H-C	SEQ ID NO: 657
AK129	SEQ ID NO: 788	-	-	-	SEQ ID NO: 154	H-C	SEQ ID NO: 658

Construct #	Cytokine or functional fragment thereof (C)	Linker (L1)	Masking moiety (MM)	Linker (L2)	Half-life extension domain (H)	Structure (N- to C-terminal direction)	Amino Acid Sequence
AK130	SEQ ID NO: 789	-	-	-	SEQ ID NO: 154	H-C	SEQ ID NO: 659
AK131	SEQ ID NO: 790	-	-	-	SEQ ID NO: 154	H-C	SEQ ID NO: 660
AK132	SEQ ID NO: 791	-	-	-	SEQ ID NO: 154	H-C	SEQ ID NO: 661
AK133	SEQ ID NO: 792	-	-	-	SEQ ID NO: 154	H-C	SEQ ID NO: 662

[0593] Masked IL-15 polypeptide constructs are generated that include an IL-15 polypeptide or functional fragment thereof, a masking moiety, and a half-life extension domain, such as albumin, an antibody or fragment thereof (e.g., an Fc region, heavy chain, and/or light chain), an albumin-binding peptide, an IgG-binding peptide, or a polyamino acid sequence. Some IL-15 polypeptide constructs are also generated that include an IL-15 polypeptide or functional fragment thereof linked to a half-life extension domain without also including a masking moiety. Some of the constructs also include a linker that comprises a cleavable peptide and links the masking moiety to the IL-15 polypeptide or functional fragment thereof, thereby resulting in an activatable masked IL-15 polypeptide construct. Some of the constructs also include a linker that links the IL-15 polypeptide or functional fragment thereof to the half-life extension domain. Some of the constructs also include a linker that links the IL-15 polypeptide or functional fragment thereof to the masking moiety. The masked IL-15 polypeptide constructs that do not include a cleavable peptide in the linker that links the IL-15 polypeptide or functional fragment thereof to the masking moiety are also referred to as non-activatable masked IL-15 polypeptide constructs or non-activatable IL-15 polypeptide constructs because they do not include a cleavable peptide. Some IL-15 polypeptide constructs are also generated that include a masking moiety comprising the amino acid sequence of SEQ ID NO: 261. The structure and composition of exemplary IL-15 polypeptide constructs are provided in Table 5.

Table 5

Construct #	Cytokine or functional fragment thereof (C)	Linker (L1)	Masking moiety (MM)	Linker (L2)	Half-life extension domain (H)	Structure (N- to C-terminal direction)
3000	SEQ ID NO: 167	SEQ ID NO: 20	SEQ ID NO: 10	SEQ ID NO: 15	SEQ ID NO: 154	H-L1-MM-L2-C
3001	SEQ ID NO: 167	SEQ ID NO: 20	SEQ ID NO: 161	SEQ ID NO: 16	SEQ ID NO: 154	H-L1-MM-L2-C
3002	SEQ ID NO: 167	SEQ ID NO: 20	SEQ ID NO: 162	SEQ ID NO: 17	SEQ ID NO: 154	H-L1-MM-L2-C
3003	SEQ ID NO: 167	SEQ ID NO: 20	SEQ ID NO: 163	SEQ ID NO: 18	SEQ ID NO: 154	H-L1-MM-L2-C
3004	SEQ ID NO: 167	SEQ ID NO: 20	SEQ ID NO: 164	SEQ ID NO: 19	SEQ ID NO: 154	H-L1-MM-L2-C
3005	SEQ ID NO: 167	SEQ ID NO: 20	SEQ ID NO: 165	SEQ ID NO: 15	SEQ ID NO: 154	H-L1-MM-L2-C
3006	SEQ ID NO: 167	SEQ ID NO: 20	SEQ ID NO: 219	SEQ ID NO: 16	SEQ ID NO: 154	H-L1-MM-L2-C
3007	SEQ ID NO: 167	SEQ ID NO: 20	SEQ ID NO: 220	SEQ ID NO: 17	SEQ ID NO: 154	H-L1-MM-L2-C
3008	SEQ ID NO: 167	SEQ ID NO: 20	SEQ ID NO: 221	SEQ ID NO: 18	SEQ ID NO: 154	H-L1-MM-L2-C
3009	SEQ ID NO: 167	SEQ ID NO: 20	SEQ ID NO: 222	SEQ ID NO: 19	SEQ ID NO: 154	H-L1-MM-L2-C
3010	SEQ ID NO: 167	SEQ ID NO: 20	SEQ ID NO: 223	SEQ ID NO: 15	SEQ ID NO: 154	C-L2-MM-L1-H
3011	SEQ ID NO: 167	SEQ ID NO: 20	SEQ ID NO: 224	SEQ ID NO: 16	SEQ ID NO: 154	C-L2-MM-L1-H
3012	SEQ ID NO: 167	SEQ ID NO: 20	SEQ ID NO: 225	SEQ ID NO: 17	SEQ ID NO: 154	C-L2-MM-L1-H
3013	SEQ ID NO: 167	SEQ ID NO: 20	SEQ ID NO: 226	SEQ ID NO: 18	SEQ ID NO: 154	C-L2-MM-L1-H
3014	SEQ ID NO: 167	SEQ ID NO: 20	SEQ ID NO: 227	SEQ ID NO: 19	SEQ ID NO: 154	C-L2-MM-L1-H
3015	SEQ ID NO: 167	SEQ ID NO: 20	SEQ ID NO: 228	SEQ ID NO: 15	SEQ ID NO: 154	C-L2-MM-L1-H
3016	SEQ ID NO: 167	SEQ ID NO: 20	SEQ ID NO: 229	SEQ ID NO: 16	SEQ ID NO: 154	C-L2-MM-L1-H
3017	SEQ ID NO: 167	SEQ ID NO: 20	SEQ ID NO: 232	SEQ ID NO: 17	SEQ ID NO: 154	C-L2-MM-L1-H
3018	SEQ ID NO: 167	SEQ ID NO: 20	SEQ ID NO: 233	SEQ ID NO: 18	SEQ ID NO: 154	C-L2-MM-L1-H
3019	SEQ ID NO: 167	SEQ ID NO: 20	SEQ ID NO: 234	SEQ ID NO: 19	SEQ ID NO: 154	C-L2-MM-L1-H

[0594] Also generated are masked IL-2 polypeptide constructs that include an IL-2 polypeptide or functional fragment thereof, a first masking moiety, a second masking moiety, and a half-life extension domain, such as albumin, an antibody or fragment thereof (e.g., an Fc region, heavy chain, and/or light chain), an albumin-binding peptide, an IgG-binding peptide, or a polyamino acid sequence. Some of the constructs also include a linker that links the first masking moiety to the IL-2 polypeptide or functional fragment thereof. Some of the constructs also include a linker that links the second masking moiety to the IL-2 polypeptide or functional fragment thereof. Some of the constructs include a cleavable peptide in the linker linking the first masking moiety to the IL-2 polypeptide or functional fragment thereof and/or the linker linking the second masking moiety to the IL-2 polypeptide or functional fragment thereof, thereby resulting in an activatable masked IL-2 polypeptide construct. Some of the constructs also include a linker linking the second masking moiety to the half-life extension domain. The masked IL-2 polypeptide constructs that do not include a cleavable peptide in either of the linkers that link the IL-2 polypeptide or functional fragment thereof to the first masking moiety or the second masking moiety are also referred to as non-activatable masked IL-2 polypeptide constructs or non-activatable IL-2 polypeptide constructs because they do not include a cleavable peptide. The structure and composition of exemplary IL-2 polypeptide constructs are provided in Table 6.

Table 6

Construct #	Masking moiety (MM1)	Linker (L1)	Cytokine or functional fragment thereof (C)	Linker (L2)	Masking moiety (MM2)	Linker (L3)	Half-life extension domain (H)	Structure (N- to C- terminal direction)	Amino Acid Sequence
2015	SEQ ID NO: 9	SEQ ID NO: 20	SEQ ID NO: 1	SEQ ID NO: 29	SEQ ID NO: 10	SEQ ID NO: 15	SEQ ID NO: 154	H-L1-MM1-L2-C-L3-MM2	
2072	SEQ ID NO: 9	SEQ ID NO: 20	SEQ ID NO: 1	SEQ ID NO: 29	SEQ ID NO: 10	SEQ ID NO: 16	SEQ ID NO: 154	H-L1-MM1-L2-C-L3-MM2	
2073	SEQ ID NO: 9	SEQ ID NO: 20	SEQ ID NO: 1	SEQ ID NO: 29	SEQ ID NO: 10	SEQ ID NO: 17	SEQ ID NO: 154	H-L1-MM1-L2-C-L3-MM2	
2074	SEQ ID NO: 9	SEQ ID NO: 20	SEQ ID NO: 1	SEQ ID NO: 29	SEQ ID NO: 10	SEQ ID NO: 18	SEQ ID NO: 154	H-L1-MM1-L2-C-L3-MM2	
2075	SEQ ID NO: 9	SEQ ID NO: 20	SEQ ID NO: 1	SEQ ID NO: 29	SEQ ID NO: 10	SEQ ID NO: 19	SEQ ID NO: 154	H-L1-MM1-L2-C-L3-MM2	
2076	SEQ ID NO: 9	SEQ ID NO: 20	SEQ ID NO: 2	SEQ ID NO: 29	SEQ ID NO: 10	SEQ ID NO: 16	SEQ ID NO: 154	H-L1-MM1-L2-C-L3-MM2	
2077	SEQ ID NO: 9	SEQ ID NO: 20	SEQ ID NO: 2	SEQ ID NO: 29	SEQ ID NO: 10	SEQ ID NO: 17	SEQ ID NO: 154	H-L1-MM1-L2-C-L3-MM2	
2078	SEQ ID NO: 9	SEQ ID NO: 20	SEQ ID NO: 2	SEQ ID NO: 29	SEQ ID NO: 10	SEQ ID NO: 18	SEQ ID NO: 154	H-L1-MM1-L2-C-L3-MM2	
2079	SEQ ID NO: 9	SEQ ID NO: 20	SEQ ID NO: 2	SEQ ID NO: 29	SEQ ID NO: 10	SEQ ID NO: 19	SEQ ID NO: 154	H-L1-MM1-L2-C-L3-MM2	
AK041	SEQ ID NO: 9	SEQ ID NO: 20	SEQ ID NO: 1	SEQ ID NO: 29	SEQ ID NO: 10	SEQ ID NO: 15	SEQ ID NO: 154	H-L1-MM1-L2-C-L3-MM2	SEQ ID NO: 567
AK072	SEQ ID NO: 9	SEQ ID NO: 20	SEQ ID NO: 1	SEQ ID NO: 29	SEQ ID NO: 10	SEQ ID NO: 16	SEQ ID NO: 154	H-L1-MM1-L2-C-L3-MM2	SEQ ID NO: 598
AK073	SEQ ID NO: 9	SEQ ID NO: 20	SEQ ID NO: 1	SEQ ID NO: 29	SEQ ID NO: 10	SEQ ID NO: 17	SEQ ID NO: 154	H-L1-MM1-L2-C-L3-MM2	SEQ ID NO: 599
AK074	SEQ ID NO: 9	SEQ ID NO: 20	SEQ ID NO: 1	SEQ ID NO: 29	SEQ ID NO: 10	SEQ ID NO: 18	SEQ ID NO: 154	H-L1-MM1-L2-C-L3-MM2	SEQ ID NO: 600
AK075	SEQ ID NO: 9	SEQ ID NO: 20	SEQ ID NO: 1	SEQ ID NO: 29	SEQ ID NO: 10	SEQ ID NO: 19	SEQ ID NO: 154	H-L1-MM1-L2-C-L3-MM2	SEQ ID NO: 601

[0595] Also generated are masked IL-15 polypeptide constructs that include an IL-15 polypeptide or functional fragment thereof, a first masking moiety, a second masking moiety, and a half-life extension domain, such as albumin, an antibody or fragment thereof (e.g., an Fc region, heavy chain, and/or light chain), an albumin-binding peptide, an IgG-binding peptide, or a polyamino acid sequence. Some of the constructs also include a linker that links the first masking moiety to the IL-15 polypeptide or functional fragment thereof. Some of the constructs also include a linker that links the second masking moiety to the IL-15 polypeptide or functional fragment thereof. Some of the constructs include a cleavable peptide in the linker linking the first masking moiety to the IL-15 polypeptide or functional fragment thereof and/or the linker linking the second masking moiety to the IL-15 polypeptide or functional fragment thereof, thereby resulting in an activatable masked IL-15 polypeptide construct. Some of the constructs also include a linker linking the second masking moiety to the half-life extension domain. Some of the constructs also include a second half-life extension domain that associates with the first half-life extension domain. The masked IL-15 polypeptide constructs that do not include a cleavable peptide in either of the linkers that link the IL-15 polypeptide or functional fragment thereof to the first masking moiety or the second masking moiety are also referred to as non-activatable masked IL-15 polypeptide constructs or non-activatable IL-2 polypeptide constructs because they do not include a cleavable peptide. The structure and composition of exemplary IL-15 polypeptide constructs are provided in Table 7.

Table 7

Construct #	Masking moiety (MM1)	Linker (L1)	Cytokine or functional fragment thereof (C)	Linker (L2)	Masking moiety (MM2)	Linker (L3)	Half-life extension domain (H)	Structure (N- to C- terminal direction)	Amino Acid Sequence
3020	SEQ ID NO: 232	SEQ ID NO: 20	SEQ ID NO: 167	SEQ ID NO: 29	SEQ ID NO: 10	SEQ ID NO: 15	SEQ ID NO: 154	H-L1-MM1-L2-C-L3-MM2	
3021	SEQ ID NO: 232	SEQ ID NO: 20	SEQ ID NO: 167	SEQ ID NO: 29	SEQ ID NO: 161	SEQ ID NO: 16	SEQ ID NO: 154	H-L1-MM1-L2-C-L3-MM2	
3022	SEQ ID NO: 232	SEQ ID NO: 20	SEQ ID NO: 167	SEQ ID NO: 29	SEQ ID NO: 162	SEQ ID NO: 17	SEQ ID NO: 154	H-L1-MM1-L2-C-L3-MM2	
3023	SEQ ID NO: 232	SEQ ID NO: 20	SEQ ID NO: 167	SEQ ID NO: 29	SEQ ID NO: 163	SEQ ID NO: 18	SEQ ID NO: 154	H-L1-MM1-L2-C-L3-MM2	
3024	SEQ ID NO: 233	SEQ ID NO: 20	SEQ ID NO: 167	SEQ ID NO: 29	SEQ ID NO: 164	SEQ ID NO: 19	SEQ ID NO: 154	H-L1-MM1-L2-C-L3-MM2	
3025	SEQ ID NO: 233	SEQ ID NO: 20	SEQ ID NO: 167	SEQ ID NO: 29	SEQ ID NO: 165	SEQ ID NO: 15	SEQ ID NO: 154	H-L1-MM1-L2-C-L3-MM2	
3026	SEQ ID NO: 233	SEQ ID NO: 20	SEQ ID NO: 167	SEQ ID NO: 29	SEQ ID NO: 219	SEQ ID NO: 16	SEQ ID NO: 154	H-L1-MM1-L2-C-L3-MM2	
3027	SEQ ID NO: 233	SEQ ID NO: 20	SEQ ID NO: 167	SEQ ID NO: 29	SEQ ID NO: 220	SEQ ID NO: 17	SEQ ID NO: 154	H-L1-MM1-L2-C-L3-MM2	
3028	SEQ ID NO: 234	SEQ ID NO: 20	SEQ ID NO: 167	SEQ ID NO: 29	SEQ ID NO: 221	SEQ ID NO: 18	SEQ ID NO: 154	H-L1-MM1-L2-C-L3-MM2	
3029	SEQ ID NO: 234	SEQ ID NO: 20	SEQ ID NO: 167	SEQ ID NO: 29	SEQ ID NO: 222	SEQ ID NO: 19	SEQ ID NO: 154	H-L1-MM1-L2-C-L3-MM2	
3030	SEQ ID NO: 234	SEQ ID NO: 20	SEQ ID NO: 167	SEQ ID NO: 29	SEQ ID NO: 227	SEQ ID NO: 15	SEQ ID NO: 154	MM2-L3-C-L2-MM1-L1-H	
3031	SEQ ID NO: 234	SEQ ID NO: 20	SEQ ID NO: 167	SEQ ID NO: 29	SEQ ID NO: 228	SEQ ID NO: 16	SEQ ID NO: 154	MM2-L3-C-L2-MM1-L1-H	
3032	SEQ ID NO: 234	SEQ ID NO: 20	SEQ ID NO: 167	SEQ ID NO: 29	SEQ ID NO: 229	SEQ ID NO: 17	SEQ ID NO: 154	MM2-L3-C-L2-MM1-L1-H	
AK401	SEQ ID NO: 261	SEQ ID NO: 28	SEQ ID NO: 167	SEQ ID NO: 318	SEQ ID NO: 825	SEQ ID NO: 27	SEQ ID NO: 155	H-L1-MM1-L2-MM2-L3-C	SEQ ID NO: 755
	-	-	-	-	-	-	SEQ ID NO: 616	H	SEQ ID NO: 616

Construct #	Masking moiety (MM1)	Linker (L1)	Cytokine or functional fragment thereof (C)	Linker (L2)	Masking moiety (MM2)	Linker (L3)	Half-life extension domain (H)	Structure (N- to C- terminal direction)	Amino Acid Sequence
AK403	SEQ ID NO: 261	SEQ ID NO: 28	SEQ ID NO: 167	SEQ ID NO: 318	SEQ ID NO: 825	SEQ ID NO: 27	SEQ ID NO: 155	H-L1-MM1-L2-MM2-L3-C	SEQ ID NO: 756
	-	-	-	-	-	-	SEQ ID NO: 616	H	SEQ ID NO: 616
AK402	SEQ ID NO: 261	SEQ ID NO: 28	SEQ ID NO: 167	SEQ ID NO: 319	SEQ ID NO: 825	SEQ ID NO: 27	SEQ ID NO: 155	H-L1-MM1-L2-MM2-L3-C	SEQ ID NO: 757
	-	-	-	-	-	-	SEQ ID NO: 616	H	SEQ ID NO: 616

[0596] Also generated are masked IL-2 polypeptide constructs that include an IL-2 polypeptide or functional fragment thereof, a masking moiety, a first half-life extension domain, and a second half-life extension domain, such as albumin, an antibody or fragment thereof (e.g., an Fc region, heavy chain, and/or light chain), an albumin-binding peptide, an IgG-binding peptide, or a polyamino acid sequence. The masking moiety is linked to the first half-life extension domain, the IL-2 polypeptide or functional fragment thereof is linked to the second half-life extension domain, and the first half-life extension domain and the second half-life extension domain contain modifications promoting the association of the first and the second half-life extension domain. In one exemplary embodiment, the masking moiety is linked to the first half-life extension domain and includes the amino acid sequence of SEQ ID NO: 267, and the IL-2 polypeptide or functional fragment thereof is linked to the second half-life extension domain and includes the amino acid sequence of SEQ ID NO: 266, and the first half-life extension domain and the second half-life extension domain contain modifications promoting the association of the first and the second half-life extension domain. In one exemplary embodiment of a non-masked IL-2 polypeptide construct, the embodiment comprises an IL-2 polypeptide or functional fragment thereof linked to a first half-life extension domain, and comprises a second half-life extension domain, where the IL-2 polypeptide or functional fragment thereof is linked to the first half-life extension domain and includes the amino acid sequence of SEQ ID NO: 266, and the second half-life extension domain includes the amino acid sequence of SEQ ID NO: 265. Some of the constructs also include a linker that links the masking moiety to the first half-life extension domain, and/or a linker that links the IL-2 polypeptide or functional fragment thereof to the second half-life extension domain. The first and second half-life extension domain of some of the constructs are also linked. In some constructs, the first and second half-life extension domain of some of the constructs are linked by a linker. Some of the constructs include a cleavable peptide in the linker linking the masking moiety to the first half-life extension domain and/or the linker linking the IL-2 polypeptide or functional fragment thereof to the second half-life extension domain, thereby resulting in an activatable masked IL-2 polypeptide construct. The masked IL-2 polypeptide constructs that do not include a cleavable peptide in either the linker that links the IL-2 polypeptide or functional fragment thereof to the second half-life extension domain or the linker that links the masking moiety to the first half-life extension domain are also referred to as non-activatable masked IL-2 polypeptide constructs or non-activatable IL-2 polypeptide constructs because they do not include a cleavable peptide. The structure and composition of exemplary IL-2 polypeptide constructs are provided in Table 8.

Table 8

Construct #	Cytokine or functional fragment thereof (C)	Linker (L1)	Masking moiety (MM)	Linker (L2)	Half-life extension domain (H)	Structure (N- to C-terminal direction)	Amino Acid Sequence
2007/2008	SEQ ID NO: 1	SEQ ID NO: 22	-	-	SEQ ID NO: 157	C-L1-H	
	-	SEQ ID NO: 23	SEQ ID NO: 9	-	SEQ ID NO: 158	MM-L1-H	
2009/2010	-	SEQ ID NO: 24	SEQ ID NO: 9	-	SEQ ID NO: 158	MM-L1-H	
	SEQ ID NO: 1	SEQ ID NO: 25	-	-	SEQ ID NO: 157	C-L1-H	
2080/2081	-	SEQ ID NO: 28	SEQ ID NO: 10	-	SEQ ID NO: 155	H-L1-MM	
	SEQ ID NO: 1	SEQ ID NO: 11	-	-	SEQ ID NO: 156	H-L1-C	
2080/2082	-	SEQ ID NO: 28	SEQ ID NO: 10	-	SEQ ID NO: 155	H-L1-MM	
	SEQ ID NO: 1	SEQ ID NO: 12	-	-	SEQ ID NO: 156	H-L1-C	
2080/2083	-	SEQ ID NO: 28	SEQ ID NO: 10	-	SEQ ID NO: 155	H-L1-MM	
	SEQ ID NO: 1	SEQ ID NO: 13	-	-	SEQ ID NO: 156	H-L1-C	
2080/2084	-	SEQ ID NO: 28	SEQ ID NO: 10	-	SEQ ID NO: 155	H-L1-MM	
	SEQ ID NO: 1	SEQ ID NO: 14	-	-	SEQ ID NO: 156	H-L1-C	
2080/2085	-	SEQ ID NO: 28	SEQ ID NO: 10	-	SEQ ID NO: 155	H-L1-MM	
	SEQ ID NO: 3	SEQ ID NO: 11	-	-	SEQ ID NO: 156	H-L1-C	
2080/2086	-	SEQ ID NO: 28	SEQ ID NO: 10	-	SEQ ID NO: 155	H-L1-MM	
	SEQ ID NO: 3	SEQ ID NO: 12	-	-	SEQ ID NO: 156	H-L1-C	
2080/2087	-	SEQ ID NO: 28	SEQ ID NO: 10	-	SEQ ID NO: 155	H-L1-MM	
	SEQ ID NO: 3	SEQ ID NO: 13	-	-	SEQ ID NO: 156	H-L1-C	
2080/2088	-	SEQ ID NO: 28	SEQ ID NO: 10	-	SEQ ID NO: 155	H-L1-MM	
	SEQ ID NO: 3	SEQ ID NO: 14	-	-	SEQ ID NO: 156	H-L1-C	
2080/2089	-	SEQ ID NO: 28	SEQ ID NO: 10	-	SEQ ID NO: 155	H-L1-MM	
	SEQ ID NO: 4	SEQ ID NO: 11	-	-	SEQ ID NO: 156	H-L1-C	
2080/2090	-	SEQ ID NO: 28	SEQ ID NO: 10	-	SEQ ID NO: 155	H-L1-MM	
	SEQ ID NO: 4	SEQ ID NO: 12	-	-	SEQ ID NO: 156	H-L1-C	
2080/2091	-	SEQ ID NO: 28	SEQ ID NO: 10	-	SEQ ID NO: 155	H-L1-MM	
	SEQ ID NO: 4	SEQ ID NO: 13	-	-	SEQ ID NO: 156	H-L1-C	
2080/2092	-	SEQ ID NO: 28	SEQ ID NO: 10	-	SEQ ID NO: 155	H-L1-MM	
	SEQ ID NO: 4	SEQ ID NO: 14	-	-	SEQ ID NO: 156	H-L1-C	
2080/2093	-	SEQ ID NO: 28	SEQ ID NO: 10	-	SEQ ID NO: 155	H-L1-MM	
	SEQ ID NO: 5	SEQ ID NO: 11	-	-	SEQ ID NO: 156	H-L1-C	
2080/2094	-	SEQ ID NO: 28	SEQ ID NO: 10	-	SEQ ID NO: 155	H-L1-MM	
	SEQ ID NO: 5	SEQ ID NO: 12	-	-	SEQ ID NO: 156	H-L1-C	

Construct #	Cytokine or functional fragment thereof (C)	Linker (L1)	Masking moiety (MM)	Linker (L2)	Half-life extension domain (H)	Structure (N- to C-terminal direction)	Amino Acid Sequence
2080/2095	-	SEQ ID NO: 28	SEQ ID NO: 10	-	SEQ ID NO: 155	H-L1-MM	
	SEQ ID NO: 5	SEQ ID NO: 13	-	-	SEQ ID NO: 156	H-L1-C	
2080/2096	-	SEQ ID NO: 28	SEQ ID NO: 10	-	SEQ ID NO: 155	H-L1-MM	
	SEQ ID NO: 5	SEQ ID NO: 14	-	-	SEQ ID NO: 156	H-L1-C	
2080/2097	-	SEQ ID NO: 28	SEQ ID NO: 10	-	SEQ ID NO: 155	H-L1-MM	
	SEQ ID NO: 6	SEQ ID NO: 11	-	-	SEQ ID NO: 156	H-L1-C	
2080/2098	-	SEQ ID NO: 28	SEQ ID NO: 10	-	SEQ ID NO: 155	H-L1-MM	
	SEQ ID NO: 6	SEQ ID NO: 12	-	-	SEQ ID NO: 156	H-L1-C	
2080/2099	-	SEQ ID NO: 28	SEQ ID NO: 10	-	SEQ ID NO: 155	H-L1-MM	
	SEQ ID NO: 6	SEQ ID NO: 13	-	-	SEQ ID NO: 156	H-L1-C	
2080/2100	-	SEQ ID NO: 28	SEQ ID NO: 10	-	SEQ ID NO: 155	H-L1-MM	
	SEQ ID NO: 6	SEQ ID NO: 14	-	-	SEQ ID NO: 156	H-L1-C	
2080/2101	-	SEQ ID NO: 28	SEQ ID NO: 10	-	SEQ ID NO: 155	H-L1-MM	
	SEQ ID NO: 7	SEQ ID NO: 11	-	-	SEQ ID NO: 156	H-L1-C	
2080/2102	-	SEQ ID NO: 28	SEQ ID NO: 10	-	SEQ ID NO: 155	H-L1-MM	
	SEQ ID NO: 7	SEQ ID NO: 12	-	-	SEQ ID NO: 156	H-L1-C	
2080/2103	-	SEQ ID NO: 28	SEQ ID NO: 10	-	SEQ ID NO: 155	H-L1-MM	
	SEQ ID NO: 7	SEQ ID NO: 13	-	-	SEQ ID NO: 156	H-L1-C	
2080/2104	-	SEQ ID NO: 28	SEQ ID NO: 10	-	SEQ ID NO: 155	H-L1-MM	
	SEQ ID NO: 7	SEQ ID NO: 14	-	-	SEQ ID NO: 156	H-L1-C	
2080/2105	-	SEQ ID NO: 28	SEQ ID NO: 10	-	SEQ ID NO: 155	H-L1-MM	
	SEQ ID NO: 8	SEQ ID NO: 11	-	-	SEQ ID NO: 156	H-L1-C	
2080/2106	-	SEQ ID NO: 28	SEQ ID NO: 10	-	SEQ ID NO: 155	H-L1-MM	
	SEQ ID NO: 8	SEQ ID NO: 12	-	-	SEQ ID NO: 156	H-L1-C	
2080/2107	-	SEQ ID NO: 28	SEQ ID NO: 10	-	SEQ ID NO: 155	H-L1-MM	
	SEQ ID NO: 8	SEQ ID NO: 13	-	-	SEQ ID NO: 156	H-L1-C	
2080/2108	-	SEQ ID NO: 28	SEQ ID NO: 10	-	SEQ ID NO: 155	H-L1-MM	
	SEQ ID NO: 8	SEQ ID NO: 14	-	-	SEQ ID NO: 156	H-L1-C	
5001/5002	SEQ ID NO: 260	SEQ ID NO: 262	-	-	SEQ ID NO: 156	H-L1-C	SEQ ID NO: 266
	-	-	-	-	SEQ ID NO: 265	H	SEQ ID NO: 265
5001/5003	SEQ ID NO: 260	SEQ ID NO: 262	-	-	SEQ ID NO: 156	H-L1-C	SEQ ID NO: 266
	-	SEQ ID NO: 28	SEQ ID NO: 261	-	SEQ ID NO: 155	H-L1-MM	SEQ ID NO: 267
AK038	SEQ ID NO: 1	SEQ ID NO: 22	-	-	SEQ ID NO: 157	C-L1-H	SEQ ID NO: 562

Construct #	Cytokine or functional fragment thereof (C)	Linker (L1)	Masking moiety (MM)	Linker (L2)	Half-life extension domain (H)	Structure (N- to C-terminal direction)	Amino Acid Sequence
	-	SEQ ID NO: 23	SEQ ID NO: 9	-	SEQ ID NO: 158	MM-L1-H	SEQ ID NO: 563
AK039	-	SEQ ID NO: 24	SEQ ID NO: 9	-	SEQ ID NO: 158	MM-L1-H	SEQ ID NO: 564
	SEQ ID NO: 1	SEQ ID NO: 25	-	-	SEQ ID NO: 157	C-L1-H	SEQ ID NO: 565
AK076	SEQ ID NO: 1	SEQ ID NO: 11	-	-	SEQ ID NO: 156	H-L1-C	SEQ ID NO: 608
	-	SEQ ID NO: 795	SEQ ID NO: 10	-	SEQ ID NO: 155	H-L1-MM	SEQ ID NO: 603
AK077	SEQ ID NO: 1	SEQ ID NO: 12	-	-	SEQ ID NO: 156	H-L1-C	SEQ ID NO: 604
	-	SEQ ID NO: 795	SEQ ID NO: 10	-	SEQ ID NO: 155	H-L1-MM	SEQ ID NO: 603
AK078	SEQ ID NO: 1	SEQ ID NO: 13	-	-	SEQ ID NO: 156	H-L1-C	SEQ ID NO: 605
	-	SEQ ID NO: 795	SEQ ID NO: 10	-	SEQ ID NO: 155	H-L1-MM	SEQ ID NO: 603
AK079	SEQ ID NO: 1	SEQ ID NO: 14	-	-	SEQ ID NO: 156	H-L1-C	SEQ ID NO: 606
	-	SEQ ID NO: 795	SEQ ID NO: 10	-	SEQ ID NO: 155	H-L1-MM	SEQ ID NO: 603
AK081	SEQ ID NO: 1	SEQ ID NO: 11	-	-	SEQ ID NO: 156	H-L1-C	SEQ ID NO: 608
	-	-	-	-	SEQ ID NO: 265	H	SEQ ID NO: 265
AK088	SEQ ID NO: 1	-	-	-	SEQ ID NO: 155	H-C	SEQ ID NO: 615
	-	-	-	-	SEQ ID NO: 616	H	SEQ ID NO: 616
AK089	SEQ ID NO: 1	-	-	-	SEQ ID NO: 155	H-C	SEQ ID NO: 615
	-	SEQ ID NO: 15	SEQ ID NO: 10	-	SEQ ID NO: 156	H-L1-MM	SEQ ID NO: 617
AK090	SEQ ID NO: 1	-	-	-	SEQ ID NO: 721	H-C	SEQ ID NO: 618
	-	-	-	-	SEQ ID NO: 619	H	SEQ ID NO: 619
AK091	SEQ ID NO: 1	-	-	-	SEQ ID NO: 721	H-C	SEQ ID NO: 618
	-	SEQ ID NO: 15	SEQ ID NO: 10	-	SEQ ID NO: 772	H-L1-MM	SEQ ID NO: 620
AK092	SEQ ID NO: 1	-	-	-	SEQ ID NO: 793	H-C	SEQ ID NO: 621
	-	-	-	-	SEQ ID NO: 622	H	SEQ ID NO: 622
AK093	SEQ ID NO: 1	-	-	-	SEQ ID NO: 793	H-C	SEQ ID NO: 621
	-	SEQ ID NO: 15	SEQ ID NO: 10	-	SEQ ID NO: 773	H-L1-MM	SEQ ID NO: 623
AK094	SEQ ID NO: 1	-	-	-	SEQ ID NO: 796	H-C	SEQ ID NO: 624
	-	-	-	-	SEQ ID NO: 625	H	SEQ ID NO: 625
AK095	SEQ ID NO: 1	-	-	-	SEQ ID NO: 796	H-C	SEQ ID NO: 624
	-	SEQ ID NO: 15	SEQ ID NO: 10	-	SEQ ID NO: 774	H-L1-MM	SEQ ID NO: 626
AK107	-	SEQ ID NO: 15	SEQ ID NO: 261	-	SEQ ID NO: 156	H-L1-MM	SEQ ID NO: 638
	SEQ ID NO: 1	-	-	-	SEQ ID NO: 155	H-C	SEQ ID NO: 615
AK108	-	SEQ ID NO: 15	SEQ ID NO: 261	-	SEQ ID NO: 772	H-L1-MM	SEQ ID NO: 639
	SEQ ID NO: 1	-	-	-	SEQ ID NO: 721	H-C	SEQ ID NO: 618

Construct #	Cytokine or functional fragment thereof (C)	Linker (L1)	Masking moiety (MM)	Linker (L2)	Half-life extension domain (H)	Structure (N- to C-terminal direction)	Amino Acid Sequence
AK109	-	SEQ ID NO: 15	SEQ ID NO: 261	-	SEQ ID NO: 773	H-L1-MM	SEQ ID NO: 640
	SEQ ID NO: 1	-	-	-	SEQ ID NO: 793	H-C	SEQ ID NO: 621
AK110	-	SEQ ID NO: 15	SEQ ID NO: 261	-	SEQ ID NO: 774	H-L1-MM	SEQ ID NO: 641
	SEQ ID NO: 1	-	-	-	SEQ ID NO: 796	H-C	SEQ ID NO: 624
AK111	SEQ ID NO: 1	SEQ ID NO: 11	-	-	SEQ ID NO: 156	H-L1-C	SEQ ID NO: 608
	-	SEQ ID NO: 28	SEQ ID NO: 261	-	SEQ ID NO: 155	H-L1-MM	SEQ ID NO: 267
AK163	SEQ ID NO: 1	SEQ ID NO: 11	-	-	SEQ ID NO: 793	H-L1-C	SEQ ID NO: 663
	-	-	-	-	SEQ ID NO: 622	H	SEQ ID NO: 622
AK164	SEQ ID NO: 1	SEQ ID NO: 11	-	-	SEQ ID NO: 793	H-L1-C	SEQ ID NO: 663
	-	SEQ ID NO: 795	SEQ ID NO: 261	-	SEQ ID NO: 773	H-L1-MM	SEQ ID NO: 664
AK165	SEQ ID NO: 1	SEQ ID NO: 11	-	-	SEQ ID NO: 796	H-L1-C	SEQ ID NO: 665
	-	-	-	-	SEQ ID NO: 625	H	SEQ ID NO: 625
AK166	SEQ ID NO: 1	SEQ ID NO: 11	-	-	SEQ ID NO: 796	H-L1-C	SEQ ID NO: 665
	-	SEQ ID NO: 795	SEQ ID NO: 261	-	SEQ ID NO: 774	H-L1-MM	SEQ ID NO: 666
AK167	SEQ ID NO: 3	SEQ ID NO: 11	-	-	SEQ ID NO: 156	H-L1-C	SEQ ID NO: 667
	-	-	-	-	SEQ ID NO: 265	H	SEQ ID NO: 265
AK168	SEQ ID NO: 3	SEQ ID NO: 11	-	-	SEQ ID NO: 156	H-L1-C	SEQ ID NO: 667
	-	SEQ ID NO: 28	SEQ ID NO: 261	-	SEQ ID NO: 155	H-L1-MM	SEQ ID NO: 267
AK169	SEQ ID NO: 6	SEQ ID NO: 11	-	-	SEQ ID NO: 156	H-L1-C	SEQ ID NO: 669
	-	-	-	-	SEQ ID NO: 265	H	SEQ ID NO: 265
AK170	-	SEQ ID NO: 28	SEQ ID NO: 261	-	SEQ ID NO: 155	H-L1-MM	SEQ ID NO: 267
	SEQ ID NO: 6	SEQ ID NO: 11	-	-	SEQ ID NO: 156	H-L1-C	SEQ ID NO: 669
AK171	SEQ ID NO: 1	SEQ ID NO: 11	-	-	SEQ ID NO: 155	H-L1-C	SEQ ID NO: 670
	-	-	-	-	SEQ ID NO: 616	H	SEQ ID NO: 616
AK172	SEQ ID NO: 1	SEQ ID NO: 11	-	-	SEQ ID NO: 155	H-L1-C	SEQ ID NO: 670
	-	SEQ ID NO: 795	SEQ ID NO: 261	-	SEQ ID NO: 156	H-L1-MM	SEQ ID NO: 671
AK184	SEQ ID NO: 1	SEQ ID NO: 800	-	-	SEQ ID NO: 156	H-L1-C	SEQ ID NO: 672
	-	SEQ ID NO: 28	SEQ ID NO: 261	-	SEQ ID NO: 155	H-L1-MM	SEQ ID NO: 267
AK185	SEQ ID NO: 1	SEQ ID NO: 185	-	-	SEQ ID NO: 156	H-L1-C	SEQ ID NO: 673
	-	SEQ ID NO: 28	SEQ ID NO: 261	-	SEQ ID NO: 155	H-L1-MM	SEQ ID NO: 267
AK186	SEQ ID NO: 1	SEQ ID NO: 802	-	-	SEQ ID NO: 156	H-L1-C	SEQ ID NO: 674
	-	SEQ ID NO: 28	SEQ ID NO: 261	-	SEQ ID NO: 155	H-L1-MM	SEQ ID NO: 267
AK187	SEQ ID NO: 1	SEQ ID NO: 803	-	-	SEQ ID NO: 156	H-L1-C	SEQ ID NO: 675

Construct #	Cytokine or functional fragment thereof (C)	Linker (L1)	Masking moiety (MM)	Linker (L2)	Half-life extension domain (H)	Structure (N- to C-terminal direction)	Amino Acid Sequence
	-	SEQ ID NO: 28	SEQ ID NO: 261	-	SEQ ID NO: 155	H-L1-MM	SEQ ID NO: 267
AK188	SEQ ID NO: 3	SEQ ID NO: 804	-	-	SEQ ID NO: 156	H-L1-C	SEQ ID NO: 676
	-	SEQ ID NO: 28	SEQ ID NO: 261	-	SEQ ID NO: 155	H-L1-MM	SEQ ID NO: 267
AK189	SEQ ID NO: 1	SEQ ID NO: 805	-	-	SEQ ID NO: 156	H-L1-C	SEQ ID NO: 677
	-	SEQ ID NO: 28	SEQ ID NO: 261	-	SEQ ID NO: 155	H-L1-MM	SEQ ID NO: 267
AK190	SEQ ID NO: 1	SEQ ID NO: 806	-	-	SEQ ID NO: 156	H-L1-C	SEQ ID NO: 678
	-	SEQ ID NO: 28	SEQ ID NO: 261	-	SEQ ID NO: 155	H-L1-MM	SEQ ID NO: 267
AK191	SEQ ID NO: 3	SEQ ID NO: 807	-	-	SEQ ID NO: 156	H-L1-C	SEQ ID NO: 679
	-	SEQ ID NO: 28	SEQ ID NO: 261	-	SEQ ID NO: 155	H-L1-MM	SEQ ID NO: 267
AK192	SEQ ID NO: 3	SEQ ID NO: 805	-	-	SEQ ID NO: 156	H-L1-C	SEQ ID NO: 680
	-	SEQ ID NO: 28	SEQ ID NO: 261	-	SEQ ID NO: 155	H-L1-MM	SEQ ID NO: 267
AK193	SEQ ID NO: 3	SEQ ID NO: 806	-	-	SEQ ID NO: 156	H-L1-C	SEQ ID NO: 681
	-	SEQ ID NO: 28	SEQ ID NO: 261	-	SEQ ID NO: 155	H-L1-MM	SEQ ID NO: 267
AK194	SEQ ID NO: 1	SEQ ID NO: 808	-	-	SEQ ID NO: 156	H-L1-C	SEQ ID NO: 682
	-	SEQ ID NO: 28	SEQ ID NO: 261	-	SEQ ID NO: 155	H-L1-MM	SEQ ID NO: 267
AK195	SEQ ID NO: 1	SEQ ID NO: 809	-	-	SEQ ID NO: 156	H-L1-C	SEQ ID NO: 683
	-	SEQ ID NO: 28	SEQ ID NO: 261	-	SEQ ID NO: 155	H-L1-MM	SEQ ID NO: 267
AK196	SEQ ID NO: 1	SEQ ID NO: 810	-	-	SEQ ID NO: 156	H-L1-C	SEQ ID NO: 684
	-	SEQ ID NO: 28	SEQ ID NO: 261	-	SEQ ID NO: 155	H-L1-MM	SEQ ID NO: 267
AK197	SEQ ID NO: 3	SEQ ID NO: 808	-	-	SEQ ID NO: 156	H-L1-C	SEQ ID NO: 685
	-	SEQ ID NO: 28	SEQ ID NO: 261	-	SEQ ID NO: 155	H-L1-MM	SEQ ID NO: 267
AK198	SEQ ID NO: 3	SEQ ID NO: 809	-	-	SEQ ID NO: 156	H-L1-C	SEQ ID NO: 686
	-	SEQ ID NO: 28	SEQ ID NO: 261	-	SEQ ID NO: 155	H-L1-MM	SEQ ID NO: 267
AK199	SEQ ID NO: 3	SEQ ID NO: 810	-	-	SEQ ID NO: 156	H-L1-C	SEQ ID NO: 687
	-	SEQ ID NO: 28	SEQ ID NO: 261	-	SEQ ID NO: 155	H-L1-MM	SEQ ID NO: 267
AK200	SEQ ID NO: 1	SEQ ID NO: 811	-	-	SEQ ID NO: 156	H-L1-C	SEQ ID NO: 688
	-	SEQ ID NO: 28	SEQ ID NO: 261	-	SEQ ID NO: 155	H-L1-MM	SEQ ID NO: 267
AK201	SEQ ID NO: 1	SEQ ID NO: 812	-	-	SEQ ID NO: 156	H-L1-C	SEQ ID NO: 689
	-	SEQ ID NO: 28	SEQ ID NO: 261	-	SEQ ID NO: 155	H-L1-MM	SEQ ID NO: 267
AK202	SEQ ID NO: 1	SEQ ID NO: 263	-	-	SEQ ID NO: 156	H-L1-C	SEQ ID NO: 690
	-	SEQ ID NO: 28	SEQ ID NO: 261	-	SEQ ID NO: 155	H-L1-MM	SEQ ID NO: 267
AK203	SEQ ID NO: 3	SEQ ID NO: 811	-	-	SEQ ID NO: 156	H-L1-C	SEQ ID NO: 266
	-	SEQ ID NO: 28	SEQ ID NO: 261	-	SEQ ID NO: 155	H-L1-MM	SEQ ID NO: 267

Construct #	Cytokine or functional fragment thereof (C)	Linker (L1)	Masking moiety (MM)	Linker (L2)	Half-life extension domain (H)	Structure (N- to C-terminal direction)	Amino Acid Sequence
AK204	SEQ ID NO: 3	SEQ ID NO: 812	-	-	SEQ ID NO: 156	H-L1-C	SEQ ID NO: 692
	-	SEQ ID NO: 28	SEQ ID NO: 261	-	SEQ ID NO: 155	H-L1-MM	SEQ ID NO: 267
AK205	SEQ ID NO: 3	SEQ ID NO: 263	-	-	SEQ ID NO: 156	H-L1-C	SEQ ID NO: 693
	-	SEQ ID NO: 28	SEQ ID NO: 261	-	SEQ ID NO: 155	H-L1-MM	SEQ ID NO: 267
AK206	SEQ ID NO: 3	SEQ ID NO: 800	-	-	SEQ ID NO: 156	H-L1-C	SEQ ID NO: 694
	-	SEQ ID NO: 28	SEQ ID NO: 261	-	SEQ ID NO: 155	H-L1-MM	SEQ ID NO: 267
AK207	SEQ ID NO: 3	SEQ ID NO: 801	-	-	SEQ ID NO: 156	H-L1-C	SEQ ID NO: 695
	-	SEQ ID NO: 28	SEQ ID NO: 261	-	SEQ ID NO: 155	H-L1-MM	SEQ ID NO: 267
AK208	SEQ ID NO: 1	SEQ ID NO: 804	-	-	SEQ ID NO: 156	H-L1-C	SEQ ID NO: 696
	-	SEQ ID NO: 28	SEQ ID NO: 261	-	SEQ ID NO: 155	H-L1-MM	SEQ ID NO: 267
AK209	SEQ ID NO: 3	SEQ ID NO: 802	-	-	SEQ ID NO: 156	H-L1-C	SEQ ID NO: 697
	-	SEQ ID NO: 28	SEQ ID NO: 261	-	SEQ ID NO: 155	H-L1-MM	SEQ ID NO: 267
AK210	SEQ ID NO: 1	SEQ ID NO: 807	-	-	SEQ ID NO: 156	H-L1-C	SEQ ID NO: 698
	-	SEQ ID NO: 28	SEQ ID NO: 261	-	SEQ ID NO: 155	H-L1-MM	SEQ ID NO: 267
AK211	SEQ ID NO: 3	SEQ ID NO: 339	-	-	SEQ ID NO: 156	H-L1-C	SEQ ID NO: 699
	-	SEQ ID NO: 28	SEQ ID NO: 261	-	SEQ ID NO: 155	H-L1-MM	SEQ ID NO: 267
AK212	SEQ ID NO: 1	SEQ ID NO: 339	-	-	SEQ ID NO: 156	H-L1-C	SEQ ID NO: 700
	-	SEQ ID NO: 28	SEQ ID NO: 261	-	SEQ ID NO: 155	H-L1-MM	SEQ ID NO: 267
AK215	SEQ ID NO: 815	SEQ ID NO: 11	-	-	SEQ ID NO: 156	H-L1-C	SEQ ID NO: 701
	-	SEQ ID NO: 28	SEQ ID NO: 261	-	SEQ ID NO: 155	H-L1-MM	SEQ ID NO: 267
AK216	SEQ ID NO: 816	SEQ ID NO: 11	-	-	SEQ ID NO: 156	H-L1-C	SEQ ID NO: 702
	-	SEQ ID NO: 28	SEQ ID NO: 261	-	SEQ ID NO: 155	H-L1-MM	SEQ ID NO: 267
AK217	SEQ ID NO: 817	SEQ ID NO: 11	-	-	SEQ ID NO: 156	H-L1-C	SEQ ID NO: 703
	-	SEQ ID NO: 28	SEQ ID NO: 261	-	SEQ ID NO: 155	H-L1-MM	SEQ ID NO: 267
AK218	SEQ ID NO: 818	SEQ ID NO: 11	-	-	SEQ ID NO: 156	H-L1-C	SEQ ID NO: 704
	-	SEQ ID NO: 28	SEQ ID NO: 261	-	SEQ ID NO: 155	H-L1-MM	SEQ ID NO: 267
AK219	SEQ ID NO: 819	SEQ ID NO: 11	-	-	SEQ ID NO: 156	H-L1-C	SEQ ID NO: 705
	-	SEQ ID NO: 28	SEQ ID NO: 261	-	SEQ ID NO: 155	H-L1-MM	SEQ ID NO: 267
AK220	SEQ ID NO: 820	SEQ ID NO: 11	-	-	SEQ ID NO: 156	H-L1-C	SEQ ID NO: 706
	-	SEQ ID NO: 28	SEQ ID NO: 261	-	SEQ ID NO: 155	H-L1-MM	SEQ ID NO: 267
AK221	SEQ ID NO: 821	SEQ ID NO: 11	-	-	SEQ ID NO: 156	H-L1-C	SEQ ID NO: 707
	-	SEQ ID NO: 28	SEQ ID NO: 261	-	SEQ ID NO: 155	H-L1-MM	SEQ ID NO: 267
AK222	SEQ ID NO: 822	SEQ ID NO: 11	-	-	SEQ ID NO: 156	H-L1-C	SEQ ID NO: 708

Construct #	Cytokine or functional fragment thereof (C)	Linker (L1)	Masking moiety (MM)	Linker (L2)	Half-life extension domain (H)	Structure (N- to C-terminal direction)	Amino Acid Sequence
	-	SEQ ID NO: 28	SEQ ID NO: 261	-	SEQ ID NO: 155	H-L1-MM	SEQ ID NO: 267
AK223	SEQ ID NO: 813	SEQ ID NO: 11	-	-	SEQ ID NO: 156	H-L1-C	SEQ ID NO: 709
	-	SEQ ID NO: 28	SEQ ID NO: 261	-	SEQ ID NO: 155	H-L1-MM	SEQ ID NO: 267
AK224	SEQ ID NO: 814	SEQ ID NO: 11	-	-	SEQ ID NO: 156	H-L1-C	SEQ ID NO: 710
	-	SEQ ID NO: 28	SEQ ID NO: 261	-	SEQ ID NO: 155	H-L1-MM	SEQ ID NO: 267
AK225	SEQ ID NO: 3	SEQ ID NO: 803	-	-	SEQ ID NO: 156	H-L1-C	SEQ ID NO: 711
	-	SEQ ID NO: 28	SEQ ID NO: 261	-	SEQ ID NO: 155	H-L1-MM	SEQ ID NO: 267
AK228	SEQ ID NO: 1	SEQ ID NO: 339	-	-	SEQ ID NO: 156	H-L1-C	SEQ ID NO: 700
	-	-	-	-	SEQ ID NO: 265	H	SEQ ID NO: 265
AK231	-	-	-	-	SEQ ID NO: 156	H	SEQ ID NO: 156
	-	SEQ ID NO: 28	SEQ ID NO: 261	-	SEQ ID NO: 155	H-L1-MM	SEQ ID NO: 267
AK232	SEQ ID NO: 3	SEQ ID NO: 11	-	-	SEQ ID NO: 156	H-L1-C	SEQ ID NO: 667
	-	SEQ ID NO: 795	SEQ ID NO: 261	-	SEQ ID NO: 155	H-L1-MM	SEQ ID NO: 712
AK233	SEQ ID NO: 1	SEQ ID NO: 691	-	-	SEQ ID NO: 156	H-L1-C	SEQ ID NO: 713
	-	SEQ ID NO: 28	SEQ ID NO: 261	-	SEQ ID NO: 155	H-L1-MM	SEQ ID NO: 267
AK234	SEQ ID NO: 3	SEQ ID NO: 691	-	-	SEQ ID NO: 156	H-L1-C	SEQ ID NO: 714
	-	SEQ ID NO: 28	SEQ ID NO: 261	-	SEQ ID NO: 155	H-L1-MM	SEQ ID NO: 267
AK235	SEQ ID NO: 3	SEQ ID NO: 802	-	-	SEQ ID NO: 156	H-L1-C	SEQ ID NO: 697
	-	-	-	-	SEQ ID NO: 265	H	SEQ ID NO: 265
AK252	-	SEQ ID NO: 15	SEQ ID NO: 261	-	SEQ ID NO: 155	H-L1-MM	SEQ ID NO: 716
	SEQ ID NO: 3	SEQ ID NO: 339	-	-	SEQ ID NO: 156	H-L1-C	SEQ ID NO: 699
AK253	SEQ ID NO: 3	SEQ ID NO: 339	-	-	SEQ ID NO: 156	H-L1-C	SEQ ID NO: 699
	-	-	-	-	SEQ ID NO: 265	H	SEQ ID NO: 265
AK304	SEQ ID NO: 815	SEQ ID NO: 802	-	-	SEQ ID NO: 156	H-L1-C	SEQ ID NO: 717
	-	-	-	-	SEQ ID NO: 265	H	SEQ ID NO: 265
AK305	SEQ ID NO: 815	SEQ ID NO: 802	-	-	SEQ ID NO: 156	H-L1-C	SEQ ID NO: 717
	-	SEQ ID NO: 28	SEQ ID NO: 261	-	SEQ ID NO: 155	H-L1-MM	SEQ ID NO: 267
AK306	SEQ ID NO: 816	SEQ ID NO: 802	-	-	SEQ ID NO: 156	H-L1-C	SEQ ID NO: 718
	-	-	-	-	SEQ ID NO: 265	H	SEQ ID NO: 265
AK307	SEQ ID NO: 816	SEQ ID NO: 802	-	-	SEQ ID NO: 156	H-L1-C	SEQ ID NO: 718
	-	SEQ ID NO: 28	SEQ ID NO: 261	-	SEQ ID NO: 155	H-L1-MM	SEQ ID NO: 267
AK308	SEQ ID NO: 818	SEQ ID NO: 802	-	-	SEQ ID NO: 156	H-L1-C	SEQ ID NO: 719
	-	-	-	-	SEQ ID NO: 265	H	SEQ ID NO: 265

Construct #	Cytokine or functional fragment thereof (C)	Linker (L1)	Masking moiety (MM)	Linker (L2)	Half-life extension domain (H)	Structure (N- to C-terminal direction)	Amino Acid Sequence
AK309	SEQ ID NO: 818	SEQ ID NO: 802	-	-	SEQ ID NO: 156	H-L1-C	SEQ ID NO: 719
	-	SEQ ID NO: 28	SEQ ID NO: 261	-	SEQ ID NO: 155	H-L1-MM	SEQ ID NO: 267
AK310	SEQ ID NO: 819	SEQ ID NO: 802	-	-	SEQ ID NO: 156	H-L1-C	SEQ ID NO: 720
	-	-	-	-	SEQ ID NO: 265	H	SEQ ID NO: 265
AK311	SEQ ID NO: 819	SEQ ID NO: 802	-	-	SEQ ID NO: 156	H-L1-C	SEQ ID NO: 720
	-	SEQ ID NO: 28	SEQ ID NO: 261	-	SEQ ID NO: 155	H-L1-MM	SEQ ID NO: 267
AK312	SEQ ID NO: 820	SEQ ID NO: 802	-	-	SEQ ID NO: 156	H-L1-C	SEQ ID NO: 722
	-	-	-	-	SEQ ID NO: 265	H	SEQ ID NO: 265
AK313	SEQ ID NO: 820	SEQ ID NO: 802	-	-	SEQ ID NO: 156	H-L1-C	SEQ ID NO: 722
	-	SEQ ID NO: 28	SEQ ID NO: 261	-	SEQ ID NO: 155	H-L1-MM	SEQ ID NO: 267
AK314	SEQ ID NO: 813	SEQ ID NO: 802	-	-	SEQ ID NO: 156	H-L1-C	SEQ ID NO: 723
	-	-	-	-	SEQ ID NO: 265	H	SEQ ID NO: 265
AK315	SEQ ID NO: 813	SEQ ID NO: 802	-	-	SEQ ID NO: 156	H-L1-C	SEQ ID NO: 723
	-	SEQ ID NO: 28	SEQ ID NO: 261	-	SEQ ID NO: 155	H-L1-MM	SEQ ID NO: 267
AK316	SEQ ID NO: 1	SEQ ID NO: 802	-	-	SEQ ID NO: 156	H-L1-C	SEQ ID NO: 674
	-	SEQ ID NO: 28	SEQ ID NO: 261	-	SEQ ID NO: 155	H-L1-MM	SEQ ID NO: 267
AK325	SEQ ID NO: 815	SEQ ID NO: 11	-	-	SEQ ID NO: 156	H-L1-C	SEQ ID NO: 701
	-	SEQ ID NO: 28	SEQ ID NO: 261	-	SEQ ID NO: 155	H-L1-MM	SEQ ID NO: 267
AK326	SEQ ID NO: 816	SEQ ID NO: 11	-	-	SEQ ID NO: 156	H-L1-C	SEQ ID NO: 702
	-	SEQ ID NO: 28	SEQ ID NO: 261	-	SEQ ID NO: 155	H-L1-MM	SEQ ID NO: 267
AK327	SEQ ID NO: 818	SEQ ID NO: 11	-	-	SEQ ID NO: 156	H-L1-C	SEQ ID NO: 704
	-	SEQ ID NO: 28	SEQ ID NO: 261	-	SEQ ID NO: 155	H-L1-MM	SEQ ID NO: 267
AK328	SEQ ID NO: 819	SEQ ID NO: 11	-	-	SEQ ID NO: 156	H-L1-C	SEQ ID NO: 705
	-	SEQ ID NO: 28	SEQ ID NO: 261	-	SEQ ID NO: 155	H-L1-MM	SEQ ID NO: 267
AK329	SEQ ID NO: 820	SEQ ID NO: 11	-	-	SEQ ID NO: 156	H-L1-C	SEQ ID NO: 706
	-	SEQ ID NO: 28	SEQ ID NO: 261	-	SEQ ID NO: 155	H-L1-MM	SEQ ID NO: 267
AK330	SEQ ID NO: 813	SEQ ID NO: 11	-	-	SEQ ID NO: 156	H-L1-C	SEQ ID NO: 709
	-	SEQ ID NO: 28	SEQ ID NO: 261	-	SEQ ID NO: 155	H-L1-MM	SEQ ID NO: 267
AK349	SEQ ID NO: 813	SEQ ID NO: 807	-	-	SEQ ID NO: 156	H-L1-C	SEQ ID NO: 728
	-	SEQ ID NO: 28	SEQ ID NO: 261	-	SEQ ID NO: 155	H-L1-MM	SEQ ID NO: 267
AK350	SEQ ID NO: 813	SEQ ID NO: 797	-	-	SEQ ID NO: 156	H-L1-C	SEQ ID NO: 729
	-	SEQ ID NO: 28	SEQ ID NO: 261	-	SEQ ID NO: 155	H-L1-MM	SEQ ID NO: 267
AK351	SEQ ID NO: 813	SEQ ID NO: 798	-	-	SEQ ID NO: 156	H-L1-C	SEQ ID NO: 730

Construct #	Cytokine or functional fragment thereof (C)	Linker (L1)	Masking moiety (MM)	Linker (L2)	Half-life extension domain (H)	Structure (N- to C-terminal direction)	Amino Acid Sequence
	-	SEQ ID NO: 28	SEQ ID NO: 261	-	SEQ ID NO: 155	H-L1-MM	SEQ ID NO: 267
AK352	SEQ ID NO: 813	SEQ ID NO: 724			SEQ ID NO: 156	H-L1-C	SEQ ID NO: 731
	-	SEQ ID NO: 28	SEQ ID NO: 261	-	SEQ ID NO: 155	H-L1-MM	SEQ ID NO: 267
AK353	SEQ ID NO: 813	SEQ ID NO: 725			SEQ ID NO: 156	H-L1-C	SEQ ID NO: 732
	-	SEQ ID NO: 28	SEQ ID NO: 261	-	SEQ ID NO: 155	H-L1-MM	SEQ ID NO: 267
AK354	SEQ ID NO: 813	SEQ ID NO: 536	-	-	SEQ ID NO: 156	H-L1-C	SEQ ID NO: 733
	-	SEQ ID NO: 28	SEQ ID NO: 261	-	SEQ ID NO: 155	H-L1-MM	SEQ ID NO: 267
AK355	SEQ ID NO: 813	SEQ ID NO: 537	-	-	SEQ ID NO: 156	H-L1-C	SEQ ID NO: 734
	-	SEQ ID NO: 28	SEQ ID NO: 261	-	SEQ ID NO: 155	H-L1-MM	SEQ ID NO: 267
AK357	SEQ ID NO: 813	SEQ ID NO: 502	-	-	SEQ ID NO: 156	H-L1-C	SEQ ID NO: 735
	-	SEQ ID NO: 28	SEQ ID NO: 261	-	SEQ ID NO: 155	H-L1-MM	SEQ ID NO: 267
AK358	SEQ ID NO: 813	SEQ ID NO: 503	-	-	SEQ ID NO: 156	H-L1-C	SEQ ID NO: 736
	-	SEQ ID NO: 28	SEQ ID NO: 261	-	SEQ ID NO: 155	H-L1-MM	SEQ ID NO: 267
AK359	SEQ ID NO: 813	SEQ ID NO: 492	-	-	SEQ ID NO: 156	H-L1-C	SEQ ID NO: 737
	-	SEQ ID NO: 28	SEQ ID NO: 261	-	SEQ ID NO: 155	H-L1-MM	SEQ ID NO: 267
AK360	SEQ ID NO: 813	SEQ ID NO: 493	-	-	SEQ ID NO: 156	H-L1-C	SEQ ID NO: 738
	-	SEQ ID NO: 28	SEQ ID NO: 261	-	SEQ ID NO: 155	H-L1-MM	SEQ ID NO: 267
AK361	SEQ ID NO: 813	SEQ ID NO: 416	-	-	SEQ ID NO: 156	H-L1-C	SEQ ID NO: 739
	-	SEQ ID NO: 28	SEQ ID NO: 261	-	SEQ ID NO: 155	H-L1-MM	SEQ ID NO: 267
AK362	SEQ ID NO: 813	SEQ ID NO: 417	-	-	SEQ ID NO: 156	H-L1-C	SEQ ID NO: 740
	-	SEQ ID NO: 28	SEQ ID NO: 261	-	SEQ ID NO: 155	H-L1-MM	SEQ ID NO: 267
AK363	SEQ ID NO: 813	SEQ ID NO: 418	-	-	SEQ ID NO: 156	H-L1-C	SEQ ID NO: 741
	-	SEQ ID NO: 28	SEQ ID NO: 261	-	SEQ ID NO: 155	H-L1-MM	SEQ ID NO: 267
AK364	SEQ ID NO: 813	SEQ ID NO: 419	-	-	SEQ ID NO: 156	H-L1-C	SEQ ID NO: 742
	-	SEQ ID NO: 28	SEQ ID NO: 261	-	SEQ ID NO: 155	H-L1-MM	SEQ ID NO: 267
AK365	SEQ ID NO: 813	SEQ ID NO: 350	-	-	SEQ ID NO: 156	H-L1-C	SEQ ID NO: 743
	-	SEQ ID NO: 28	SEQ ID NO: 261	-	SEQ ID NO: 155	H-L1-MM	SEQ ID NO: 267
AK366	SEQ ID NO: 813	SEQ ID NO: 351	-	-	SEQ ID NO: 156	H-L1-C	SEQ ID NO: 744
	-	SEQ ID NO: 28	SEQ ID NO: 261	-	SEQ ID NO: 155	H-L1-MM	SEQ ID NO: 267
AK367	SEQ ID NO: 813	SEQ ID NO: 352	-	-	SEQ ID NO: 156	H-L1-C	SEQ ID NO: 745
	-	SEQ ID NO: 28	SEQ ID NO: 261	-	SEQ ID NO: 155	H-L1-MM	SEQ ID NO: 267
AK368	SEQ ID NO: 813	SEQ ID NO: 353	-	-	SEQ ID NO: 156	H-L1-C	SEQ ID NO: 746
	-	SEQ ID NO: 28	SEQ ID NO: 261	-	SEQ ID NO: 155	H-L1-MM	SEQ ID NO: 267

Construct #	Cytokine or functional fragment thereof (C)	Linker (L1)	Masking moiety (MM)	Linker (L2)	Half-life extension domain (H)	Structure (N- to C-terminal direction)	Amino Acid Sequence
AK317	SEQ ID NO: 1	SEQ ID NO: 802	-	-	SEQ ID NO: 156	H-L1-C	SEQ ID NO: 674
	-	SEQ ID NO: 28	SEQ ID NO: 826	-	SEQ ID NO: 155	H-L1-MM	SEQ ID NO: 828
AK324	SEQ ID NO: 1	SEQ ID NO: 802	-	-	SEQ ID NO: 156	H-L1-C	SEQ ID NO: 674
	-	SEQ ID NO: 28	SEQ ID NO: 827	-	SEQ ID NO: 155	H-L1-MM	SEQ ID NO: 829
AK341	SEQ ID NO: 3	SEQ ID NO: 802	-	-	SEQ ID NO: 156	H-L1-C	SEQ ID NO: 726
	-	SEQ ID NO: 28	SEQ ID NO: 826	-	SEQ ID NO: 155	H-L1-MM	SEQ ID NO: 830
AK342	SEQ ID NO: 3	SEQ ID NO: 802	-	-	SEQ ID NO: 156	H-L1-C	SEQ ID NO: 726
	-	SEQ ID NO: 28	SEQ ID NO: 827	-	SEQ ID NO: 155	H-L1-MM	SEQ ID NO: 829

[0597] Also generated are masked IL-15 polypeptide constructs that include an IL-15 polypeptide or functional fragment thereof, a masking moiety, a first half-life extension domain, and a second half-life extension domain, such as albumin, an antibody or fragment thereof (e.g., an Fc region, heavy chain, and/or light chain), an albumin-binding peptide, an IgG-binding peptide, or a polyamino acid sequence. The masking moiety is linked to the first half-life extension domain, the IL-15 polypeptide or functional fragment thereof is linked to the second half-life extension domain, and the first half-life extension domain and the second half-life extension domain contain modifications promoting the association of the first and the second half-life extension domain. Some of the constructs also include a linker that links the masking moiety to the first half-life extension domain, and/or a linker that links the IL-15 polypeptide or functional fragment thereof to the second half-life extension domain. The first and second half-life extension domain of some of the constructs are also linked. In some constructs, the first and second half-life extension domain of some of the constructs are linked by a linker. Some of the constructs include a cleavable peptide in the linker linking the masking moiety to the first half-life extension domain and/or the linker linking the IL-15 polypeptide or functional fragment thereof to the second half-life extension domain, thereby resulting in an activatable masked IL-15 polypeptide construct. The masked IL-15 polypeptide constructs that do not include a cleavable peptide in either the linker that links the IL-15 polypeptide or functional fragment thereof to the second half-life extension domain or the linker that links the masking moiety to the first half-life extension domain are also referred to as non-activatable masked IL-15 polypeptide constructs or non-activatable IL-15 polypeptide constructs because they do not include a cleavable peptide. The structure and composition of exemplary IL-15 polypeptide constructs are provided in Table 9.

Table 9

Construct #	Cytokine or functional fragment thereof (C)	Linker (L1)	Masking moiety (MM)	Linker (L2)	Half-life extension domain (H)	Structure (N- to C-terminal direction)	Amino Acid Sequence
3033	-	SEQ ID NO: 28	SEQ ID NO: 10	-	SEQ ID NO: 155	H-L1-MM	
	SEQ ID NO: 167	SEQ ID NO: 11	-	-	SEQ ID NO: 156	H-L1-C	
3034	-	SEQ ID NO: 28	SEQ ID NO: 10	-	SEQ ID NO: 155	MM-L1-H	
	SEQ ID NO: 167	SEQ ID NO: 11	-	-	SEQ ID NO: 156	C-L1-H	
3035	-	SEQ ID NO: 28	SEQ ID NO: 10	-	SEQ ID NO: 155	MM-L1-H	
	SEQ ID NO: 167	SEQ ID NO: 11	-	-	SEQ ID NO: 156	C-L1-H	
3036	-	SEQ ID NO: 28	SEQ ID NO: 232	-	SEQ ID NO: 155	H-L1-MM	
	SEQ ID NO: 167	SEQ ID NO: 11	-	-	SEQ ID NO: 156	H-L1-C	
3037	-	SEQ ID NO: 28	SEQ ID NO: 233	-	SEQ ID NO: 155	MM-L1-H	
	SEQ ID NO: 167	SEQ ID NO: 11	-	-	SEQ ID NO: 156	C-L1-H	
3038		SEQ ID NO: 28	SEQ ID NO: 233	-	SEQ ID NO: 155	H-L1-MM	
	SEQ ID NO: 167	SEQ ID NO: 11	-	-	SEQ ID NO: 156	H-L1-C	
AK243	SEQ ID NO: 167	SEQ ID NO: 668	-	-	SEQ ID NO: 156	H-L1-C	SEQ ID NO: 715
	-	-	-	-	SEQ ID NO: 265	H	SEQ ID NO: 265
AK247	SEQ ID NO: 167	SEQ ID NO: 845			SEQ ID NO: 156	H-L1-C	SEQ ID NO: 747
	-	SEQ ID NO: 799	SEQ ID NO: 261	-	SEQ ID NO: 156	H-L1-MM	SEQ ID NO: 671
AK248	SEQ ID NO: 167	SEQ ID NO: 668	-	-	SEQ ID NO: 156	H-L1-C	SEQ ID NO: 715
	-	SEQ ID NO: 28	SEQ ID NO: 261	-	SEQ ID NO: 155	H-L1-MM	SEQ ID NO: 267
AK248b	SEQ ID NO: 167	SEQ ID NO: 668	-	-	SEQ ID NO: 156	H-L1-C	SEQ ID NO: 715
	-	SEQ ID NO: 799	SEQ ID NO: 261	-	SEQ ID NO: 156	H-L1-MM	SEQ ID NO: 671
AK249	SEQ ID NO: 167	SEQ ID NO: 355			SEQ ID NO: 156	H-L1-C	SEQ ID NO: 748
	-	SEQ ID NO: 799	SEQ ID NO: 261	-	SEQ ID NO: 156	H-L1-MM	SEQ ID NO: 671
AK250	SEQ ID NO: 167	SEQ ID NO: 354	SEQ ID NO: 823	SEQ ID NO: 27	SEQ ID NO: 156	H-L1-C-L2-MM	SEQ ID NO: 749
	-	SEQ ID NO: 799	SEQ ID NO: 261	-	SEQ ID NO: 156	H-L1-MM	SEQ ID NO: 671
AK251	SEQ ID NO: 167	SEQ ID NO: 354	SEQ ID NO: 824	SEQ ID NO: 27	SEQ ID NO: 156	H-L1-C-L2-MM	SEQ ID NO: 750
	-	SEQ ID NO: 799	SEQ ID NO: 261	-	SEQ ID NO: 156	H-L1-MM	SEQ ID NO: 671
AK418	SEQ ID NO: 167	SEQ ID NO: 348	-	-	SEQ ID NO: 156	H-L1-C	SEQ ID NO: 751
	-	SEQ ID NO: 799	SEQ ID NO: 261	-	SEQ ID NO: 156	H-L1-MM	SEQ ID NO: 671
AK419	SEQ ID NO: 167	SEQ ID NO: 668	SEQ ID NO: 823	SEQ ID NO: 27	SEQ ID NO: 156	H-L1-C-L2-MM	SEQ ID NO: 752
	-	SEQ ID NO: 799	SEQ ID NO: 261	-	SEQ ID NO: 156	H-L1-MM	SEQ ID NO: 671
AK420	SEQ ID NO: 167	SEQ ID NO: 668	SEQ ID NO: 824	SEQ ID NO: 27	SEQ ID NO: 156	H-L1-C-L2-MM	SEQ ID NO: 753

Construct #	Cytokine or functional fragment thereof (C)	Linker (L1)	Masking moiety (MM)	Linker (L2)	Half-life extension domain (H)	Structure (N- to C-terminal direction)	Amino Acid Sequence
	-	SEQ ID NO: 799	SEQ ID NO: 261	-	SEQ ID NO: 156	H-L1-MM	SEQ ID NO: 671
AK421	SEQ ID NO: 167	SEQ ID NO: 349	-	-	SEQ ID NO: 156	H-L1-C	SEQ ID NO: 754
	-	SEQ ID NO: 799	SEQ ID NO: 261	-	SEQ ID NO: 156	H-L1-MM	SEQ ID NO: 671
AK399	SEQ ID NO: 167	SEQ ID NO: 320	SEQ ID NO: 823	SEQ ID NO: 321	SEQ ID NO: 156	H-L1-C-L2-MM	SEQ ID NO: 758
	-	SEQ ID NO: 799	SEQ ID NO: 261	-	SEQ ID NO: 156	H-L1-MM	SEQ ID NO: 671
AK405	SEQ ID NO: 167	SEQ ID NO: 320	SEQ ID NO: 823	SEQ ID NO: 322	SEQ ID NO: 156	H-L1-C-L2-MM	SEQ ID NO: 759
	-	SEQ ID NO: 799	SEQ ID NO: 261	-	SEQ ID NO: 156	H-L1-MM	SEQ ID NO: 671
AK400	SEQ ID NO: 167	SEQ ID NO: 349	SEQ ID NO: 824	SEQ ID NO: 30	SEQ ID NO: 156	H-L1-C-L2-MM	SEQ ID NO: 760
	-	SEQ ID NO: 799	SEQ ID NO: 261	-	SEQ ID NO: 156	H-L1-MM	SEQ ID NO: 671
AK404	SEQ ID NO: 167	SEQ ID NO: 349	SEQ ID NO: 823	SEQ ID NO: 30	SEQ ID NO: 156	H-L1-C-L2-MM	SEQ ID NO: 761
	-	SEQ ID NO: 799	SEQ ID NO: 261	-	SEQ ID NO: 156	H-L1-MM	SEQ ID NO: 671

[0598] Also generated are masked IL-2 polypeptide constructs that include an IL-2 polypeptide or functional fragment thereof, a first masking moiety, a second masking moiety, a first half-life extension domain, and a second half-life extension domain, such as albumin, an antibody or fragment thereof (e.g., an Fc region, heavy chain, and/or light chain), an albumin-binding peptide, an IgG-binding peptide, or a polyamino acid sequence. The first masking moiety is linked to the first half-life extension domain, the second masking moiety is linked to the IL-2 polypeptide or functional fragment thereof, either the second masking moiety or the IL-2 polypeptide or functional fragment thereof is linked to the second half-life extension domain, and the first half-life extension domain and the second half-life extension domain contain modifications promoting the association of the first and second half-life extension domain. Some of the constructs also include a linker that links the first masking moiety to the first half-life extension domain, and/or a linker that linkers the second masking moiety to the IL-2 polypeptide or functional fragment thereof. The first and second half-life extension domain of some of the constructs are also linked. In some constructs, the first and second half-life extension domain of some of the constructs are linked by a linker. Some of the constructs include a cleavable peptide in the linker linking the first masking moiety to the first half-life extension domain, and/or include a cleavable peptide in the linker linking the second masking moiety to the IL-2 polypeptide or functional fragment thereof, thereby resulting in an activatable masked IL-2 polypeptide construct. The masked IL-2 polypeptide constructs that do not include a cleavable peptide in either the linker that links the first masking moiety to the first half-life extension domain or the linker linking the second masking moiety to the IL-2 polypeptide or functional fragment thereof are also referred to as non-activatable masked IL-2 polypeptide constructs or non-activatable IL-2 polypeptide constructs because they do not include a cleavable peptide. The structure and composition of exemplary IL-2 polypeptide constructs are provided in Table 10.

Table 10

Construct #	Cytokine or functional fragment thereof (C)	Linker (L1)	Masking moiety (MM)	Linker (L2)	Half-life extension domain (H)	Structure (N- to C-terminal direction)
4000	-	SEQ ID NO: 28	SEQ ID NO: 10	-	SEQ ID NO: 155	H-L1-MM
	SEQ ID NO: 1	SEQ ID NO: 11	SEQ ID NO: 9	SEQ ID NO: 15	SEQ ID NO: 156	H-L1-C-L2-MM
4001	-	SEQ ID NO: 28	SEQ ID NO: 10	-	SEQ ID NO: 155	H-L1-MM
	SEQ ID NO: 3	SEQ ID NO: 11	SEQ ID NO: 9	SEQ ID NO: 16	SEQ ID NO: 156	H-L1-C-L2-MM
4002	-	SEQ ID NO: 28	SEQ ID NO: 10	-	SEQ ID NO: 155	H-L1-MM
	SEQ ID NO: 4	SEQ ID NO: 11	SEQ ID NO: 9	SEQ ID NO: 17	SEQ ID NO: 156	H-L1-C-L2-MM
4003	-	SEQ ID NO: 28	SEQ ID NO: 10	-	SEQ ID NO: 155	MM-L1-H
	SEQ ID NO: 5	SEQ ID NO: 11	SEQ ID NO: 9	SEQ ID NO: 18	SEQ ID NO: 156	MM-L2-C-L1-H
4004	-	SEQ ID NO: 28	SEQ ID NO: 10	-	SEQ ID NO: 155	MM-L1-H
	SEQ ID NO: 6	SEQ ID NO: 11	SEQ ID NO: 9	SEQ ID NO: 19	SEQ ID NO: 156	MM-L2-C-L1-H
4005	-	SEQ ID NO: 28	SEQ ID NO: 10	-	SEQ ID NO: 155	MM-L1-H
	SEQ ID NO: 7	SEQ ID NO: 11	SEQ ID NO: 9	SEQ ID NO: 15	SEQ ID NO: 156	MM-L2-C-L1-H
4006	-	SEQ ID NO: 28	SEQ ID NO: 10	-	SEQ ID NO: 155	H-L1-MM
	SEQ ID NO: 8	SEQ ID NO: 11	SEQ ID NO: 9	SEQ ID NO: 16	SEQ ID NO: 156	H-L1-C-L2-MM

[0599] Also generated are masked IL-15 polypeptide constructs that include an IL-15 polypeptide or functional fragment thereof, a first masking moiety, a second masking moiety, a first half-life extension domain, and a second half-life extension domain, such as albumin, an antibody or fragment thereof (e.g., an Fc region, heavy chain, and/or light chain), an albumin-binding peptide, an IgG-binding peptide, or a polyamino acid sequence. The first masking moiety is linked to the first half-life extension domain, the second masking moiety is linked to the IL-15 polypeptide or functional fragment thereof, either the second masking moiety or the IL-15 polypeptide or functional fragment thereof is linked to the second half-life extension domain, and the first half-life extension domain and the second half-life extension domain contain modifications promoting the association of the first and second half-life extension domain. Some of the constructs also include a linker that links the first masking moiety to the first half-life extension domain, and/or a linker that linkers the second masking moiety to the IL-15 polypeptide or functional fragment thereof. The first and second half-life extension domain of some of the constructs are also linked. In some constructs, the first and second half-life extension domain of some of the constructs are linked by a linker. Some of the constructs include a cleavable peptide in the linker linking the first masking moiety to the first half-life extension domain, and/or include a cleavable peptide in the linker linking the second masking moiety to the IL-15 polypeptide or functional fragment thereof, thereby resulting in an activatable masked IL-15 polypeptide construct. The masked IL-15 polypeptide constructs that do not include a cleavable peptide in either the linker that links the first masking moiety to the first half-life extension domain or the linker linking the second masking moiety to the IL-15 polypeptide or functional fragment thereof are also referred to as non-activatable masked IL-15 polypeptide constructs or non-activatable IL-15 polypeptide constructs because they do not include a cleavable peptide. The structure and composition of exemplary IL-2 polypeptide constructs are provided in Table 11.

Table 11

Construct #	Cytokine or functional fragment thereof (C)	Linker (L1)	Masking moiety (MM)	Linker (L2)	Half-life extension domain (H)	Structure (N- to C-terminal direction)
3034	-	SEQ ID NO: 28	SEQ ID NO: 10	-	SEQ ID NO: 155	H-L1-MM
	SEQ ID NO: 167	SEQ ID NO: 11	SEQ ID NO: 232	SEQ ID NO: 235	SEQ ID NO: 156	H-L1-C-L2-MM
3035	-	SEQ ID NO: 28	SEQ ID NO: 10	-	SEQ ID NO: 155	H-L1-MM
	SEQ ID NO: 167	SEQ ID NO: 11	SEQ ID NO: 233	SEQ ID NO: 235	SEQ ID NO: 156	H-L1-C-L2-MM
3036	-	SEQ ID NO: 28	SEQ ID NO: 10	-	SEQ ID NO: 155	H-L1-MM
	SEQ ID NO: 167	SEQ ID NO: 11	SEQ ID NO: 234	SEQ ID NO: 235	SEQ ID NO: 156	H-L1-C-L2-MM
3038	-	SEQ ID NO: 28	SEQ ID NO: 10	-	SEQ ID NO: 155	MM-L1-H
	SEQ ID NO: 167	SEQ ID NO: 11	SEQ ID NO: 232	SEQ ID NO: 235	SEQ ID NO: 156	MM-L2-C-L1-H
3039	-	SEQ ID NO: 28	SEQ ID NO: 10	-	SEQ ID NO: 155	MM-L1-H
	SEQ ID NO: 167	SEQ ID NO: 11	SEQ ID NO: 233	SEQ ID NO: 235	SEQ ID NO: 156	MM-L2-C-L1-H
3040	-	SEQ ID NO: 28	SEQ ID NO: 10	-	SEQ ID NO: 155	MM-L1-H
	SEQ ID NO: 167	SEQ ID NO: 11	SEQ ID NO: 234	SEQ ID NO: 235	SEQ ID NO: 156	MM-L2-C-L1-H

Example 2: In vitro characterization of masked IL-2 and IL-15 polypeptides

[0600] The masked IL-2 polypeptide constructs and masked IL-15 polypeptide constructs generated in Example 1 are characterized using several cellular and functional assays in vitro.

Production

[0601] Plasmids encoding the constructs (e.g., masked IL-2 polypeptide constructs and masked IL-15 polypeptide constructs) were transfected into either Expi293 cells (Life Technologies A14527) or HEK293-6E cells (National Research Council; NRC). Transfections were performed using 1 mg of total DNA using PEIpro (Polyplus Transfection, 115-100) in a 1:1 ratio with the total DNA. The DNA and PEI were each added to 50 mL of OptiMem (Life Technologies 31985088) medium and sterile filtered. The DNA and PEI were combined for 10 minutes and added to the Expi293 cells with a cell density of 1.8 – 2.8 x 10^6 cells/mL or 0.85-1.20 x 10^6 cells/m, for expi293 cells or HEK293 cells, respectively, and a viability of at least 95%. The HEK293-6E transfection was performed with a cell density of and a viability of at least 95%, following the same protocol used for the Expi293 transfections. After 5-7 days, the cells were pelleted by centrifugation at 3000 x g and the supernatant was filtered through a 0.2 μm membrane. Protein A resin (CaptivA, Repligen CA-PRI-0005) was added to the filtered supernatant and incubated for at least 2 hours at 4 °C with shaking. The resin was packed into a column, washed with 15 column volumes of 20 mM citrate, pH 6.5, and then washed with 15 column volumes of 20 mM citrate, 500 mM sodium chloride, pH 6.5. The bound protein was eluted from the column with 20 mM citrate, 100 mM NaCl, pH 2.9.

[0602] The titer (mg/L) of exemplary constructs produced, including parental (e.g., non-masked) and masked constructs, is provided in Table 12, below.

Table 12

Construct ID	Titer (mg/L)		Construct ID	Titer (mg/L)		Construct ID	Titer (mg/L)		Construct ID	Titer (mg/L)
AK032	5.8		AK063	3.5		AK165	13.5		AK314	60
AK033	9.6		AK064	1.5		AK166	17.1		AK315	59.8
AK034	13.9		AK065	3.2		AK167	56.4		AK316	69.2
AK035	16.7		AK066	3.5		AK168	36.1		AK325	3.2
AK036	25		AK076	1.4		AK184	21.6		AK326	33.1
AK037	11.1		AK077	1.5		AK188	12.8		AK327	68.5
AK039	3.5		AK078	4.4		AK203	83.2		AK328	28.8
AK040	0.7		AK079	4.3		AK209	27.3		AK329	181
AK042	1.9		AK080	2.3		AK211	43.8		AK330	51
AK043	1.1		AK081	23.5		AK212	18.2		AK341	58
AK044	15		AK083	3.3		AK225	44.1		AK342	24
AK045	9.3		AK084	3.2		AK226	20.2		AK349	39.6
AK046	12.5		AK085	2.1		AK227	27.4		AK350	7.8
AK047	18.5		AK086	3.2		AK228	20.1		AK351	9.3
AK048	24		AK087	3.2		AK231	19.3		AK352	9.9
AK049	12.2		AK088	41		AK233	36.4		AK353	11
AK050	12.8		AK090	14.8		AK234	33.3		AK354	9.8
AK051	11.9		AK092	6.3		AK235	35.9		AK355	13.7
AK052	10		AK094	17.1		AK252	68		AK357	13.1
AK053	15.2		AK106	10.5		AK253	41.4		AK358	12.4
AK054	11.9		AK107	0		AK304	19.9		AK359	10.4
AK055	13.2		AK109	12.6		AK305	53.2		AK360	11.1
AK056	9.2		AK110	23.8		AK306	29.3		AK361	13.7
AK057	10.8		AK111	12.7		AK307	62.9		AK362	9.3
AK058	13.5		AK112	21.6		AK308	74.5		AK363	13.2
AK059	3.7		AK113	25.3		AK309	90.8		AK364	7.9
AK060	1.2		AK114	29		AK310	44		AK365	10.9
AK061	3.5		AK115	15		AK311	64.9		AK366	8.3
AK062	0.6		AK163	7.5		AK312	154		AK367	10.3
AK248	47.7		AK164	4		AK313	81.2		AK368	7.1

SDS-PAGE Analysis

[0603] For SDS-PAGE analysis, protein samples were made with 4x Laemmli sample buffer (BioRad Catalog Number 1610747). For the reduced samples, 0.1 M Bond Breaker TCEP Solution (Thermo Scientific 77720) was added and the samples were heated for 5 minutes at 65 °C. The proteins were loaded into a 12-well NuPage 4-12 % Bis-Tris Protein Gel (Invitrogen NP0322BOX), with 4 µg of protein loaded per well. The gel was stained using SimplyBlue SafeStain (Invitrogen LC6065).

[0604] As depicted in FIG. 8, SDS-PAGE analysis was performed on the flow-through (FT) samples (i.e., proteins that did not bind to the Protein A column) and the eluted (E) samples (i.e., proteins that bound to the Protein A column and were eluted from it) following production and purification of exemplary constructs (AK304, AK305, AK307, AK308, AK309, AK310, AK311, AK312, AK313, AK314, and AK315). This exemplary data demonstrates that constructs as described herein can be successfully produced and purified.

Reporter Bioassays

[0605] Reporter bioassays are performed on masked IL-2 polypeptide constructs and masked IL-15 polypeptide constructs, along with non-masked parental constructs or other controls, to monitor activation of a downstream pathway, such as the JAK-STAT pathway.

[0606] In some studies, HEK-Blue IL-2 reporter cells (Invivogen) were used to test activation of the JAK-STAT pathway in accordance with the following method. HEK-Blue IL-2 cells passage 6 (p6) (97% live) were washed 2x with assay medium (DMEM + 10% heat-inactivated FBS), plated in 3 plated at 5e4 cells/well in 150 uL of assay medium, and rested in assay medium for about 2 hours to allow adherence to plate. Each construct tested was diluted to 300 pM in assay medium, then diluted 1:2 down the plate. 50 uL of each dilution was added, for a final starting concentration of 75 pM. HEK-Blue IL-2 cell supernatant was harvested after 24 hours, an incubated with Quantiblue (180 uL + 20 uL supernatant), plus 3 wells/plate of assay medium, at 37 deg C for 1 hour. The absorbance was read using a Biotek Neo2 at 625 nm. In one study, the exemplary masked IL-15 polypeptide construct AK248 was tested in accordance with this protocol, with or without prior exposure to an MMP10 protease, along with recombinant human IL-15 (rhIL-15) as a positive control. As shown in FIGs. 22A and 22B, there was no detectable activation of the JAK-STAT pathway when using the masked IL-15 polypeptide construct AK248 (without protease cleavage), but following cleavage by an activating protease, strong levels of activation of the JAK-STAT pathway were observed. This demonstrates that an exemplary IL-15 polypeptide can be effectively masked and also activated through protease cleavage.

[0607] In some studies, CTLL2 cells were used to test activation of the JAK-STAT pathway in accordance with the following method. CTLL2 cells were plated at 40,000 cell per well in RPMI with 10% FBS. Dilutions of the constructs of interest (e.g., the masked IL-15 polypeptide construct AK248, with or without prior exposure to an MMP protease, or a positive control such as rhIL-15) were added and incubated at 37 degrees. After 6 hours, the Bio-Glo reagent was added and luminescence measured with a BioTek Synergy Neo2 plate reader.

Receptor Binding

[0608] The binding of the masked IL-2 polypeptide constructs and the masked IL-15 polypeptide constructs generated in Example 1 is assessed. For the masked IL-2 polypeptide constructs, in some experiments, ELISA plates are coated with a receptor subunit, such as IL-2Rα (also referred to as CD25), IL-2Rβ (also referred to as CD122), or IL-2Rγ (also referred to as CD132), or combinations thereof. For the masked IL-15 polypeptide constructs, in some experiments, ELISA plates are coated with a receptor subunit,

such as IL-15Rα, IL-2Rβ (also referred to as CD122), or IL-2Rγ (also referred to as CD132), or combinations thereof. Dilutions of masked IL-2 polypeptide constructs or masked IL-15 polypeptide constructs are allowed to bind to the receptor subunit(s) and are detected using an anti-huFc-HRP detection antibody. The binding of the masked IL-2 polypeptide constructs and masked IL-15 polypeptide constructs is determined in conditions with and without protease cleavage.

On-Cell Receptor Binding

[0609] The on-cell receptor binding of the masked IL-2 polypeptide constructs and the masked IL-15 polypeptide constructs generated in Example 1 is assessed. Dilutions of masked IL-2 polypeptide constructs or IL-15 polypeptide constructs are allowed to bind to peripheral blood lymphocytes or tissue culture cells, such as CTLL2 cells and are detected by fluorescence activated cell sorting (FACS) using an anti-huFc-FITC or anti-albumin-FITC detection antibody. The binding of the masked IL-2 polypeptide constructs and IL-15 polypeptide constructs is determined in conditions with and without protease cleavage.

Receptor Binding Affinity

[0610] The binding affinity of the masked IL-2 polypeptide constructs and the masked IL-15 polypeptide constructs generated in Example 1 is assessed. For example, surface plasmon resonance (SPR) is performed at room temperature and/or 37 °C. The IL-2 receptors (e.g., IL-2Rα, IL-2Rβ, or IL-2Rγ, or combinations thereof) are coupled to CM5 chips (GE Healthcare) via EDC/NHS chemistry. The IL-15 receptors (e.g., IL-15Rα, IL-2Rβ, or IL-2Rγ, or combinations thereof) are coupled to CM5 chips (GE Healthcare) via EDC/NHS chemistry. Masked IL-2 polypeptide constructs or masked IL-15 polypeptide constructs are flowed over the chips at a range of concentrations to obtain dissociation constants for on- and off-rates. The binding affinity of the masked IL-2 polypeptide constructs and the IL-15 polypeptide constructs is determined in conditions with and without protease cleavage.

[0611] For some SPR studies testing binding of masked and non-masked IL-2 polypeptide constructs, Reichert Carboxymethyl Dextran Hydrogel Surface Sensor Chips were coated and immobilized with the construct of interest (e.g., a masked IL-2 polypeptide construct or non-masked IL-2 polypeptide construct) at 30ug/ml in 10mM Sodium Acetate, pH 5.0 diluted 1:1 in EDC and NHS. Dilutions of CD25-Fc or Fc-CD122 in PBS (CD25: 16 nM, 8 nM, 4 nM, 2 nM, 1 nM and CD122: 500 nM, 250 nM, 125 nM, 62.5 nM, 31.25 nM) were prepared. Using a Reichert 4Channel SPR, dilutions of CD25 or CD122 were flowed over the clips with the immobilized construct to determine the on rate at 25 degrees C. At equilibrium (approximately 3-4 minutes), the flow buffer was changed to PBS, to determine the off rates over 1 minute. Between each run the chip was regenerated with 10mM glycine, pH 2.0. A similar approach is taken to test

binding of masked and unmasked IL-15 polypeptide constructs to appropriate binding partners at appropriate concentrations in accordance with the teachings and examples herein.

[0612] FIGs. 9A-9D depict results from SPR analysis that tested the binding of exemplary masked IL-2 polypeptide constructs (AK215 and AK216) to CD25-Fc. FIG. 9A depicts the interaction between AK215 and CD25-Fc, FIG. 9B depicts the interaction between AK216 and CD25-Fc, and FIG. 9C depicts the interaction between a recombinant human IL2 (rhIL2) control and CD25-Fc. FIG. 9D provides a table summarizing the data obtained for the association constant (ka), dissociation constant (kd), equilibrium dissociation constant (KD), as well as the Chi^2 value and U-value for each interaction. These results demonstrate that these exemplary masked IL-2 polypeptide constructs did not demonstrate detectable binding to CD25-Fc, while the rhIL2 control did demonstrate detectable binding.

[0613] FIGs. 10A-10D depict results from SPR analysis that tested the binding of exemplary masked IL-2 polypeptide constructs (AK216 and AK218) to CD122-Fc. FIG. 10A depicts the interaction between AK216 and CD122-Fc, FIG. 10B depicts the interaction between AK218 and CD122-Fc, and FIG. 10C depicts the interaction between a recombinant human IL2 (rhIL2) control and CD122-Fc. FIG. 10D provides a table summarizing the data obtained for the association constant (ka), dissociation constant (kd), equilibrium dissociation constant (KD), as well as the Chi^2 value and U-value for each interaction. These results demonstrate that these exemplary masked IL-2 polypeptide constructs did not demonstrate detectable binding to CD122-Fc, while the rhIL2 control did demonstrate detectable binding. Additional exemplary SPR data is provided below in Table 13 for various constructs tested, including masked and non-masked constructs. For some structures, when applicable, the KD was determined for the construct with or without having been previously cleaved by a protease.

Table 13

Construct	KD for CD25 (without protease cleavage)	KD for CD122 (without protease cleavage)	KD for CD122 (after protease cleavage)
rhIL2	1.2 nM	124 nM	N/A
AK032	1.76 nM	260 nM	N/A
AK033	No binding detected	368 nM*	N/A
AK034	No binding detected	Not determined	N/A
AK035	No binding detected	110 nM	N/A
AK042	No binding detected	4.1 nM	N/A
AK049	No binding detected	4.67 nM	N/A
AK056	No binding detected	Not determined	N/A
AK076	2.28 nM	No binding detected	
AK077	4.77 nM	No binding detected	
AK078	3.41 nM	No binding detected	
AK081	1.66 nM	489 nM*	N/A
AK109	1.67 nM	No binding detected	118 nM
AK110	0.911 nM	No binding detected	195 nM

AK111	0.4 nM	No binding detected	235 nM
AK112	0.724 nM	No binding detected	No binding detected
AK113	No binding detected	191 nM	74.3 nM
AK114	No binding detected	10.2 nM	13.8 nM
AK168	No binding detected	Not determined	175 nM
AK215	No binding detected		
AK216	No binding detected		
AK217	1.9 nM		
AK218	Weak binding		
AK219	Weak binding		
AK220	Weak or no binding detected		
AK221	Weak binding		
AK222	Weak or no binding detected		
AK223	No binding detected		
AK224	No binding detected		

Cleavage

[0614] The cleavage rate of the masked IL-2 polypeptide constructs is assessed by conducting receptor-binding assays, as described above, after incubation of the masked IL-2 peptide constructs in the presence or absence of a protease, and with the protease, if any, inactivated at various time points, such as by the addition of EDTA. The cleavage rate of the masked IL-15 polypeptide constructs is assessed by conducting receptor-binding assays, as described above, after incubation of the masked IL-15 peptide constructs in the presence or absence of a protease, and with the protease, if any, inactivated at various time points, such as by the addition of EDTA. The cleavage rate is also assessed using reducing and non-reducing polyacrylamide gel electrophoresis (PAGE) and by mass spectrometry whole mass and peptide map analyses. The cleavage rate is also assessed using an ex vivo assay in which the masked IL-2 polypeptide constructs or the masked IL-15 polypeptide constructs are exposed to human, mouse, or cynomolgus monkey peripheral blood lymphocytes, or normal human tissue or human tumor tissue.

[0615] For some protease activation studies, MMP10 was diluted to 50 ng/uL in MMP cleavage buffer and activated with 1mM APMA for 2 h at 37 ºC. 5 µL of protease (250 ng total) of the activated protease was incubated with 1uM of masked cytokine constructs (e.g., masked IL-2 polypeptide constructs) and incubated at 37 degrees for 2 hours. Cleavage was assessed by SDS-PAGE using AnykD™ Criterion™ TGX Stain-Free™ Protein Gels. A similar approach is taken to test cleavage by other proteases.

[0616] FIG. 11A depicts an exemplary structure of a masked IL-2 polypeptide prior to (left) and after (right) cleavage by a protease, such as a protease associated with the tumor environment. FIG. 11B depicts SDS-PAGE analysis of an exemplary masked IL-2 polypeptide construct that was incubated in the absence (left lane) or presence (right lane) of the MMP10 protease.

Proliferation

[0617] Proliferation of IL-2 and IL-15 responsive tissue culture cell lines, such as CTLL2, YT, TF1B, LGL, HH, and CT6, following treatment with the masked IL-2 polypeptide constructs or the masked IL-15 polypeptide constructs generated in Example 1 is assessed. For experiments involving the masked IL-2 polypeptide constructs, cells are plated in 96 well tissue culture plates in media lacking IL-2 for 2-4 hours and then treated with the masked IL-2 polypeptide constructs at various concentrations. For experiments involving the masked IL-15 polypeptide constructs, cells are plated in 96 well tissue culture plates in media lacking IL-15 for 2-4 hours and then treated with the masked IL-15 polypeptide constructs at various concentrations. After incubation at 37 degrees for 24-48 hours, the cell number is determined by the addition of MTS, alamar blue, luciferase, or a similar metabolic detection reagent, and the colorimetric, fluorescent or luciferase readout detected by a plate spectrophotometer reader.

[0618] The proliferation of immune cells following treatment with the masked IL-2 polypeptide constructs or the masked IL-15 polypeptide constructs generated in Example 1 is also assessed. Human, mouse, or cynomolgus peripheral blood mononuclear cells (PBMCs) are treated with the constructs at various concentrations, and the proliferation of cell types, such as Natural Killer (NK) cells, CD8+ T cells, CD4+ T cells, and/or Treg cells, is determined by staining for the particular cell type and analysis via fluorescence activated cell sorting (FACS). In some experiments, some PBMCs are treated with controls for comparison. In some experiments, some PBMCs are treated with aldesleukin as a control for the masked IL-2 polypeptide treatment. In some experiments, the masked IL-2 polypeptide constructs and the masked IL-15 polypeptide constructs are tested in conditions with and without protease cleavage (e.g., activation). In some experiments, the NK cells are stained as CD45+ CD3- CD56+, the CD8+ T cells are stained as CD45+ CD3+ CD8+, the CD4+ T cells are stained as CD45+ CD3+ CD4+ CD25-, and the Treg cells are stained as CD45+ CD3+ CD4+ CD25+ FOXP3+. In some experiments, the PBMCs are treated for a period of five days. In some experiments, the PBMCs are also stained with Ki67, a marker of cell proliferation. In some experiments, the PBMCs are labeled with CFSE (Sigma-Aldrich) prior to treatment and proliferation is measured by determining the extent of CFSE dilution. In some experiments, each construct, as well as aldesleukin and/or other controls, is administered at one or more concentrations, such as one or more concentrations ranging from 0.0001 nM to 500 nM.

STAT5 Activation

[0619] The activation of Signal Transducer and Activator of Transcription 5 (STAT5) following treatment with the masked IL-2 polypeptide constructs or the masked IL-15 polypeptide constructs generated in Example 1 is also assessed. PBMCs are treated with the constructs for a specified period of time and are then immediately fixed to preserve the phosphorylation status of proteins, such as STAT5. In some

experiments, some PBMCs are treated with controls for comparison. In some experiments, some PBMCs are treated with aldesleukin as a control for the masked IL-2 polypeptide treatment. In some experiments, the masked IL-2 polypeptide constructs and the masked IL-15 polypeptide constructs are tested in conditions with and without protease cleavage (e.g., activation). In some experiments, the PBMCs are treated for 10 minutes, 15 minutes, 20 minutes, or 25 minutes. In some experiments, each construct, as well as aldesleukin and/or other controls, is administered at one or more concentrations, such as one or more concentrations ranging from 0.0001 nM to 500 nM. In some experiments, the fixed and permeabilized PBMCs are then stained with an antibody specific for phosphorylated STAT5 (phospho-STAT5) and are analyzed by flow cytometry. In some experiments, total and phosphorylated levels of STAT5 are measured. The phospho-STAT5 status of certain cell types, such as NK cells, CD8+ T cells, CD4+ T cells, and/or Treg cells, is determined by staining for the particular cell type. In some experiments, the NK cells are stained as CD45+ CD3- CD56+, the CD8+ T cells are stained as CD45+ CD3+ CD8+, the CD4+ T cells are stained as CD45+ CD3+ CD4+ CD25-, and the Treg cells are stained as CD45+ CD3+ CD4+ CD25+ FOXP3+.

[0620] The activation of STAT5 in the mouse cell lines, such as CTLL-2 cells, following treatment with the masked IL-2 polypeptide constructs or the masked IL-15 polypeptide constructs generated in Example 1 is also assessed. In some experiments, some CTLL-2 cells are treated with controls for comparison. In some experiments, some CTLL-2 cells are treated with aldesleukin as a control for the masked IL-2 polypeptide treatment. In some experiments, the masked IL-2 polypeptide constructs and the masked IL-15 polypeptide constructs are tested in conditions with and without protease cleavage (e.g., activation). In some experiments, the CTLL-2 cells are treated for 10 minutes, 15 minutes, 20 minutes, or 25 minutes, and are then fixed to preserve the phosphorylation status of proteins, such as STAT5. In some experiments, each construct, as well as aldesleukin and/or other controls, is administered at one or more concentrations. In some experiments, total and phosphorylated levels of STAT5 are measured.

[0621] In some studies, the levels of intracellular STAT5 activation (pSTAT5 signal) induced by IL-2 was determined by the following method. Frozen human PBMCs were thawed in water bath and added to 39 mL pre-warmed media (RPMI1640 medium plus 10% FBS, 1%P/S, 1% NEA), spun and reconstitute in media at 10E6 cells/mL. Cells were plated at 5E5 per well cells in a 96 well plate. IL-2 (e.g., rhIL-2 or an exemplary IL-2-containing polypeptide construct) diluted in medium was added to each well, and incubated at 37 °C for 20 min. Cells were then fix with 200ul/well Fixation buffer (eBiosciences) at 4 °C, overnight. After centrifugation, the fixed cells were resuspended in 200ul cold BD Phosflow buffer and incubated at 4 °C for 30 min. After washing the cells twice, they were treated with Biolegend Human TruStain FcX (2.5 uL in 50 uL total per sample in Staining buffer) for 5 min on ice. Staining antibodies were added; 5ul pSTAT5-APC (pY694, BD), 10ul CD56-BV421 (5.1H11, Biolegend), 10ul CD4-PerCP/Cy5.5 (A161A1, Biolegend),

and 10ul CD3-FITC (UCHT1, Biolegend) and incubated for 30 min, on ice, protected from light. Cells were washed 2 times and resuspended, and analyzed by flow cytometry.

[0622] FIGs. 12A-12D depict the results from STAT5 activation studies, as described above, using the exemplary constructs AK032, AK035, AK041, or rhIL-2 as a control. The levels of STAT5 activation (%) are shown for NK cells, CD8+ T cells, effector T cells (Teff), and regulatory T cells (Treg). The AK032 and AK035 constructs include an IL-2 polypeptide linked to an Fc domain, and the AK041 construct includes an IL-2 polypeptide linked to a CD25 domain and a CD122 domain. As shown, engineered IL-2 polypeptide constructs can, in some embodiments, reduce activation of Treg cells while retaining or enhancing activation of CD8+ T cells and NK cells.

[0623] FIGs. 13A-13C depict the results from STAT5 activation studies, as described above, using the exemplary constructs AK081 and AK032. The AK081 construct with and without prior exposure to MMP10 was tested. An isotype control as well as a no IL-2 negative control was also tested. The levels of STAT5 activation (%) are shown for NK cells, CD8+ T cells, and CD4+ T cells. The AK032 and AK081 constructs include an IL-2 polypeptide linked to an Fc domain, and the AK081 construct includes a cleavable peptide in the linker connecting the IL-2 polypeptide to the Fc domain. As shown, the non-masked monomeric AK081 IL-2 polypeptide construct stimulates STAT5 activation of PBMCs with or without protease activation similarly to the non-masked dimeric AK032 IL-2 polypeptide construct.

[0624] FIGs. 14A-14D depict the results from STAT5 activation studies, as described above, using the exemplary constructs AK081 and AK111, as well as controls that included an rhIL-2 and anti-RSV antibody. A no-treatment control was also tested. The AK111 construct is an exemplary masked IL-2 polypeptide construct that includes a wildtype form of an IL-2 polypeptide (except for a C125A mutation). As shown in FIGs. 14A-14C, the masked IL-2 polypeptide construct AK111 demonstrated reduced STAT5 activation as compared to the non-masked IL-2 polypeptide construct AK081. FIG. 14D provides EC50 (pM) and fold-change data for the AK081, AK111 constructs, as well as the rhIL-2 control.

[0625] FIGs. 15A-15D depict the results from STAT5 activation studies, as described above, using the exemplary constructs AK167 and AK168, as well as controls that included an rhIL-2 and anti-RSV antibody. A no-treatment control was also tested. The AK168 construct is an exemplary masked IL-2 polypeptide construct that includes a mutant form of an IL-2 polypeptide that eliminates or reduces CD25 binding. The AK167 construct is a parental, non-masked form of the AK168 construct that includes the same mutant IL-2 polypeptide. As shown in FIGs. 15A-15C, the non-masked AK167 construct demonstrated reduced STAT5 activation as compared to the rhIL-2 control, and the masked IL-2 polypeptide construct AK168 did not induce detectable STAT5 activation. FIG. 15D provides EC50 (pM) and fold-change data for the AK167,

AK168 constructs, as well as the rhIL-2 control. The EC50 of the AK168 construct was non-detectable (n.d.).

[0626] FIGs. 16A-16D depict the results from STAT5 activation studies, as described above, using the exemplary constructs AK165 and AK166, as well as an isotype control and an IL-2-Fc control, that were (+ MMP10) or were not previously exposed to the MMP10 protease. The AK166 construct is an exemplary masked IL-2 polypeptide construct that includes a wildtype form of an IL-2 polypeptide (except for a C125A mutation). The AK165 construct is a parental, non-masked form of the AK166 construct that includes the same IL-2 polypeptide. The key as shown in FIG. 16A also applies to FIG. 16B, and the key as shown in FIG. 16C also applies to FIG. 16D. As shown in FIGs. 16A-16D, STAT5 activation was greatly diminished for the masked AK166 construct (without protease cleavage), but was restored to levels resembling the IL2-Fc control following exposure to the activating protease MMP10.

[0627] FIGs. 17A-17C depict the results from STAT5 activation studies, as described above, using the exemplary constructs AK109 and AK110, as well as an isotype control and an IL-2-Fc control, that were (+ MMP10) or were not previously exposed to the MMP10 protease. The AK109 and AK110 construct are exemplary masked IL-2 polypeptide constructs that include half-life extension domains having different heterodimerization mutations. The key as shown in FIG. 17B also applies to FIG. 17A. As shown in FIGs. 17A-17C, STAT5 activation was greatly diminished for the masked AK109 and AK110 construct (without protease cleavage), but was greatly increased to levels approaching the IL2-Fc control following exposure to the activating protease MMP10.

[0628] FIGs. 18A-18D depict the results from STAT5 activation studies, as described above, using the constructs AK211, AK235, AK253, AK306, AK310, AK314, and AK316, as well as an an rhIL-2 control. This includes constructs that are parental, non-masked constructs (AK235, AK253, AK306, AK310, AK314) that include various mutations that modulate CD25 binding. FIG. 18D provides EC50 data for each of the tested constructs as well as the rhIL-2 control.

[0629] FIGs. 19A-19D depict the results from STAT5 activation studies, as described above, using the constructs AK081, AK167, AK216, AK218, AK219, AK220, and AK223 that have been activated by protease, as well as an an rhIL-2 control. A no-treatment control was also tested. This includes masked IL-2 polypeptide constructs (AK216, AK218, AK219, AK220, and AK223) that include various mutations that modulate CD25 binding. The constructs were previously exposed to an activating protease prior to testing their ability to activate STAT5. FIG. 19D provides EC50 data for each of the tested constructs as well as the rhIL-2 control.

[0630] FIGs. 20A-20C depict the results from STAT5 activation studies, as described above, using the constructs AK081, AK189, AK190, and AK210, as well as an an anti-RSV control. This includes masked

IL-2 polypeptide constructs (AK189, AK190, AK210) that include an IL-2 polypeptide having a C125A mutation and include the same cleavable peptide sequence (RAAAVKSP; SEQ ID NO: 121) but having different linker sequences due to differences in the amino acid residues on the N-terminus of the protease cleavage sequence. The key as shown in FIG. 20A also applies to FIGs. 20B and 20C.

[0631] FIGs. 21A-21C depict the results from STAT5 activation studies, as described above, using the constructs AK167, AK191, AK192, and AK193, as well as an an anti-RSV control. This includes masked IL-2 polypeptide constructs (AK189, AK190, AK210) that include an IL-2 polypeptide having R38A, F42A, Y45A, E62A, and C125A mutations and include the same cleavable peptide sequence (RAAAVKSP; SEQ ID NO: 121) but having different linker sequences due to differences in the amino acid residues on the N-terminus of the protease cleavage sequence. The key as shown in FIG. 21A also applies to FIGs. 20B and 20C.

Example 3: In vivo characterization of masked IL-2 and IL-15 polypeptides

Pharmacokinetics

[0632] The pharmacokinetics of the masked IL-2 polypeptide constructs and the masked IL-15 polypeptide constructs generated in Example 1 is assessed in vivo using mouse models.

[0633] Mice are treated intravenously or subcutaneously with the constructs and the concentration of the construct in the plasma is measured over time. In some experiments, some mice are treated with controls for comparison. In some experiments, some mice are treated with aldesleukin as a control for masked IL-2 polypeptide treatment. In some experiments, the mice that are treated have tumors. In some experiments, the mice that are treated are tumor-free. In some experiments, mice are treated with the constructs and blood is drawn at various times over the course of treatment, which may include drawing blood prior to the initiation of treatment and processing it to obtain plasma. In some experiments, blood is drawn at various time points over the course of two weeks, three weeks, or four weeks or more of treatment. In some experiments, the mean plasma concentration of the administered constructs, as well as aldesleukin and/or other controls, is measured. Masked IL-2 polypeptide constructs are detected in the plasma samples after dilution into PBS Tween with IL-2- and human Fc-specific ELISAs and are quantified using a standard curve generated for each construct. Masked IL-15 polypeptide constructs are detected in the plasma samples after dilution into PBS Tween with IL-15- and human Fc-specific ELISAs and are quantified using a standard curve generated for each construct. The percentage of full length and cleaved constructs is determined by western blot with anti-huFc-HRP and anti-huIL-2-HRP and by whole mass and peptide mass spectrometry.

[0634] The pharmacokinetics of the masked IL-2 polypeptide constructs and the masked IL-15 polypeptide constructs in tumors is also assessed in vivo using mouse models. Mice having tumors are

treated intravenously or subcutaneously with the constructs and the concentration of the construct in tumors of the mice is assessed. In some experiments, some mice are treated with controls for comparison. In some experiments, some mice are treated with aldesleukin as a control for masked IL-2 polypeptide treatment. Tumors are analyzed for the presence of the constructs as well as the presence of particular proteases. In some experiments, the tumors are analyzed for the presence and percentage of full length and cleaved constructs.

[0635] Some pharmacokinetic studies were carried out according to the following method. C57BL/6 female mice were purchased from Charles River Laboratories and were 8-10 weeks old at the start of study. MC38 tumor cells (5 x10^5 cells per mouse) were injected subcutaneously into the right flank of each mouse. Upon reaching ~100 mm^3 sized tumors (day 0), the mice received a single 2 mg/kg intravenous dose of the construct of interest (e.g., a non-masked parental IL-2 polypeptide construct, a masked IL-2 polypeptide construct, or a non-cleavable masked IL-2 polypeptide construct) in PBS. Constructs tested include, for instance, AK032, AK081, AK111, AK167, AK168, AK191, AK197, AK203, AK209, and AK211. Plasma were collected at 5 min, days 1, 2 and 5 after dosing. Drug levels were determined using ELISAs utilizing anti-human IgG (clone M1310G05, Biolegend) as the capture antibody and various detection antibodies. HRP or biotin conjugated detection antibodies against human IgG (ab97225, Abcam) or CD122 (clone 9A2, Ancell) and IL-2 (Poly5176, Biolegend) were utilized to detect total and non-cleaved drug levels, respectively.

[0636] FIGs. 23A-23D describe results from pharmacokinetic studies carried out, as described above, in tumor-bearing mice using the constructs AK032, AK081, AK111, AK167, and AK168, as well as an anti-RSV control. FIG. 23A provides a simplistic depiction of the structure of each of the constucts tested. As indicated, AK111 and AK168 are exemplary masked IL-2 polypeptide constructs. The AK167 and AK168 constructs include mutations (R38A, F42A, Y45A, and E62A) that eliminate or reduce binding to CD25. FIG. 23B shows Fc levels in plasma (µg/mL) by detecting human IgG, FIG. 23C shows Fc-CD122 levels in plasma (µg/mL) by detecting human CD122, and FIG. 23D shows Fc-IL2 levels in plasma (µg/mL) by detecting human IL-2.

[0637] FIGs. 24A-24D describe results from pharmacokinetic studies carried out, as described above, in tumor-bearing mice using the constructs AK167, AK191 AK197, AK203, AK209, and AK211, as well as an anti-RSV control. FIG. 24A provides a simplistic depiction of the structure of each of the constucts tested. As indicated, AK168, AK191, AK197, AK203, and AK209 are exemplary masked IL-2 polypeptide constructs that each include a different cleavable peptide sequence in the linker connecting the IL-2 polypeptide to the half-life extension domain. FIG. 24B shows Fc levels in plasma (µg/mL) by detecting human IgG, FIG. 24C shows Fc-IL2 levels in plasma (µg/mL) by detecting human IL-2, and FIG. 24D

shows Fc-CD122 levels in plasma (μg/mL) by detecting human CD122. As shown in FIGs. 24B, 24C, and 24D, the Fc levels, Fc-IL2 levels, and Fc-CD122 levels in the plasma are similar among the masked IL-2 polypeptide constructs tested.

Bioactivity in mice

[0638] The in vivo bioactivity of the masked IL-2 polypeptide constructs and the masked IL-15 polypeptide constructs generated in Example 1 is assessed in vivo using mouse models, such as C57BL/6 mice. Mice are treated with the constructs and in vivo bioactivity is assessed. In some experiments, some mice are treated with controls for comparison. In some experiments, some mice are treated with aldesleukin as a control for masked IL-2 polypeptide treatment. In some experiments, the mice that are treated have tumors. In some experiments, the mice that are treated are tumor-free. In some experiments, the dose-dependent expansion of immune cells is assessed in the mice. In some experiments, the mice are treated with various doses of a construct, aldesleukin, or other control. In some experiments, the mice are treated over the course of two weeks. Blood is collected from the mice at various time points and is then stained using antibodies to immune cell markers of interest. In some experiments, the longitudinal kinetics of the proliferation and expansion of certain circulating cell types, such as CD8+ T cells, NK cells,, and Treg cells, is also determined, as well as the ratio of CD8+ T cells and NK cells to CD4+ CD25+ FoxP3+ Treg cells. In some experiments, the mice are assessed for vascular leakage, such as by assessing for edema and lymphocyte infiltration in certain organs like the lung and liver as determined by organ wet weight and histology.

[0639] In some studies, vascular leakage was assessed in order to assess potential toxicity-related effects mediated by IL-2 based therapies by performing the following method. Repeated dose toxicity studies were conducted using C57BL/6 female mice that were purchased from Charles River Laboratories and were 8-10 weeks old weighing 18-22 grams at the start of study. Groups of 5 mice received daily intraperitoneal injections of masked and non-masked IL-2 constructs in PBS daily for 4 or 5 days. The constructs tested included AK081, AK111, AK167, and AK168. A control antibody was also administered as a control. Two hours after the last dose, all mice received an intravenous injection of 0.1 ml of 1% Evans blue (Sigma, cat# E2129) in PBS. Two hours after Evans blue administration, mice were anesthetized and perfused with 10 U/ml heparin in PBS. Spleen, lung and liver were harvested and fixed in 3 ml of 4% PFA 2 days at 4°C prior to measuring the absorbance of the supernatant at 650 nm with NanoDrop OneC (Thermo Fisher Scientific, Waltham, MA) as an indicator of vascular leak of Evans blue. Fixed organs were embedded in paraffin, sectioned, and stained with hematoxylin and eosin. Histopathological studies and quantification were carried out by NovoVita Histopath Laboratory, LLC. (Allston, MA) according to standard procedures. FIGs. 30A-

30D depict results from an in vivo study as described above for assessing vascular leakage using the exemplary masked IL-2 polypeptide constructs AK111 and AK168, as well as the non-masked IL-2 polypeptide constructs AK081 and AK167, and an anti-RSV control. FIG.30A shows the percentage (%) of body weight loss, and FIGs. 30B, 30C, and 30D shows the weight in grams of the liver, lung, and spleen, respectively, for each.

[0640] Vascular leakage as indicated by measuring the extent of dye leakage into tissues was also assessed for the AK081, AK111, AK167, and AK168 constructs, along with an anti-RSV control, with results shown in FIGs. 31A and 31B for the liver and lung, respectively. The extent of dye leakage was measured based on absorbance at 650nm.

[0641] Vascular leakage as indicated by measuring the extent of mononuclear cell perivascular invasion into the liver and lung was also assessed for the AK081, AK111, AK167, and AK168 constructs, along with an anti-RSV control, with results shown in FIGs. 32A and 32B for the liver and lung, respectively. The average number of mononuclear cells in the liver (FIG. 32A) and the average number of mononuclear cells in the lung (FIG. 32B) depicted for each. As shown in FIG. 32B, for instance, the masked IL-2 polypeptide constructs AK111 and AK168 did not result in a detectable number of mononuclear cells in the lung, unlike the non-masked constructs AK081 and AK167.

Infiltrating Immune Cell Phenotype

[0642] The phenotype of immune cells infiltrating tumors in vivo in mouse models treated with the masked IL-2 polypeptide constructs or the masked IL-15 polypeptide constructs generated in Example 1 is assessed. Mice are treated with the constructs and the phenotype of tumor-infiltrating immune cells is assessed. In some experiments, some mice are treated with controls for comparison. In some experiments, some mice are treated with aldesleukin as a control for masked IL-2 polypeptide treatment. Mice bearing tumors are treated with a construct, aldesleukin, or another control, and tumors, tissues such as liver, lung, and spleen, and blood, are collected at various time points following the initial dose, such as five days, seven days, or ten days after the initial dose. In some experiments, immune cells are isolated from the tumors, tissues, and blood, and are subject to phenotypic assessment using flow cytometry. In some experiments, the isolated immune cells are assessed using markers of interest, such as those for CD8+ T cells, Memory CD8+ T cells, activated NK cells, CD4+ T cells, and CD4+ Treg cells.

[0643] In some studies, the phenotype of immune cells infiltrating tumors in vivo was assessed using the following method. C57BL/6 female mice were purchased from Charles River Laboratories and were 8-10 weeks old at the start of study. MC38 tumor cells (5 $x10^5$ cells per mouse) were injected subcutaneously into the right flank of each mouse. Upon reaching ~100 mm^3 sized tumors (day 0), the mice received a

single 2 mg/kg intravenous dose of the construct of interest (e.g., a non-masked parental IL-2 polypeptide construct, a masked IL-2 polypeptide construct, or a non-cleavable masked IL-2 polypeptide construct) in PBS. On day 5, mice were euthanized by CO2 asphyxiation and tumors, livers, spleens and blood were harvested. Cell suspensions were prepared from spleens by mechanical disruption and and passing through a 40 μm cell strainer. The tumor tissues were enzymatically digested using Miltenyi Tumor Dissociation Kit reagents (Miltenyi cat# 130-096-730) and the gentleMACS Dissociator (Miltenyi) was used for the mechanical dissociation steps. Red blood cells in the spleen and tumor cell suspensions and blood were lysed using ACK buffer (Gibco cat# A10492). The cell suspensions were stained with the following antibodies: CD45 (clone 30-F11, eBioscience), CD3 (clone 2C11, Biolegend), CD8 (clone 53-6.7, BD Biosciences), CD4 (clone RM-45, BD Biosciences), FOXP3 (MF-14, Biolegend), CD25 (3C7, Biolegend), CD44 (clone IM7, eBioscience), and NKp46 (29A1.4, eBioscience). Data acquisition was carried out on the MACSQuant Analyzer flow cytometer (Milenyi) and data were analyzed using the FlowJo.

[0644] Results from studies testing the in vivo responses of CD4, CD8, NK, and Treg percentages in spleen, blood, and tumor, as carried out as described above, using the AK032, AK081, AK111, AK167, and AK168 constructs, as well as an anti-RSV IgG control, are shown in FIGs. 25A-25L. AK111 and AK168 are exemplary masked IL-2 polypeptide constructs.

[0645] Results from studies testing the in vivo responses of CD4, CD8, NK, and Treg percentages in spleen, blood, and tumor, as carried out as described above, using the AK167, AK168, AK191, AK197, AK203, AK209, and AK211 constructs, as well as an anti-RSV IgG control, are shown in FIGs. 26A-26L. AK168, AK191, AK197, AK203, and AK209 are exemplary masked IL-2 polypeptide constructs that each include a different cleavable peptide sequence in the linker connecting the IL-2 polypeptide to the half-life extension domain. Statistical analysis was performed using One-way ANOVA as compared to the non-cleavable AK211 construct.

[0646] Results from studies testing the in vivo responses of CD4, CD8, NK, and Treg percentages in spleen, blood, and tumor, as carried out as described above, using the AK235, AK191, AK192, AK193, AK210, AK189, AK190, and AK211 constructs are shown in FIGs. 27A-27L. AK191, AK192, AK193, AK210, AK189, and AK190 are exemplary masked IL-2 polypeptide constructs that each include a cleavable peptide sequence in the linker connecting the IL-2 polypeptide to the half-life extension domain. The linker sequence also differs among these constructs, depending on the linker sequence utilized. AK189, AK190, and AK210 include an IL-2 polypeptide having a C125A mutation, and AK191, AK192, and AK193 include an IL-2 polypeptide having C125A, R38A, F42A, Y45A, and E62A mutations. The AK235 construct is a non-masked construct and the AK211 construct includes a non-cleavable linker sequence. Statistical analysis was performed using One-way ANOVA as compared to the non-cleavable AK211 construct.

[0647] Results from studies testing the in vivo T cell activation in spleen, blood, and tumor, as carried out as described above, using the AK235, AK191, AK192, AK193, AK210, AK189, AK190, and AK211 constructs, as described above, are shown in FIGs. 28A-28I. T cell activation was measured as the mean fluorescence intensity (MFI) of CD25 in CD8+ T cells, CD4+ T cells, or Foxp3+ cells in the spleen, blood, and tumor. Statistical analysis was performed using One-way ANOVA as compared to the non-cleavable AK211 construct.

In Vivo Cleavage

[0648] The in vivo cleavage of masked cytokine constructs (e.g., masked IL-2 polypeptide constructs or masked IL-15 polypeptide constructs) is assessed. In some studies, a control antibody is administered for comparison. In some studies, in vivo cleavage is assessed by administering the construct of interest in a mouse and, after a certain period of time, capturing human IgG and then measuring the levels of, e.g., human IgG, CD122, and IL-2 or IL-15.

[0649] In some studies testing the in vivo cleavage of masked IL-2 polypeptide constructs, drug levels (i.e., levels of the administered construct, including cleavage byproducts) were determined using ELISAs utilizing anti-human IgG (clone M1310G05, Biolegend) as the capture antibody and various detection antibodies. HRP or biotin conjugated detection antibodies against human IgG (ab97225, Abcam) or CD122 (clone 9A2, Ancell) and IL-2 (Poly5176, Biolegend) were utilized to detect total and non-cleaved drug levels, respectively. The concentrations of cleaved and released IL-2 is calculated by subtracting non-cleaved (i.e., intact) from total drug concentrations. FIGs. 29A-29D depict the results from studies testing the in vivo cleavage of the exemplary masked IL-2 polypeptide constructs AK168 (cleavable peptide sequence: MPYDLYHP; SEQ ID NO: 96) and AK209 (cleavable peptide sequence: VPLSLY; SEQ ID NO: 135). The AK167 construct is a cleavable non-masked IL-2 polypeptide construct that includes the same IL-2 polypeptide as the masked AK168 construct. As shown in FIGs. 29B-29D, both the masked (AK168 and AK209) and non-masked (AK167) constructs were effectively cleaved, and both cleavable peptide sequences were cleaved. FIG. 29E depicts results from a pharmacokinetic study of total plasma IgG concentration (μg/mL) for total levels of the AK167, AK168, and AK209 constructs, and for levels of non-cleaved forms of each construct.

Tumor Eradication and Inhibition of Metastasis

[0650] The ability of the masked IL-2 polypeptide constructs and the masked IL-15 polypeptide constructs generated in Example 1 to promote tumor eradication and to inhibit metastasis is assessed in vivo using mouse models, such as syngeneic MC38, CT26, and B16F10 tumor models.

[0651] Mice are implanted with tumor cells subcutaneously, and tumors are allowed to grow to a palpable size. Tumor-bearing mice are treated with the masked IL-2 constructs or the masked IL-15 polypeptide constructs and tumor volume is measured over the course of treatment. In some experiments, some mice are treated with controls for comparison. In some experiments, some mice are treated with aldesleukin as a control for masked IL-2 polypeptide treatment. Tumor volume is measured periodically over the course of treatment. In some experiments, body weight is also measured periodically over the course of treatment. In some experiments, plasma samples are produced over the course of the treatment and analyzed for pharmacokinetics, pharmacodynamics, cleavage, and blood markers, such as those for CD8+ T cells, Memory CD8+ T cells, activated NK cells, CD4+ T cells, and CD4+ Treg cells.

[0652] The capability of the masked IL-2 polypeptide constructs and the masked IL-15 polypeptide constructs to inhibit metastasis is also assessed in vivo using mouse models suitable for metastasis studies, such as syngeneic CT26 tumor models for assessing lung metastasis. Mice are implanted with tumor cells subcutaneously. In some experiments, tumors are allowed to grow to a palpable size prior to treatment. In some experiments, treatment begins before tumors grow to palpable size. Tumor-bearing mice are treated with the masked IL-2 constructs or the masked IL-15 polypeptide constructs and are assessed for tumor cell metastasis into tissues such as lungs, liver, and lymph nodes.

[0653] In some studies, a syngeneic tumor model was used to assess the ability of masked IL-2 polypeptide constructs to reduce tumor volume in accordance with the following method. C57BL/6 female mice were purchased from Charles River Laboratories and were 8-10 weeks old at the start of study. MC38 tumor cells (5 x105 cells per mouse) were injected subcutaneously into the right flank of each mouse. Upon reaching ~125 mm3 sized tumors (day 0), the mice were randomized to receive 2 mg/kg doses of AK081, AK111, AK167, or AK168, or an anti-RSV antibody as a control, in PBS. Mice were dosed intraperitoneally, three times a week for 6 doses. Tumor volume was calculated (Length*(Width^2)/2) using dial calipers and body weights were recorded twice weekly. FIGs. 33A and 33B show results from a syngeneic tumor model study that assessed tumor volume and body weight over the course of treatment. As shown in FIG. 33A, treatment using exemplary IL-2 polypeptide constructs, including the masked constructs AK111 and AK168, resulted in tumor growth inhibition over time as compared to the anti-RSV control. As shown in FIG. 33B, there was a general lack of body weight reduction observed when the mice were treated with the masked constructs AK111 and AK168.

Bioactivity in cynomolgus monkeys

[0654] The in vivo bioactivity of the masked IL-2 polypeptide constructs and the masked IL-15 polypeptide constructs generated in Example 1 is assessed in vivo in cynomolgus monkeys. Cynomolgus

monkeys are treated with the constructs and in vivo bioactivity, pharmacokinetics, and cleavage is assessed. In some experiments, some monkeys are treated with controls for comparison. In some experiments, some monkeys are treated with aldesleukin as a control for masked IL-2 polypeptide treatment. In some experiments, the monkeys are treated with various doses of the construct, aldesluekin, or other control. Blood is collected from the monkeys at various time points and is then evaluated for certain cell types, such as CD8+ T cells, Memory CD8+ T cells, activated NK cells, CD4+ T cells, and CD4+ Treg cells, and/or markers of interest, such as for the dose-response of total lymphocytes, Ki67+, and of soluble CD25. In some experiments, the longitudinal kinetics of the proliferation and expansion of certain circulating T and NK cell types is assessed. In some experiments, pharmacokinetics and cleavage of the masked IL-2 polypeptide constructs and the masked IL-15 polypeptide constructs are determined by ELISA, PAGE, and mass spectrometry.

[0655] To test the safety profile of exemplary masked IL-2 polypeptide constructs in non-human primates, a dose ranging study is performed in accordance with the following method. Groups of 3 healthy male cynomolgus monkeys (Macaca fascicularis) are randomly assigned to receive a single intravenous bolus dose of 2 mL/kg of activatable (i.e., cleavable) masked IL-2 polypeptide proteins or non-cleavable masked IL-2 polypeptide proteins at 10, 30 and 100 nmol/kg in 100 mM sodium citrate buffer (pH 5.5). A third group receives the parental non-masked, cleavable protein at 3, 10 and 30 nmol/kg as a positive control. This third group is dosed at a lower range to account for higher potency of the parental non-masked molecules. Doses are calculated in moles to account for differences in molecular weight. Blood samples are collected before dosing and 1, 24, 48, 72, 96, 168, 264 and 336 hours post-dosing. An automated hematology analyzer is used to monitor changes in lymphocyte subsets and serum chemistry. Total and intact (i.e., non-cleaved) drug levels are measured from plasma using custom ELISA as described above. Soluble CD25 levels are measured with an ELISA (R&D systems, cat# DR2A00) to monitor immune stimulation. Plasma levels of inflammatory cytokines are quantified using custom multiplexed electrochemiluminescence assay (Meso Scale Discovery). Blood pressure is monitored as an indicator of vascular leak syndrome. PK is analyzed using an ELISA that captures IL-2 and detects human Fc and by an ELISA that captures human Fc and detects human Fc.

[0656] The present invention is not intended to be limited in scope to the particular disclosed embodiments, which are provided, for example, to illustrate various aspects of the invention. Various modifications to the compositions and methods described will become apparent from the description and teachings herein. Such variations may be practiced without departing from the true scope and spirit of the disclosure and are intended to fall within the scope of the present disclosure.

IX. SEQUENCES

SEQ ID	AMINO ACID SEQUENCE
1	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLE EELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWI TFAQSIISTLT
2	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLE EELKPLEEVLNLAQSKNFHFDPRDVVSNINVFVLELKGSETTFMCEYADETATIVEFLNR WITFAQSIISTLT
3	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTAMLTAKFAMPKKATELKHLQCLE EALKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWI TFAQSIISTLT
4	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTKKFYMPKKATELKHLQCLE EELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWI TFAQSIISTLT
5	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFAFAMPKKATELKHLQCLE EELKPLEEVLNGAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWI TFAQSIISTLT
6	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTAMLTAKFAMPKKATELKHLQCLE EALKPLEEVLNLAQSKNFHFDPRDVVSNINVFVLELKGSETTFMCEYADETATIVEFLNR WITFAQSIISTLT
7	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTKKFYMPKKATELKHLQCLE EELKPLEEVLNLAQSKNFHFDPRDVVSNINVFVLELKGSETTFMCEYADETATIVEFLNR WITFAQSIISTLT
8	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTAKFAMPKKATELKHLQCLE EELKPLEEVLNGAQSKNFHFDPRDVVSNINVFVLELKGSETTFMCEYADETATIVEFLNR WITFAQSIISTLT
9	ELCDDDPPEIPHATFKAMAYKEGTMLNCECKRGFRRIKSGSLYMLCTGNSSHSSWDNQC QCTSSATRNTTKQVTPQPEEQKERKTTEMQSPMQPVDQASLPGHCREPPPWENEATERIY HFVVGQMVYYQCVQGYRALHRGPAESVCKMTHGKTRWTQPQLICT
10	AVNGTSQFTCFYNSRANISCVWSQDGALQDTSCQVHAWPDRRRWNQTCELLPVSQASW ACNLILGAPDSQKLTTVDIVTLRVLCREGVRWRVMAIQDFKPFENLRLMAPISLQVVHVE THRCNISWEISQASHYFERHLEFEARTLSPGHTWEEAPLLTLKQKQEWICLETLTPDTQYE FQVRVKPLQ
11	GGSSPPMPYDLYHPSGP
12	GSPMPYDLYHP
13	GSPPMPYDLYHPSGP
14	GSPSMPYDLYHPSGP
15	GPPSGSSPMPYDLYHPSGGG
16	GSSGGPPGGMPYDLYHPSGGG
17	SGSPSGSGGGMPYDLYHPSGGG
18	GPPGPPGSSGMPYDLYHPSGGG
19	GSSSGPPGPPSMPYDLYHPSGGG
20	PA

SEQ ID	AMINO ACID SEQUENCE
21	GGGGSGGGGSGGGGS
22	PSGPSAGGAA
23	GGPPASAGS
24	GSPPAGGAP
25	GPGSGSGGAA
26	GGGGSGGGGS
27	GGGGSGGGGSGGGGSGGGGS
28	PGSGS
29	GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
30	GGGGSGGGGSGGGGSGGGGSGGGGS
31	GGGGSGGGGSGGGGSGGGGSGGGGSGGGGS
32	GGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGS
33	GGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGS
34	GGSSPP
35	SGP
36	GSP
37	GSPP
38	GSPS
39	GPPSGSSP
40	GSSGGPPGG
41	SGSPSGSGGG
42	GPPGPPGSSG
43	SGGG
44	GSSSGPPGPPS
45	GGS
46	GGGSSGGS
47	GGSGG
48	GGGS
49	GS
50	GSGGGSSGGS
51	GSSGGS
52	GGGSSGGSG
53	GGSAGGS
54	GHS
55	GPS
56	GAS
57	SGG
58	SGGSGG
59	SSG
60	GGGSGG
61	GG
62	GGG
63	SHGG
64	HGGG
65	SGAA
66	SGPA

SEQ ID	AMINO ACID SEQUENCE
67	GGSGGS
68	GGSGGP
69	GGSGGG
70	GSGGPGPS
71	SGPPGSS
72	SSGGSGP
73	SSPSPSGG
74	SPGGSS
75	GGPGSSP
76	SGPPGGPSS
77	GPGPGSPPGGSS
78	SGPP
79	PGSPSSS
80	PSPGGPS
81	GGPPS
82	PSPPSS
83	SGGPGP
84	GPSPGS
85	GSPGPSP
86	PSSGGSS
87	SGSSGP
88	GGSSSPP
89	GSPGSP
90	PPPS
91	APPPS
92	AAPPPS
93	SAPPPS
94	SSGP
95	SSPGP
96	MPYDLYHP
97	GGIGQLTA
98	DLGRFQTF
99	DSGGFMLT
100	TSVLMAAP
101	TSEFVFAPDQ
102	KLVLPVLP
103	KPILFFRL
104	ANQLKG
105	QSQLKE
106	HEQLTV
107	PANLVAPDP
108	PAPGVYPGP
109	APAGLIVPYN
110	PQALVA
111	VGNLNF
112	VANLLYE

SEQ ID	AMINO ACID SEQUENCE
113	VYNLMD
114	TFNIKQ
115	DLWKLLP
116	PGSTKRA
117	QQYRALKS
118	YVPRAVL
119	GVNKWPT
120	LAQAVRSS
121	RAAAVKSP
122	DLLAVVAAS
123	VQTVTWPD
124	AIPMSIPP
125	GYEVHHQK
126	VHHQKLVF
127	IRRVSYSF
128	MPYDLYHPILFFRL
129	GGIGQLTSVLMAAP
130	DSGGFMLTLVLPVLP
131	TSEFVFAPDLGRFQTF
132	TSTSGRSANPR
133	TSTSGRSANPG
134	TSTSGRSANPH
135	VPLSLY
136	TSASGASASAA
137	PSSPGGGSSP
138	ISSGLLSGRSDNH
139	ISSGLLSGRSDDH
140	ISSGLLSGRSDIH
141	ISSGLLSGRSDQH
142	ISSGLLSGRSDTH
143	ISSGLLSGRSANP
144	ISSGLLSGRSDNP
145	ISSGLLSGRSANPRG
146	AVGLLAPPGGLSGRSDNH
147	AVGLLAPPGGLSGRSDDH
148	AVGLLAPPGGLSGRSDIH
149	AVGLLAPPGGLSGRSDQH
150	AVGLLAPPGGLSGRSDTH
151	AVGLLAPPGGLSGRSANP
152	AVGLLAPPGGLSGRSDNP
153	AVGLLAPPSGRSANPRG
154	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG

SEQ ID	AMINO ACID SEQUENCE
155	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVCTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLVSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
156	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
157	EIVLTQSPDFQSVTPKEKVTITCSANSALSYMYWYQQKPDQSPKLWVHGTSNLASGVPSR FSGSGSGTDFTLTINSLEAEDAATYYCHHWSNTQWTFGGGTKVEIKRTVAAPSVFIFPPSD EQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLS KADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
158	QVQLVQSGAEVKKPGSSVKVSCKASGYTFTNYFMNWVRQAPGQGLEWMGRVDPEQGR ADYAEKFKKRVTITADKSTSTAYMELSSLRSEDTAVYYCARRAMDNYGFAYWGQGTLV TVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL QSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPDVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPEEKTISKAKGQPREPQVYTLPP SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
159	MYRMQLLSCIALSLALVTNSAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRML TFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSET TFMCEYADETATIVEFLNRWITFCQSIISTLT
160	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLE EELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWI TFCQSIISTLT
161	CGGHQYERRGGC
162	CSGHQYERREGC
163	CGGHYFERHGGC
164	CSGHYFERHEGC
165	CSFHQYERHEGC
166	MRISKPHLRSISIQCYLCLLLNSHFLTEAGIHVFILGCFSAGLPKTEANWVNVISDLKKIEDL IQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLSSN GNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS
167	NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHD TVENLIILANNSLSSNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS
168	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGP SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPGK
169	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA

SEQ ID	AMINO ACID SEQUENCE
	KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
170	TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS KDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
171	DAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPFEDHVKLVNEVTEFAKTCVADESA ENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLPRLVRP EVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLF FAKRYKAAFTECCQAADKAACLLPKLDELRDEGKASSAKQGLKCASLQKFGERAFKAW AV ARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICENQDSISSKLK ECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVGSKDVCKNYAEAKDVFLGMFLYEYA R RHPDYSVVLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFE QLGEYKFQNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDCLSV F LNQLCVLHEKTPVSDRVTKCCTESLVNGRPCFSALEVDETYVPKEFNAETFTFHADICTL SEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKK LV AASQAALGL
172	LAEAKVLANRELDKYGVSDYYKNLINNAKTVEGVKALIDEILAALP
173	DICLPRWGCLW
174	RLIEDICLPRWGCLWEDD
175	DCAWHLGELVWCT
176	NKFRGKYK
177	NARKFYKG
178	FYWHCLDE
179	FYCHWALE
180	FYCHTIDE
181	AQQNAFYQVLNMPNLNADQRNGFIQSLKDDPSQSANVLGEAQKLNDSQAPK
182	ADAQQNKFNKDQQSAFYEILNMPNLNEEQRNGFIQSLKDDPSQSTNVLGEAKKLNESQA PK
183	ADNNFNKEQQNAFYEILNMPNLNEEQRNGFIQSLKDDPSQSANLLAEAKKLNESQAPK
184	ADNKFNKEQQNAFYEILHLPNLNEEQRNGFIQSLKDDPSQSANLLAEAKKLNDAQAPK
185	ADNKFNKEQQNAFYEILHLPNLTEEQRNGFIQSLKDDPSVSKEILAEAKKLNDAQAPK
186	VDNKFNKEQQNAFYEILHLPNLNEEQRNAFIQSLKDDPSQSANLLAEAKKLNDAQAPK
187	QVQLVESGGGVVQPGRSLRLSCAASGFTFSIYGMHWVRQAPGKGLEWVTVIWYDGSNE YYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAREDWLGEADYGMDVWGQG TTVTVSS
188	DIVMTQTPLSSPVTLGQPASISCRSSQSLVHSDGNTYLSWLQQRPGQPPRLLIYKISNRFSG VPDRFSGSGAGTDFTLKISRVEAEDVGVYYCMQATQFPTFGQGTKVEIKR
189	QVQLVESGGGVVQPGRSLRLSCAASGFTFSIYGMHWVRQAPGKGLEWVTVIWYDGSNE YYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDGEQWRGFDYWGQGTTV TVSS
190	DIVMTQTPLSSPVTLGQPASISCRSSQSLVHSDGNTYLSWLQQRPGQPPRLLIYKISNRFSG VPDRFSGSGAGTDFTLKISRVEAEDVGVYYCMQATQFPTFGQGTKVEIKR

SEQ ID	AMINO ACID SEQUENCE
191	QVQLVESGGGVVQPGRSLRLSCAASGFTFSIYGMHWVRQAPGKGLEWVTVIWYDGSNE YYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDQEQWRLAFDYWGQGTT VTVSS
192	DIVMTQTPLSSPVTLGQPASISCRSSQSLVHSDGNTYLSWLQQRPGQPPRLLIYKISNRFSG VPDRFSGSGAGTDFTLKISRVEAEDVGVYYCMQATQFPTFGQGTKVEIKR
193	QVQLVESGGGVVQPGRSLRLSCAASGFTFSIYGMHWVRQAPGKGLEWVTVIWYDGSNE YYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARGAVAGTGRDYYYYGMDV WGQGTTVTVSS
194	DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRAS GVPDRFSGSGSGTDFTLKLSRVEAEDVGVYYCMQALQTPLTFGGGTKVEIKR
195	QVQLVESGGGVVQPGRSLRLSCAASGFTFSIYGMHWVRQAPGKGLEWVTVIWYDGSNE YYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARGSYYDSSGYYYGEDFDYW GQGTTVTVSS
196	DIVMTQTPLSSPVTLGQPASISCRSSQSLVHSDGNTYLSWLQQRPGQPPRLLIYKISNRFSG VPDRFSGSGAGTDFTLKISRVEAEDVGVYYCMQTSQFPTFGQGTKVEIKR
197	QVQLVESGGGVVQPGRSLRLSCAASGFTFSIYGMHWVRQAPGKGLEWVTVIWYDGSNE YYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAREEWELEDYGMDVWGQGT TVTVSS
198	DIVMTQTPLSSPVTLGQPASISCRSSQSLVHSDGNTYLSWLQQRPGQPPRLLIYKISNRFSG VPDRFSGSGAGTDFTLKISRVEAEDVGVYYCMQITQFPTFGQGTKVEIKR
199	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWYDGSNK YYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAREDFDSHYGMDVWGQGTTV TVSS
200	DIVMTQTPLSSPVTLGQPASISCRSSQSLVHSDGNTYLSWLQQRPGQPPRLLIYKISNRFSG VPDRFSGSGAGTDFTLKISRVEAEDVGVYYCMQTTQFPTFGQGTKVEIKR
201	QVQLVESGGGVVQPGRSLRLSCAASGFTFSIYGMHWVRQAPGKGLEWVTVIWYDGSNE YYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDNWGSDAFDIWGQGTTVT VSS
202	DIVMTQTPLSSPVTLGQPASISCRSSQSLVHSDGNTYLSWLQQRPGQPPRLLIYKISNRFSG VPDRFSGSGAGTDFTLKISRVEAEDVGVYYCMQVTQFPTFGQGTKVEIKR
203	QVQLVESGGGVVQPGRSLRLSCAASGFTFSIYGMHWVRQAPGKGLEWVTVIWYDGSNE YYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDDWFGEADYGMDVWGQG TTVTVSS
204	DIVMTQTPLSSPVTLGQPASISCRSSQSLVHSDGNTYLSWLQQRPGQPPRLLIYKISNRFSG VPDRFSGSGAGTDFTLKISRVEAEDVGVYYCMQTTQFPTFGQGTKVEIKR
205	QVQLVESGGGVVQPGRSLRLSCAASGFTFSIYGMHWVRQAPGKGLEWVTVIWYDGSNE YYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARRISITPFDYWGQGTTVTVSS
206	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDR FSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPLTFGGGTKVEIKR
207	EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTR YSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCARQQVAGMLDYWGQGTTVTVSS
208	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDR FSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPLTFGGGTKVEIKR
209	QVQLVESGGGVVQPGRSLRLSCAASGFTFSIYGMHWVRQAPGKGLEWVTVIWYDGSNE YYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDDFWSDYPFDYWGQGTTV TVSS

SEQ ID	AMINO ACID SEQUENCE
210	DIVMTQTPLSSPVTLGQPASISCRSSQSLVHSDGNTYLSWLQQRPGQPPRLLIYKISNRFSG VPDRFSGSGAGTDFTLKISRVEAEDVGVYYCMQTTQFPTFGQGTKVEIKR
211	QVQLVESGGGVVQPGRSLRLSCAASGFTFSIYGMHWVRQAPGKGLEWVTVIWYDGSNE YYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAREEWFGEADYGMDVWGQG TTVTVSS
212	DIVMTQTPLSSPVTLGQPASISCRSSQSLVHSDGNTYLSWLQQRPGQPPRLLIYKISNRFSG VPDRFSGSGAGTDFTLKISRVEAEDVGVYYCMQTTQFPTFGQGTKVEIKR
213	QVQLVESGGGVVQPGRSLRLSCAASGFTFSIYGMHWVRQAPGKGLEWVTVIWYDGSNE YYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARGAVAGTGRDYYYYGMDV WGQGTTVTVSS
214	DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRAS GVPDRFSGSGSGTDFTLKLISRVEAEDVGVYYCMQALQTPLTFGGGTKVEIKR
215	QVQLVESGGGVVQPGRSLRLSCAASGFTFSIYGMHWVRQAPGKGLEWVTVIWYDGSNE YYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARGSYYDSSGYYFGEDFDYW GQGTTVTVSS
216	DIVMTQTPLSSPVTLGQPASISCRSSQSLVHSDGNTYLSWLQQRPGQPPRLLIYKISNRFSG VPDRFSGSGAGTDFTLKISRVEAEDVGVYYCMQVTQFPTFGQGTKVEIKR
217	QVQLVESGGGVVQPGRSLRLSCAASGFTFSIYGMHWVRQAPGKGLEWVTVIWYDGSNE YYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARGTVAGTGRDYYYYGMDV WGQGTTVTVSS
218	DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRAS GVPDRFSGSGSGTDFTLKLISRVEAEDVGVYYCMQALQTPLTFGGGTKVEIKR
219	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDR FSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSHTFGQGTKLEISR
220	EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTR YSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCARGGNWNCFDYWGQGTLVTVSS
221	GMLSLAVNGTSQFTCFYNSRANISCVWSQDGALQDTSCQVHAWPDRRRWNQTCELLPV SQASWACNLILGAPDSQKLTTVDIVTLRVLCREGVRWRVMAIQDFKPFENLRLMAPISLQ VVHVETHRCNISWEISQASHYFERHLEFEARTLSPGHTWEEAPLLTLKQKQEWICLETLTP DTQYEFQVRVKPLQAFRTLTGH
222	QKLTTVDI
223	CQKLTTVDIC
224	SHYFER
225	CSHYFERC
226	AVNGTSQFTCFYNSRANISCVWSQDGALQDTSCQVHAWPDRRRWNQTCELLPVSQASW ACNLILGAPDSQKLTTVDIVTLRVLCREGVRWRVMAIQDF
227	LNTTILTPNGNEDITADFFLTTMPTDSLSVSTLPLPEVQCFVFNVEYMNCTWNSSSEPQPT NLTLHYWYKNSDNDKVQKCSHYLFSEEITSGCQLQKKEIHLYQTFVVQLQDPREPRRQA TQMLKLQNLVIPWAPENLTLHKLSESQLELNWNNRFLN HCLEHLVQYRTDWDHSWTEQSVDYRHKFSL PSVDGQKRYTFRVRSRFNPLCGSAQHWSEW SHPIHWGSNTSKENPFLFALEAV
228	TLPLPEVQCFVFNVEYMNCTWNSSSEPQPTNLTLHYWYKNSDNDKVQKCSHYLFSEEITS GCQLQKKEIHLYQTFVVQLQDPREPRRQATQMLKLQNLVIPWAPENLTLHKLSESQLELN WNNRFLNHCLEHLVQYRTDWDHSWTEQSVDYRHKFSLPSVDGQKRYTFRVRSRFNPLC GSAQHWSEWSHPIHWGSNT

SEQ ID	AMINO ACID SEQUENCE
229	TLPLPEVQCFVFNVEYMNCTWNSSSEPQPTNLTLHYWYKNSDNDKVQKCSHYLFSEEITS GCQLQKKEIHLYQTFVVQLQDPREPRRQATQMLKLQNLVI
230	SSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEEL KPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFC QSIISTLT
231	ELCDDDPPEIPHATFKAMAYKEGTMLNCECKRGFRRIKSGSLYMLCTGNSSHSSWDNQC QCTSSATRNTTKQVTPQPEEQKERKTTEMQSPMQPVDQASLPGHCREPPPWENEATERIY HFVVGQMVYYQCVQGYRALHRGPAESVCKMTHGKTRWTQPQLICTGEMETSQFPGEEK PQASPEGRPESETSCLVTTTDFQIQTEMAATMETS
232	ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPS LKCIRDPALVHQRPAPP
233	ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPS LKCIRDP
234	ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPS LKCIR
235	SGGSGGGGSGGGSGGGGSLQ
236	SGRSA
237	SGRSANA
238	SGRNAQ
239	SGRNAQVR
240	SGRSDN
241	SGRSDNPN
242	GSGKSA
243	APASSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLE EELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWI TFAQSIISTLT
244	APASSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLE EELKPLEEVLNLAQSKNFHFDPRDVVSNINVFVLELKGSETTFMCEYADETATIVEFLNR WITFAQSIISTLT
245	APASSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTAMLTAKFAMPKKATELKHLQCL EEALKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNR WITFAQSIISTLT
246	APASSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTKKFYMPKKATELKHLQCL EEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRW ITFAQSIISTLT
247	APASSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFAFAMPKKATELKHLQCLE EELKPLEEVLNGAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWI TFAQSIISTLT

SEQ ID	AMINO ACID SEQUENCE
248	APASSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTAMLTAKFAMPKKATELKHLQCL EEALKPLEEVLNLAQSKNFHFDPRDVVSNINVFVLELKGSETTFMCEYADETATIVEFLNR WITFAQSIISTLT
249	APASSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTKKFYMPKKATELKHLQCL EEELKPLEEVLNLAQSKNFHFDPRDVVSNINVFVLELKGSETTFMCEYADETATIVEFLNR WITFAQSIISTLT
250	APASSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTAKFAMPKKATELKHLQCL EEELKPLEEVLNGAQSKNFHFDPRDVVSNINVFVLELKGSETTFMCEYADETATIVEFLNR WITFAQSIISTLT
251	APASSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLE EELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWI TFCQSIISTLT
252	EVQLVESGGGLVQPGGSLRLSCAASGFTFRSFGMSWVRQAPGKEPEWVSSISGSGSDTLY ADSVKGRFTISRDNAKTTLYLQMNSLKPEDTAVYYCTIGGSLSRSSQGTQVTVSS
253	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSFGMSWVRQAPGKEPEWVSSISGSGSDTLY ADSVKGRFTISRDNAKTTLYLQMNSLKPEDTAVYYCTIGGSLSRSSQGTQVTVSS
254	EVQLVESGGGLVQPGGSLRLSCAASGFTFRSFGMSWVRQAPGKGLEWVSSISGSGSDTLY ADSVKGRFTISRDNAKTTLYLQMNSLKPEDTA VYYCTIGGSLSRSSQGTQVTVSS
255	EVQLVESGGGLVQPGNSLRLSCAASGFTFRSFGMSWVRQAPGKGLEWVSSISGSGSDTLY ADSVKGRFTISRDNAKTTLYLQMNSLKPEDTAVYYCTIGGSLSRSSQGTLVTVSS
256	EVQLVESGGGLVQPGNSLRLSCAASGFTFRSFGMSWVRQAPGKGLEWVSSISGSGSDTLY ADSVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSRSSQGTLVTVSS
257	EVQLVESGGGLVQPGNSLRLSCAASGFTFSSFGMSWVRQAPGKGLEWVSSISGSGSDTLY ADSVKGRETISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSRSSQGTLVTVSS
258	EVQLVESGGGLVQPGNSLRLSCAASGFTFSSFGMSWVRQAPGKGLEWVSSISGSGSDTLY ADSVKGRETISRDNAKNTLYLQMNSLRPEDTAVYYCTIGGSLSRSSQGTLVTVSS
259	EVQLVESGGGLVQPGNSLRLSCAASGFTFSSFGMSWVRQAPGKGLEWVSSISGSGSDTLY ADSVKGRFTISRDNAKNTLYLQMNSLRPEDTAVYYCTIGGSLSRSGQGTLVTVSS
260	TSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTAMLTAKFAMPKKATELKHLQCLEE ALKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWIT FAQSIISTLT
261	AVNGTSQFTCFYNSRANISCVWSQDGALQDTSCQVHAWPDRRRWNQTCELLPVSQASW ACNLILGAPDSQKLTTVDIVTLRVLCREGVRWRVMAIQDFKPFENLRLMAPISLQVVHVE THRCNISWEISQASHYFERHLEFEARTLSPGHTWEEAPLLTLKQKQEWICLETLTPDTQYE FQVRVKPLQGEFTTWSPWSQPLAFRTKPAALGKD
262	GSGPDSGGFMLTSGPAP
263	GSSPPGDSGGFMLTSGP
264	DSGGFMLTS
265	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVCTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLVSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
266	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPCRDELTKNQVS

SEQ ID	AMINO ACID SEQUENCE
	LWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVF SCSVMHEALHNHYTQKSLSLSPGGSGPDSGGFMLTSGPAPTSSSTKKTQLQLEHLLLDLQ MILNGINNYKNPKLTAMLTAKFAM PKKATELKHLQCLEEALKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEY ADETATIVEFLNRWITFAQSIISTLT
267	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVCTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLVSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGPGSGSAVNGTSQ FTCFYNSRANISCVWSQDGALQDTSCQVHAWPDRRRWNQTCELLPVSQASWACNLILG APDSQKLTTVDIVTLRVLCREGVRWRVMAIQDFKPFENLRLMAPISLQVVHVETHRCNIS WEISQASHYFERHLEFEARTLSPGHTWEEAPLLTLKQKQEWICLETLTPDTQYEFQVRVK PLQGEFTTWSPWSQPLAFRTKPAALGKD
268	GSGP
269	GPAP
270	ISSGLLGGLSGRSDQP
271	ISSGLLSGRSDQG
272	ISSGLLSGRSDQA
273	ISSGLLSGRSDSP
274	ISSGLLSGRSDTP
275	ISSGLLSGRSDMP
276	ISSGLLSGRSD
277	ISSGLLSGRSDQP
278	ISSGLLGGLSGRSDNP
279	ISSGLLSSGGLSGRSDQP
280	ISSGLLSSGGLSGRSDNP
281	ISSGLLSGRS
282	ISSGLLSGRSESP
283	ISSGLLSGRSEQP
284	ISSGLLSGRSEQH
285	LSSGLLSGRSDQP
286	LSSGLLGGLSGRSDQP
287	LSSGLLSGRSDQG
288	LSSGLLSGRSDQA
289	LSSGLLSGRSDSP
290	LSSGLLSGRSDTP
291	LSSGLLSGRSDMP
292	LSSGLLSGRSD
293	GKQLRVVNEYSSMDNMLLG
294	LSSGLLGGLSGRSDNP
295	LSSGLLSSGGLSGRSDQP
296	LSSGLLSSGGLSGRSDNP
297	GKQLRVVNEYSSEDNMLLG
298	LSSGLLSGRSESP
299	LSSGLLSGRSEQP

SEQ ID	AMINO ACID SEQUENCE
300	LSSGLLSGRSEQH
301	MPYDLYH
302	LSGRSDNH
303	GGGSSP
304	SGGP
305	SGPSGSPG
306	GSIPVSLRSG
307	GPSGPAGLKGAPG
308	GPPGPAGMKGLPG
309	GYVADAPK
310	KKLADEPE
311	GGSRPAHLRDSGK
312	SFTQARVVGG
313	VHMPLGFLGPRQARVVN
314	LSGRSDNHSPLGLAGS
315	VPLSLYSG
316	IPESLRAG
317	IPVSLRSG
318	SGSGGSPVPLSLYSGGP
319	GGGSSPVPLSLYSGGP
320	GGSSPPVPLSLYSGPSGSPG
321	GGSGGGSGGGSGGGSGGGSG
322	GGSGGGSGGGSGGGSGGGSGGGSG
323	PGPGP
324	SGGCGGHQYERRGGC
325	SGGCSGHQYERREGC
326	SGGCGGHYFERHGGC
327	SGGCSGHYFERHEGC
328	SGGCSFHQYERHEGC
329	PSGSS
330	GSPG
331	GGSPGG
332	GGPGGP
333	GGSG
334	GSPPGG
335	GPGSPG
336	GSSPPG
337	GGP
338	SGPGSGS
339	GGSSPPGGGSSGGGSGP
340	SGPGSGS
341	SGSGGSP
342	IYDQKT
343	AHNYKT

SEQ ID	AMINO ACID SEQUENCE
344	MMDQAN
345	MLGEFVSE
346	GLVALRGA
347	KEHKYKAE
348	GGSSPPGGGSSGGGSGPGSGS
349	GGSSPPVPLSLYSGPGSGS
350	GNPMGSEPVNFKQLRVVNGGP
351	GNPMGSEPVNFKLLRVVNGGP
352	GNPMGSDPVNFKQLRVVNGGP
353	GNPMGSDPVNFKLLRVVNGGP
354	GGSSPPMPYDLYHPSGPSGSPG
355	GGSSPPGGGSSGGGSGPSGSPG
356	RQARVVG
357	LGGSGRSNAQVRLE
358	LGGSGRKASLSLE
359	SGRIGFLRTA
360	SGAIGFLRTA
361	RPARSGRSAGGSVA
362	VTGRGDSPASS
363	PRFKIIGG
364	LSGRIGFLRTA
365	LSGRSNAMPYDLYHP
366	LSGRSNAGGIGQLTA
367	LSGRSNAVPLSLY
368	LSGRSNADSGGFMLT
369	LSGRSNAHEQLTA
370	LSGRSNARAAAVKSP
371	LSGRSNATSVLMAAP
372	VPLSLYLSGRSNA
373	DSGGFMLTLSGRSNA
374	GGIGQLTALSGRSNA
375	MPYDLYHPLSGRSNA
376	HEQLTVLSGRSNA
377	RAAAVKSPLSGRSNA
378	TSVLMAAPLSGRSNA
379	IPVSLRSGRSNAQRLE
380	VPLSLYRQARVVG
381	DSGGFMLTRQARVVG
382	GGIGQLTARQARVVG
383	MPYDLYHPRQARVVG
384	HEQLTVRQARVVG
385	RAAAVKSPRQARVVG
386	TSVLMAAPRQARVVG
387	KQLRVVNEYSSMDNMLLG
388	KQLRVVNEYSSEDNMLLG
389	KQLRVVNGYSSEDNMLLG

SEQ ID	AMINO ACID SEQUENCE
390	KQLRVVGGLVHLKNTMET
391	TRDRLDEVNFKQLRVVNG
392	TRDRLDEVNFKLLRVVNG
393	TRDRLDPVNFKQLRVVNG
394	TRDRLDPVNFKLLRVVNG
395	NPMGSEPVNFKQLRVVNG
396	NPMGSEPVNFKLLRVVNG
397	NPMGSDPVNFKQLRVVNG
398	NPMGSDPVNFKLLRVVNG
399	TYSRSKYLATA
400	TYSRSRYLATA
401	KQLRVVNEYSSE
402	KQLRVVNGYSSE
403	KQLRVVGGLVAL
404	KQLRVVNGLVAL
405	SPGRVVGGLVAL
406	PQPRTYSRSRYL
407	PQPRTTSRSRYL
408	VVNEYSSSRGPYH
409	VVNEYSSERGPYH
410	NKVSMSSSRGPYH
411	NKVSMSSTRGPYH
412	APAMMRGSVILTV
413	APAMMEGSVILTV
414	RGSVIITVQTVTW
415	RGSVILTVQTVTW
416	GTRDRLDEVNFKQLRVVNGGP
417	GTRDRLDEVNFKLLRVVNGGP
418	GTRDRLDPVNFKQLRVVNGGP
419	GTRDRLDPVNFKLLRVVNGGP
420	RKGKALAAYRLE
421	RKGKAGAAYRLE
422	RQARVVGGLVAL
423	GGVRGPRFKIIGG
424	GGVRGPRVKIIGG
425	VTGRGDSHSLTTN
426	VTGRGDSPSLTTN
427	TGHGQASQGLLDR
428	TGHGQASSGLLDR
429	KQLRVVNENLENY
430	KQLRVVNGNLENY
431	SNVNDVANYNFF
432	SNVNDVSNYNFF
433	IDFNAAQNLYEK
434	IDFNAAYNLYEK
435	IQWNAGQPLQER

SEQ ID	AMINO ACID SEQUENCE
436	IQWNAPQPLQER
437	SMDNRLLGLFGE
438	SMDNMLLGLFGE
439	VPIDDPQDLLEG
440	VPIDDPEDLLEG
441	IPENLPPGLPLT
442	IPENLPPLLPLT
443	QPPSLTKNQVSL
444	QPPSLTRNQVSL
445	DSHSLTKNQVSL
446	DSHSLTTNQVSL
447	KAIQLTKNQVSL
448	KAIQLTYNQVSL
449	AEPWTNRNTDGS
450	AEPWTVRNTDGS
451	KQLRVVNG
452	KQLRVVTGRGDSP
453	KQLRVVNGRGDSP
454	PSSRRRVVRKGVS
455	PSSRRRVNRKGVS
456	SPGRVVTGRGDSP
457	SPGRVVGGRGDSP
458	NSGRAVTGRGDSP
459	NSGRAVTYRGDSP
460	TGHGQPSSRRRVN
461	TGHGQASSRRRVN
462	TGHGQSSSRGPYH
463	TGHGQASSRGPYH
464	RGSVILTKNQVSL
465	RGSVILTVNQVSL
466	SPGRVVGINYWLA
467	SPGRVVGGNYWLA
468	SPGRVVGSNKGAI
469	SPGRVVGGNKGAI
470	PGARGRAPNHAVV
471	PGARGRAFNHAVV
472	PGARGNAFNNLDR
473	PGARGRAFNNLDR
474	VSNKYISNNEQLP
475	VSNKYFSNNEQLP
476	KVSNKALHVTNI
477	KVSNKALPVTNI
478	VTGRGPSPDVPLT
479	VTGRGDSPDVPLT
480	TGHGQRSSNIRTS
481	TGHGQASSNIRTS

SEQ ID	AMINO ACID SEQUENCE
482	TGHGQHSSNIANI
483	TGHGQASSNIANI
484	TGHGQASRNDYSY
485	TGHGQASSNDYSY
486	KALHVTNRNTDGS
487	KALHVTNINTDGS
488	RVVRKKVSNKALP
489	RVVRKGVSNKALP
490	RQARVVGINYWLA
491	RQARVVGGNYWLA
492	GKQLRVVNGYSSEDNMLLGGP
493	GKQLRVVGGLVHLKNTMETGP
494	AGQPKQLRVVNG
495	AGQPLQLRVVNG
496	AGQPLQERVVNG
497	AGQPKQERVVNG
498	GTANKQLRVVNG
499	GTANKQLHVVNG
500	GTANIQLRVVNG
501	GTANIQLHVVNG
502	GKQLRVVNEYSSMDNMLLGGP
503	GKQLRVVNEYSSEDNMLLGGP
504	KQLRTVAGLAGK
505	KQLRTVNGLAGK
506	KQLRVVAGLAGK
507	KQLRVVNGLAGK
508	GIKYKQLRVVNG
509	GIKYKYLRVVNG
510	GIKYLQLRVVNG
511	GIKYLYLRVVNG
512	THLDLTYSRSKYLATA
513	THLDLTPSRSKYLATA
514	THLDLTYSRSRYLATA
515	THLDLTPSRSRYLATA
516	TYSRSKYLAPANGNAE
517	TYSRSKYLATANGNAE
518	TYSRSRYLAPANGNAE
519	TYSRSRYLATANGNAE
520	DPVNFKQLRVVNEYSSE
521	DPVNFKQLRVVNGYSSE
522	DPVNFKKLRVVNEYSSE
523	DPVNFKKLRVVNGYSSE
524	RKGKAGAAKNLNEKDY
525	RKGKAGAAKNLYEKDY
526	RKGKAGAAQNLNEKDY
527	RKGKAGAAQNLYEKDY

SEQ ID	AMINO ACID SEQUENCE
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529	VTGRGDSHSLTTNQVSL
530	VTGRGDSPSLTKNQVSL
531	VTGRGDSPSLTTNQVSL
532	TGHGQASSERSSNIRTS
533	TGHGQASSERSSNSRTS
534	TGHGQASSERSSTIRTS
535	TGHGQASSERSSTSRTS
536	GISSGLLSGRSDQPSGP
537	GGSGISSGLLSGRSDQPSGP
538	DPVNFKLLRVVNEYSSE
539	DPVNFKLLRVVNGYSSE
540	DPVNFKQLRVVGGLVAL
541	DPVNFKQLRVVNGLVAL
542	DPVNFKLLRVVGGLVAL
543	DPVNFKLLRVVNGLVAL
544	KQLRVQNGDSTE
545	KQLRVVNNDATE
546	KQLRVVNGDSTE
547	ISNNKQLRVVNG
548	ISNNKQLPVVNG
549	ISNNEQLRVVNG
550	ISNNEQLPVVNG
551	KVSNKQLRVVNG
552	KVSNKQLPVVNG
553	KVSNKALRVVNG
554	KVSNKALPVVNG
555	KQLRVQNNDATE
556	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGAPTSSSTKKTQLQ LEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLA QSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFAQSIISTLT
557	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGPAELCDDDPPEIP HATFKAMAYKEGTMLNCECKRGFRRIKSGSLYMLCTGNSSHSSWDNQCQCTSSATRNTT KQVTPQPEEQKERKTTEMQSPMQPVDQASLPGHCREPPPWENEATERIYHFVVGQMVYY QCVQGYRALHRGPAESVCKMTHGKTRWTQPQLICTGGGGGGGGGGGGGGGGGGGGGGGG GGGGGGGGGGGGGAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFY MPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCE YADETATIVEFLNRWITFAQSIISTLT
558	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLE EELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWI

SEQ ID	AMINO ACID SEQUENCE
	TFAQSIISTLTGGGGSGGGGSGGGGSELCDDDPPEIPHATFKAMAYKEGTMLNCECKRGF RRIKSGSLYMLCTGNSSHSSWDNQCQCTSSATRNTTKQVTPQPEEQKERKTTEMQSPMQ PVDQASLPGHCREPPPWENEATERIYHFVVGQMVYYQCVQGYRALHRGPAESVCKMTH GKTRWTQPQLICTDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH EDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP G
559	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGAPTSSSTKKTQLQ LEHLLLDLQMILNGINNYKNPKLTAMLTAKFAMPKKATELKHLQCLEEALKPLEEVLNL AQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFAQSIISTLT
560	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGAPTSSSTKKTQLQ LEHLLLDLQMILNGINNYKNPKLTRMLTKKFYMPKKATELKHLQCLEEELKPLEEVLNLA QSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFAQSIISTLT
561	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGAPTSSSTKKTQLQ LEHLLLDLQMILNGINNYKNPKLTRMLTFAFAMPKKATELKHLQCLEEELKPLEEVLNGA QSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFAQSIISTLT
562	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLE EELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWI TFAQSIISTLTPSGPSAGGAAEIVLTQSPDFQSVTPKEKVTITCSANSALSYMYWYQQKPD QSPKLWVHGTSNLASGVPSRFSGSGSGTDFTLTINSLEAEDAATYYCHHWSNTQWTFGG GTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQ ESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
563	ELCDDDPPEIPHATFKAMAYKEGTMLNCECKRGFRRIKSGSLYMLCTGNSSHSSWDNQC QCTSSATRNTTKQVTPQPEEQKERKTTEMQSPMQPVDQASLPGHCREPPPWENEATERIY HFVVGQMVYYQCVQGYRALHRGPAESVCKMTHGKTRWTQPQLICTGGPPASAGSQVQL VQSGAEVKKPGSSVKVSCKASGYTFTNYFMNWVRQAPGQGLEWMGRVDPEQGRADYA EKFKKRVTITADKSTSTAYMELSSLRSEDTAVYYCARRAMDNYGFAYWGQGTLVTVSS ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGP DVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPEEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
564	ELCDDDPPEIPHATFKAMAYKEGTMLNCECKRGFRRIKSGSLYMLCTGNSSHSSWDNQC QCTSSATRNTTKQVTPQPEEQKERKTTEMQSPMQPVDQASLPGHCREPPPWENEATERIY HFVVGQMVYYQCVQGYRALHRGPAESVCKMTHGKTRWTQPQLICTGSPPAGGAPQVQL VQSGAEVKKPGSSVKVSCKASGYTFTNYFMNWVRQAPGQGLEWMGRVDPEQGRADYA

SEQ ID	AMINO ACID SEQUENCE
	EKFKKRVTITADKSTSTAYMELSSLRSEDTAVYYCARRAMDNYGFAYWGQGTLVTVSS ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGP DVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPEEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
565	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLE EELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWI TFAQSIISTLTGPGSGSGGAAEIVLTQSPDFQSVTPKEKVTITCSANSALSYMYWYQQKPD QSPKLWVHGTSNLASGVPSRFSGSGSGTDFTLTINSLEAEDAATYYCHHWSNTQWTFGG GTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQ ESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
566	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGAPTSSSTKKTQLQ LEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLA QSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFAQSIISTLTGPPS GSSPMPYDLYHPSGGGAVNGTSQFTCFYNSRANISCVWSQDGALQDTSCQVHAWPDRR RWNQTCELLPVSQASWACNLILGAPDSQKLTTVDIVTLRVLCREGVRWRVMAIQDFKPF ENLRLMAPISLQVVHVETHRCNISWEISQASHYFERHLEFEARTLSPGHTWEEAPLLTLKQ KQEWICLETLTPDTQYEFQVRVKPLQ
567	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGPAELCDDDPPEIP HATFKAMAYKEGTMLNCECKRGFRRIKSGSLYMLCTGNSSHSSWDNQCQCTSSATRNTT KQVTPQPEEQKERKTTEMQSPMQPVDQASLPGHCREPPPWENEATERIYHFVVGQMVYY QCVQGYRALHRGPAESVCKMTHGKTRWTQPQLICTGGGGGGGGGGGGGGGGGGGG GGGGGGGGGGGGGAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFY MPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCE YADETATIVEFLNRWITFAQSIISTLTGPPSGSSPMPYDLYHPSGGGAVNGTSQFTCFYNSR ANISCVWSQDGALQDTSCQVHAWPDRRRWNQTCELLPVSQASWACNLILGAPDSQKLT TVDIVTLRVLCREGVRWRVMAIQDFKPFENLRLMAPISLQVVHVETHRCNISWEISQASH YFERHLEFEARTLSPGHTWEEAPLLTLKQKQEWICLETLTPDTQYEFQVRVKPLQ
568	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGAPTSSSTKKTQLQ LEHLLLDLQMILNGINNYKNPKLTAMLTAKFAMPKKATELKHLQCLEEALKPLEEVLNL AQSKNFHFDPRDVVSNINVFVLELKGSETTFMCEYADETATIVEFLNRWITFAQSIISTLT
569	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGAPTSSSTKKTQLQ

SEQ ID	AMINO ACID SEQUENCE
	LEHLLLDLQMILNGINNYKNPKLTRMLTKKFYMPKKATELKHLQCLEEELKPLEEVLNLA QSKNFHFDPRDVVSNINVFVLELKGSETTFMCEYADETATIVEFLNRWITFAQSIISTLT
570	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGAPTSSSTKKTQLQ LEHLLLDLQMILNGINNYKNPKLTRMLTAKFAMPKKATELKHLQCLEEELKPLEEVLNG AQSKNFHFDPRDVVSNINVFVLELKGSETTFMCEYADETATIVEFLNRWITFAQSIISTLT
571	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGPAELCDDDPPEIP HATFKAMAYKEGTMLNCECKRGFRRIKSGSLYMLCTGNSSHSSWDNQCQCTSSATRNTT KQVTPQPEEQKERKTTEMQSPMQPVDQASLPGHCREPPPWENEATERIYHFVVGQMVYY QCVQGYRALHRGPAESVCKMTHGKTRWTQPQLICTGGGGSGGGGSGGGGSGGGGSGG GGSAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQ CLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLN RWITFAQSIISTLT
572	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGPAELCDDDPPEIP HATFKAMAYKEGTMLNCECKRGFRRIKSGSLYMLCTGNSSHSSWDNQCQCTSSATRNTT KQVTPQPEEQKERKTTEMQSPMQPVDQASLPGHCREPPPWENEATERIYHFVVGQMVYY QCVQGYRALHRGPAESVCKMTHGKTRWTQPQLICTGGGGSGGGGSGGGGSGGGGSGG GGSGGGGSAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATE LKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATI VEFLNRWITFAQSIISTLT
573	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGPAELCDDDPPEIP HATFKAMAYKEGTMLNCECKRGFRRIKSGSLYMLCTGNSSHSSWDNQCQCTSSATRNTT KQVTPQPEEQKERKTTEMQSPMQPVDQASLPGHCREPPPWENEATERIYHFVVGQMVYY QCVQGYRALHRGPAESVCKMTHGKTRWTQPQLICTGGGGSGGGGSGGGGSGGGGSGG GGSGGGGSGGGGSAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMP KKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYA DETATIVEFLNRWITFAQSIISTLT
574	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGPAELCDDDPPEIP HATFKAMAYKEGTMLNCECKRGFRRIKSGSLYMLCTGNSSHSSWDNQCQCTSSATRNTT KQVTPQPEEQKERKTTEMQSPMQPVDQASLPGHCREPPPWENEATERIYHFVVGQMVYY QCVQGYRALHRGPAESVCKMTHGKTRWTQPQLICTGGGGSGGGGSGGGGSGGGGSGG GGSGGGGSGGGGSGGGGSAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTF

SEQ ID	AMINO ACID SEQUENCE
	KFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTF MCEYADETATIVEFLNRWITFAQSIISTLT
575	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGPAELCDDDPPEIP HATFKAMAYKEGTMLNCECKRGFRRIKSGSLYMLCTGNSSHSSWDNQCQCTSSATRNTT KQVTPQPEEQKERKTTEMQSPMQPVDQASLPGHCREPPPWENEATERIYHFVVGQMVYY QCVQGYRALHRGPAESVCKMTHGKTRWTQPQLICTGGGGGGGGGGGGGGGGGGGGGGG GGGGGGGGGGGGGAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFY MPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHFDPRDVVSNINVFVLELKGSETTFMC EYADETATIVEFLNRWITFAQSIISTLT
576	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGPAELCDDDPPEIP HATFKAMAYKEGTMLNCECKRGFRRIKSGSLYMLCTGNSSHSSWDNQCQCTSSATRNTT KQVTPQPEEQKERKTTEMQSPMQPVDQASLPGHCREPPPWENEATERIYHFVVGQMVYY QCVQGYRALHRGPAESVCKMTHGKTRWTQPQLICTGGGGSGGGGSGGGGSGGGGSGG GGSAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQ CLEEELKPLEEVLNLAQSKNFHFDPRDVVSNINVFVLELKGSETTFMCEYADETATIVEFL NRWITFAQSIISTLT
577	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGPAELCDDDPPEIP HATFKAMAYKEGTMLNCECKRGFRRIKSGSLYMLCTGNSSHSSWDNQCQCTSSATRNTT KQVTPQPEEQKERKTTEMQSPMQPVDQASLPGHCREPPPWENEATERIYHFVVGQMVYY QCVQGYRALHRGPAESVCKMTHGKTRWTQPQLICTGGGGSGGGGSGGGGSGGGGSGG GGSGGGGSAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATE LKHLQCLEEELKPLEEVLNLAQSKNFHFDPRDVVSNINVFVLELKGSETTFMCEYADETA TIVEFLNRWITFAQSIISTLT
578	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGPAELCDDDPPEIP HATFKAMAYKEGTMLNCECKRGFRRIKSGSLYMLCTGNSSHSSWDNQCQCTSSATRNTT KQVTPQPEEQKERKTTEMQSPMQPVDQASLPGHCREPPPWENEATERIYHFVVGQMVYY QCVQGYRALHRGPAESVCKMTHGKTRWTQPQLICTGGGGSGGGGSGGGGSGGGGSGG GGSGGGGSGGGGSAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMP KKATELKHLQCLEEELKPLEEVLNLAQSKNFHFDPRDVVSNINVFVLELKGSETTFMCEY ADETATIVEFLNRWITFAQSIISTLT
579	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGPAELCDDDPPEIP HATFKAMAYKEGTMLNCECKRGFRRIKSGSLYMLCTGNSSHSSWDNQCQCTSSATRNTT

SEQ ID	AMINO ACID SEQUENCE
	KQVTPQPEEQKERKTTEMQSPMQPVDQASLPGHCREPPPWENEATERIYHFVVGQMVYY QCVQGYRALHRGPAESVCKMTHGKTRWTQPQLICTGGGGSGGGGSGGGGSGGGGSGG GGSGGGGSGGGGSGGGGSAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTF KFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHFDPRDVVSNINVFVLELKGSETT FMCEYADETATIVEFLNRWITFAQSIISTLT
580	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLE EELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWI TFAQSIISTLTGGGGSGGGGSELCDDDPPEIPHATFKAMAYKEGTMLNCECKRGFRRIKSG SLYMLCTGNSSHSSWDNQCQCTSSATRNTTKQVTPQPEEQKERKTTEMQSPMQPVDQAS LPGHCREPPPWENEATERIYHFVVGQMVYYQCVQGYRALHRGPAESVCKMTHGKTRWT QPQLICTDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF NWYVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE KTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT TPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
581	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLE EELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWI TFAQSIISTLTGGGGSGGGGSGGGGSGGGGSELCDDDPPEIPHATFKAMAYKEGTMLNCE CKRGFRRIKSGSLYMLCTGNSSHSSWDNQCQCTSSATRNTTKQVTPQPEEQKERKTTEM QSPMQPVDQASLPGHCREPPPWENEATERIYHFVVGQMVYYQCVQGYRALHRGPAESV CKMTHGKTRWTQPQLICTDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYK CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEW ESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPG
582	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLE EELKPLEEVLNLAQSKNFHFDPRDVVSNINVFVLELKGSETTFMCEYADETATIVEFLNR WITFAQSIISTLTGGGGSGGGGSGGGGSELCDDDPPEIPHATFKAMAYKEGTMLNCECKR GFRRIKSGSLYMLCTGNSSHSSWDNQCQCTSSATRNTTKQVTPQPEEQKERKTTEMQSP MQPVDQASLPGHCREPPPWENEATERIYHFVVGQMVYYQCVQGYRALHRGPAESVCKM THGKTRWTQPQLICTDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDV SHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESN GQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSL SPG
583	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLE EELKPLEEVLNLAQSKNFHFDPRDVVSNINVFVLELKGSETTFMCEYADETATIVEFLNR WITFAQSIISTLTGGGGSGGGGSELCDDDPPEIPHATFKAMAYKEGTMLNCECKRGFRRIK SGSLYMLCTGNSSHSSWDNQCQCTSSATRNTTKQVTPQPEEQKERKTTEMQSPMQPVDQ ASLPGHCREPPPWENEATERIYHFVVGQMVYYQCVQGYRALHRGPAESVCKMTHGKTR WTQPQLICTDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENN YKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
584	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLE EELKPLEEVLNLAQSKNFHFDPRDVVSNINVFVLELKGSETTFMCEYADETATIVEFLNR WITFAQSIISTLTGGGGSGGGGSGGGGSGGGGSELCDDDPPEIPHATFKAMAYKEGTMLN CECKRGFRRIKSGSLYMLCTGNSSHSSWDNQCQCTSSATRNTTKQVTPQPEEQKERKTTE

SEQ ID	AMINO ACID SEQUENCE
	MQSPMQPVDQASLPGHCREPPPWENEATERIYHFVVGQMVYYQCVQGYRALHRGPAES VCKMTHGKTRWTQPQLICTDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCV VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEY KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQ KSLSLSPG
585	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGAPTSSSTKKTQLQ LEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLA QSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFAQSIISTLTGSS GGPPGGMPYDLYHPSGGGAVNGTSQFTCFYNSRANISCVWSQDGALQDTSCQVHAWPD RRRWNQTCELLPVSQASWACNLILGAPDSQKLTTVDIVTLRVLCREGVRWRVMAIQDFK PFENLRLMAPISLQVVHVETHRCNISWEISQASHYFERHLEFEARTLSPGHTWEEAPLLTL KQKQEWICLETLTPDTQYEFQVRVKPLQ
586	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGAPTSSSTKKTQLQ LEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLA QSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFAQSIISTLTGSP SGSGGGMPYDLYHPSGGGAVNGTSQFTCFYNSRANISCVWSQDGALQDTSCQVHAWPD RRRWNQTCELLPVSQASWACNLILGAPDSQKLTTVDIVTLRVLCREGVRWRVMAIQDFK PFENLRLMAPISLQVVHVETHRCNISWEISQASHYFERHLEFEARTLSPGHTWEEAPLLTL KQKQEWICLETLTPDTQYEFQVRVKPLQ
587	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGAPTSSSTKKTQLQ LEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLA QSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFAQSIISTLTGPP GPPGSSGMPYDLYHPSGGGAVNGTSQFTCFYNSRANISCVWSQDGALQDTSCQVHAWP DRRRWNQTCELLPVSQASWACNLILGAPDSQKLTTVDIVTLRVLCREGVRWRVMAIQDF KPFENLRLMAPISLQVVHVETHRCNISWEISQASHYFERHLEFEARTLSPGHTWEEAPLLT LKQKQEWICLETLTPDTQYEFQVRVKPLQ
588	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGAPTSSSTKKTQLQ LEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLA QSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFAQSIISTLTGSSS GPPGPPSMPYDLYHPSGGGAVNGTSQFTCFYNSRANISCVWSQDGALQDTSCQVHAWPD RRRWNQTCELLPVSQASWACNLILGAPDSQKLTTVDIVTLRVLCREGVRWRVMAIQDFK PFENLRLMAPISLQVVHVETHRCNISWEISQASHYFERHLEFEARTLSPGHTWEEAPLLTL KQKQEWICLETLTPDTQYEFQVRVKPLQ

SEQ ID	AMINO ACID SEQUENCE
589	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGAPTSSSTKKTQLQ LEHLLLDLQMILNGINNYKNPKLTAMLTAKFAMPKKATELKHLQCLEEALKPLEEVLNL AQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFAQSIISTLTGS SGGPPGGMPYDLYHPSGGGAVNGTSQFTCFYNSRANISCVWSQDGALQDTSCQVHAWP DRRRWNQTCELLPVSQASWACNLILGAPDSQKLTTVDIVTLRVLCREGVRWRVMAIQDF KPFENLRLMAPISLQVVHVETHRCNISWEISQASHYFERHLEFEARTLSPGHTWEEAPLLT LKQKQEWICLETLTPDTQYEFQVRVKPLQ
590	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGAPTSSSTKKTQLQ LEHLLLDLQMILNGINNYKNPKLTAMLTAKFAMPKKATELKHLQCLEEALKPLEEVLNL AQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFAQSIISTLTSG SPSGSGGGMPYDLYHPSGGGAVNGTSQFTCFYNSRANISCVWSQDGALQDTSCQVHAW PDRRRWNQTCELLPVSQASWACNLILGAPDSQKLTTVDIVTLRVLCREGVRWRVMAIQD FKPFENLRLMAPISLQVVHVETHRCNISWEISQASHYFERHLEFEARTLSPGHTWEEAPLL TLKQKQEWICLETLTPDTQYEFQVRVKPLQ
591	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGAPTSSSTKKTQLQ LEHLLLDLQMILNGINNYKNPKLTAMLTAKFAMPKKATELKHLQCLEEALKPLEEVLNL AQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFAQSIISTLTGP PGPPGSSGMPYDLYHPSGGGAVNGTSQFTCFYNSRANISCVWSQDGALQDTSCQVHAWP DRRRWNQTCELLPVSQASWACNLILGAPDSQKLTTVDIVTLRVLCREGVRWRVMAIQDF KPFENLRLMAPISLQVVHVETHRCNISWEISQASHYFERHLEFEARTLSPGHTWEEAPLLT LKQKQEWICLETLTPDTQYEFQVRVKPLQ
592	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGAPTSSSTKKTQLQ LEHLLLDLQMILNGINNYKNPKLTAMLTAKFAMPKKATELKHLQCLEEALKPLEEVLNL AQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFAQSIISTLTGS SSGPPGPPSMPYDLYHPSGGGAVNGTSQFTCFYNSRANISCVWSQDGALQDTSCQVHAW PDRRRWNQTCELLPVSQASWACNLILGAPDSQKLTTVDIVTLRVLCREGVRWRVMAIQD FKPFENLRLMAPISLQVVHVETHRCNISWEISQASHYFERHLEFEARTLSPGHTWEEAPLL TLKQKQEWICLETLTPDTQYEFQVRVKPLQ
593	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGAPTSSSTKKTQLQ LEHLLLDLQMILNGINNYKNPKLTAMLTAKFAMPKKATELKHLQCLEEALKPLEEVLNL AQSKNFHFDPRDVVSNINVFVLELKGSETTFMCEYADETATIVEFLNRWITFAQSIISTLTG PPSGSSPMPYDLYHPSGGGAVNGTSQFTCFYNSRANISCVWSQDGALQDTSCQVHAWPD

SEQ ID	AMINO ACID SEQUENCE
	RRRWNQTCELLPVSQASWACNLILGAPDSQKLTTVDIVTLRVLCREGVRWRVMAIQDFK PFENLRLMAPISLQVVHVETHRCNISWEISQASHYFERHLEFEARTLSPGHTWEEAPLLTL KQKQEWICLETLTPDTQYEFQVRVKPLQ
594	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGAPTSSSTKKTQLQ LEHLLLDLQMILNGINNYKNPKLTAMLTAKFAMPKKATELKHLQCLEEALKPLEEVLNL AQSKNFHFDPRDVVSNINVFVLELKGSETTFMCEYADETATIVEFLNRWITFAQSIISTLTG SSGGPPGGMPYDLYHPSGGGAVNGTSQFTCFYNSRANISCVWSQDGALQDTSCQVHAW PDRRRWNQTCELLPVSQASWACNLILGAPDSQKLTTVDIVTLRVLCREGVRWRVMAIQD FKPFENLRLMAPISLQVVHVETHRCNISWEISQASHYFERHLEFEARTLSPGHTWEEAPLL TLKQKQEWICLETLTPDTQYEFQVRVKPLQ
595	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGAPTSSSTKKTQLQ LEHLLLDLQMILNGINNYKNPKLTAMLTAKFAMPKKATELKHLQCLEEALKPLEEVLNL AQSKNFHFDPRDVVSNINVFVLELKGSETTFMCEYADETATIVEFLNRWITFAQSIISTLTS GSPSGSGGGMPYDLYHPSGGGAVNGTSQFTCFYNSRANISCVWSQDGALQDTSCQVHA WPDRRRWNQTCELLPVSQASWACNLILGAPDSQKLTTVDIVTLRVLCREGVRWRVMAIQ DFKPFENLRLMAPISLQVVHVETHRCNISWEISQASHYFERHLEFEARTLSPGHTWEEAPL LTLKQKQEWICLETLTPDTQYEFQVRVKPLQ
596	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGAPTSSSTKKTQLQ LEHLLLDLQMILNGINNYKNPKLTAMLTAKFAMPKKATELKHLQCLEEALKPLEEVLNL AQSKNFHFDPRDVVSNINVFVLELKGSETTFMCEYADETATIVEFLNRWITFAQSIISTLTG PPGPPGSSGMPYDLYHPSGGGAVNGTSQFTCFYNSRANISCVWSQDGALQDTSCQVHAW PDRRRWNQTCELLPVSQASWACNLILGAPDSQKLTTVDIVTLRVLCREGVRWRVMAIQD FKPFENLRLMAPISLQVVHVETHRCNISWEISQASHYFERHLEFEARTLSPGHTWEEAPLL TLKQKQEWICLETLTPDTQYEFQVRVKPLQ
597	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGAPTSSSTKKTQLQ LEHLLLDLQMILNGINNYKNPKLTAMLTAKFAMPKKATELKHLQCLEEALKPLEEVLNL AQSKNFHFDPRDVVSNINVFVLELKGSETTFMCEYADETATIVEFLNRWITFAQSIISTLTG SSSGPPGPPSMPYDLYHPSGGGAVNGTSQFTCFYNSRANISCVWSQDGALQDTSCQVHA WPDRRRWNQTCELLPVSQASWACNLILGAPDSQKLTTVDIVTLRVLCREGVRWRVMAIQ DFKPFENLRLMAPISLQVVHVETHRCNISWEISQASHYFERHLEFEARTLSPGHTWEEAPL LTLKQKQEWICLETLTPDTQYEFQVRVKPLQ
598	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGPAELCDDDPPEIP

SEQ ID	AMINO ACID SEQUENCE
	HATFKAMAYKEGTMLNCECKRGFRRIKSGSLYMLCTGNSSHSSWDNQCQCTSSATRNTT KQVTPQPEEQKERKTTEMQSPMQPVDQASLPGHCREPPPWENEATERIYHFVVGQMVYY QCVQGYRALHRGPAESVCKMTHGKTRWTQPQLICTGGGGGGGGGGGGGGGGGGGG GGGGGGGGGGGGGGAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFY MPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCE YADETATIVEFLNRWITFAQSIISTLTGSSGGPPGGMPYDLYHPSGGGAVNGTSQFTCFYN SRANISCVWSQDGALQDTSCQVHAWPDRRRWNQTCELLPVSQASWACNLILGAPDSQK LTTVDIVTLRVLCREGVRWRVMAIQDFKPFENLRLMAPISLQVVHVETHRCNISWEISQA SHYFERHLEFEARTLSPGHTWEEAPLLTLKQKQEWICLETLTPDTQYEFQVRVKPLQ
599	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGPAELCDDDPPEIP HATFKAMAYKEGTMLNCECKRGFRRIKSGSLYMLCTGNSSHSSWDNQCQCTSSATRNTT KQVTPQPEEQKERKTTEMQSPMQPVDQASLPGHCREPPPWENEATERIYHFVVGQMVYY QCVQGYRALHRGPAESVCKMTHGKTRWTQPQLICTGGGGGGGGGGGGGGGGGGGG GGGGGGGGGGGGGGAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFY MPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCE YADETATIVEFLNRWITFAQSIISTLTGSGSPSGSGGGMPYDLYHPSGGGAVNGTSQFTCFY NSRANISCVWSQDGALQDTSCQVHAWPDRRRWNQTCELLPVSQASWACNLILGAPDSQ KLTTVDIVTLRVLCREGVRWRVMAIQDFKPFENLRLMAPISLQVVHVETHRCNISWEISQ ASHYFERHLEFEARTLSPGHTWEEAPLLTLKQKQEWICLETLTPDTQYEFQVRVKPLQ
600	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGPAELCDDDPPEIP HATFKAMAYKEGTMLNCECKRGFRRIKSGSLYMLCTGNSSHSSWDNQCQCTSSATRNTT KQVTPQPEEQKERKTTEMQSPMQPVDQASLPGHCREPPPWENEATERIYHFVVGQMVYY QCVQGYRALHRGPAESVCKMTHGKTRWTQPQLICTGGGGGGGGGGGGGGGGGGGG GGGGGGGGGGGGGGAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFY MPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCE YADETATIVEFLNRWITFAQSIISTLTGPPGPPGSSGMPYDLYHPSGGGAVNGTSQFTCFYN SRANISCVWSQDGALQDTSCQVHAWPDRRRWNQTCELLPVSQASWACNLILGAPDSQK LTTVDIVTLRVLCREGVRWRVMAIQDFKPFENLRLMAPISLQVVHVETHRCNISWEISQA SHYFERHLEFEARTLSPGHTWEEAPLLTLKQKQEWICLETLTPDTQYEFQVRVKPLQ
601	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGPAELCDDDPPEIP HATFKAMAYKEGTMLNCECKRGFRRIKSGSLYMLCTGNSSHSSWDNQCQCTSSATRNTT KQVTPQPEEQKERKTTEMQSPMQPVDQASLPGHCREPPPWENEATERIYHFVVGQMVYY QCVQGYRALHRGPAESVCKMTHGKTRWTQPQLICTGGGGGGGGGGGGGGGGGGGG GGGGGGGGGGGGGGAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFY MPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCE YADETATIVEFLNRWITFAQSIISTLTGSSSGPPGPPSMPYDLYHPSGGGAVNGTSQFTCFY NSRANISCVWSQDGALQDTSCQVHAWPDRRRWNQTCELLPVSQASWACNLILGAPDSQ

SEQ ID	AMINO ACID SEQUENCE
	KLTTVDIVTLRVLCREGVRWRVMAIQDFKPFENLRLMAPISLQVVHVETHRCNISWEISQ ASHYFERHLEFEARTLSPGHTWEEAPLLTLKQKQEWICLETLTPDTQYEFQVRVKPLQ
602	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGAPTSSSTKKTQLQ LEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLA QSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFAQSIISTLTGPPS GSSPMPYDLYHPSGGGAVNGTSQFTCFYNSRANISCVWSQDGALQDTSCQVHAWPDRR RWNQTCELLPVSQASWACNLILGAPDSQKLTTVDIVTLRVLCREGVRWRVMAIQDFKPF ENLRLMAPISLQVVHVETHRCNISWEISQASHYFERHLEFEARTLSPGHTWEEAPLLTLKQ KQEWICLETLTPDTQYEFQVRVKPLQGEFTTWSPWSQPLAFRTKPAALGKD
603	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVCTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLVSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGPGSGAVNGTSQF TCFYNSRANISCVWSQDGALQDTSCQVHAWPDRRRWNQTCELLPVSQASWACNLILGA PDSQKLTTVDIVTLRVLCREGVRWRVMAIQDFKPFENLRLMAPISLQVVHVETHRCNISW EISQASHYFERHLEFEARTLSPGHTWEEAPLLTLKQKQEWICLETLTPDTQYEFQVRVKPL Q
604	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGSPMPYDLYHP APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLE EELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWI TFAQSIISTLT
605	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGSPPMPYDLYH PSGPAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHL QCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFL NRWITFAQSIISTLT
606	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGSPSMPYDLYH PSGPAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHL QCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFL NRWITFAQSIISTLT
607	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGAPTSSSTKKTQLQ LEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLA QSKNFHFDPRDVVSNINVFVLELKGSETTFMCEYADETATIVEFLNRWITFAQSIISTLT

SEQ ID	AMINO ACID SEQUENCE
608	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGGSSPPMPYDL YHPSGPAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELK HLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVE FLNRWITFAQSIISTLT
609	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVCTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLVSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGPGSGSAVNGTSQ FTCFYNSRANISCVWSQDGALQDTSCQVHAWPDRRRWNQTCELLPVSQASWACNLILG APDSQKLTTVDIVTLRVLCREGVRWRVMAIQDFKPFENLRLMAPISLQVVHVETHRCNIS WEISQASHYFERHLEFEARTLSPGHTWEEAPLLTLKQKQEWICLETLTPDTQYEFQVRVK PLQ
610	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGAPTSSSTKKTQLQ LEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLA QSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFAQSIISTLTGPPS GSSPMPYDLYHPSGGGAVNGTSQFTCFYNSRANISCVWSQDGALQDTSCQVHAWPDRR RWNQTCELLPVSQASWACNLILGAPDSQKLTTVDIVTLRVLCREGVRWRVMAIQDF
611	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGAPTSSSTKKTQLQ LEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLA QSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFAQSIISTLTGSS GGPPGGMPYDLYHPSGGGAVNGTSQFTCFYNSRANISCVWSQDGALQDTSCQVHAWPD RRRWNQTCELLPVSQASWACNLILGAPDSQKLTTVDIVTLRVLCREGVRWRVMAIQDF
612	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGAPTSSSTKKTQLQ LEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLA QSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFAQSIISTLTSGSP SGSGGGMPYDLYHPSGGGAVNGTSQFTCFYNSRANISCVWSQDGALQDTSCQVHAWPD RRRWNQTCELLPVSQASWACNLILGAPDSQKLTTVDIVTLRVLCREGVRWRVMAIQDF
613	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGAPTSSSTKKTQLQ LEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLA QSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFAQSIISTLTGPP GPPGSSGMPYDLYHPSGGGAVNGTSQFTCFYNSRANISCVWSQDGALQDTSCQVHAWP DRRRWNQTCELLPVSQASWACNLILGAPDSQKLTTVDIVTLRVLCREGVRWRVMAIQDF

SEQ ID	AMINO ACID SEQUENCE
614	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGAPTSSSTKKTQLQ LEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLA QSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFAQSIISTLTGSSS GPPGPPSMPYDLYHPSGGGAVNGTSQFTCFYNSRANISCVWSQDGALQDTSCQVHAWPD RRRWNQTCELLPVSQASWACNLILGAPDSQKLTTVDIVTLRVLCREGVRWRVMAIQDF
615	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVCTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLVSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGAPTSSSTKKTQLQ LEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLA QSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFAQSIISTLT
616	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
617	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGPPSGSSPMPY DLYHPSGGGAVNGTSQFTCFYNSRANISCVWSQDGALQDTSCQVHAWPDRRRWNQTCE LLPVSQASWACNLILGAPDSQKLTTVDIVTLRVLCREGVRWRVMAIQDFKPFENLRLMAP ISLQVVHVETHRCNISWEISQASHYFERHLEFEARTLSPGHTWEEAPLLTLKQKQEWICLE TLTPDTQYEFQVRVKPLQ
618	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVCTLPPSRDELTKNQVSLTCLVEGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQESLSLSPGAPTSSSTKKTQLQ LEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLA QSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFAQSIISTLT
619	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPCRKKLTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
620	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPCRKKLTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGPPSGSSPMPYDL YHPSGGGAVNGTSQFTCFYNSRANISCVWSQDGALQDTSCQVHAWPDRRRWNQTCELL PVSQASWACNLILGAPDSQKLTTVDIVTLRVLCREGVRWRVMAIQDFKPFENLRLMAPIS LQVVHVETHRCNISWEISQASHYFERHLEFEARTLSPGHTWEEAPLLTLKQKQEWICLETL TPDTQYEFQVRVKPLQ
621	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVCTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEWESNGQPENNYDTTPPVLD

SEQ ID	AMINO ACID SEQUENCE
	SDGSFFLVSDLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGAPTSSSTKKTQLQ LEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLA QSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFAQSIISTLT
622	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPCRKELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL KSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
623	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPCRKELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL KSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGPPSGSSPMPY DLYHPSGGGAVNGTSQFTCFYNSRANISCVWSQDGALQDTSCQVHAWPDRRRWNQTCE LLPVSQASWACNLILGAPDSQKLTTVDIVTLRVLCREGVRWRVMAIQDFKPFENLRLMAP ISLQVVHVETHRCNISWEISQASHYFERHLEFEARTLSPGHTWEEAPLLTLKQKQEWICLE TLTPDTQYEFQVRVKPLQ
624	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVCTLPPSRDELTKNQVSLSCAVEGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLVSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQESLSLSPGAPTSSSTKKTQLQ LEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLA QSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFAQSIISTLT
625	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPCRKKLTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
626	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPCRKKLTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGPPSGSSPMPY DLYHPSGGGAVNGTSQFTCFYNSRANISCVWSQDGALQDTSCQVHAWPDRRRWNQTCE LLPVSQASWACNLILGAPDSQKLTTVDIVTLRVLCREGVRWRVMAIQDFKPFENLRLMAP ISLQVVHVETHRCNISWEISQASHYFERHLEFEARTLSPGHTWEEAPLLTLKQKQEWICLE TLTPDTQYEFQVRVKPLQ
627	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGAPTSSSTKKTQLQ LEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLA QSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFAQSIISTLTPGP GPMPYDLYHPSGGCGGHQYERRGGC
628	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGAPTSSSTKKTQLQ LEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLA QSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFAQSIISTLTPGP GPMPYDLYHPSGGCSGHQYERREGC

SEQ ID	AMINO ACID SEQUENCE
629	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGAPTSSSTKKTQLQ LEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLA QSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFAQSIISTLTPGP GPMPYDLYHPSGGCGGHYFERHGGC
630	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGAPTSSSTKKTQLQ LEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLA QSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFAQSIISTLTPGP GPMPYDLYHPSGGCSGHYFERHEGC
631	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGAPTSSSTKKTQLQ LEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLA QSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFAQSIISTLTPGP GPMPYDLYHPSGGCSFHQYERHEGC
632	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGAPTSSSTKKTQLQ LEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLA QSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFAQSIISTLTPSGS SMPYDLYHPSGGCGGHQYERRGGC
633	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGAPTSSSTKKTQLQ LEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLA QSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFAQSIISTLTPSGS SMPYDLYHPSGGCSGHQYERREGC
634	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGAPTSSSTKKTQLQ LEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLA QSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFAQSIISTLTPSGS SMPYDLYHPSGGCGGHYFERHGGC
635	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGAPTSSSTKKTQLQ LEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLA

SEQ ID	AMINO ACID SEQUENCE
	QSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFAQSIISTLTPSGS SMPYDLYHPSGGCSGHYFERHEGC
636	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGAPTSSSTKKTQLQ LEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLA QSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFAQSIISTLTPSGS SMPYDLYHPSGGCSFHQYERHEGC
637	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGPGSGSAVNGTSQ FTCFYNSRANISCVWSQDGALQDTSCQVHAWPDRRRWNQTCELLPVSQASWACNLILG APDSQKLTTVDIVTLRVLCREGVRWRVMAIQDFKPFENLRLMAPISLQVVHVETHRCNIS WEISQASHYFERHLEFEARTLSPGHTWEEAPLLTLKQKQEWICLETLTPDTQYEFQVRVK PLQGEFTTWSPWSQPLAFRTKPAALGKD
638	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGPPSGSSPMPY DLYHPSGGGAVNGTSQFTCFYNSRANISCVWSQDGALQDTSCQVHAWPDRRRWNQTCE LLPVSQASWACNLILGAPDSQKLTTVDIVTLRVLCREGVRWRVMAIQDFKPFENLRLMAP ISLQVVHVETHRCNISWEISQASHYFERHLEFEARTLSPGHTWEEAPLLTLKQKQEWICLE TLTPDTQYEFQVRVKPLQGEFTTWSPWSQPLAFRTKPAALGKD
639	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPCRKKLTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGPPSGSSPMPYDL YHPSGGGAVNGTSQFTCFYNSRANISCVWSQDGALQDTSCQVHAWPDRRRWNQTCELL PVSQASWACNLILGAPDSQKLTTVDIVTLRVLCREGVRWRVMAIQDFKPFENLRLMAPIS LQVVHVETHRCNISWEISQASHYFERHLEFEARTLSPGHTWEEAPLLTLKQKQEWICLETL TPDTQYEFQVRVKPLQGEFTTWSPWSQPLAFRTKPAALGKD
640	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPCRKELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL KSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGPPSGSSPMPY DLYHPSGGGAVNGTSQFTCFYNSRANISCVWSQDGALQDTSCQVHAWPDRRRWNQTCE LLPVSQASWACNLILGAPDSQKLTTVDIVTLRVLCREGVRWRVMAIQDFKPFENLRLMAP ISLQVVHVETHRCNISWEISQASHYFERHLEFEARTLSPGHTWEEAPLLTLKQKQEWICLE TLTPDTQYEFQVRVKPLQGEFTTWSPWSQPLAFRTKPAALGKD
641	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPCRKKLTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGPPSGSSPMPY DLYHPSGGGAVNGTSQFTCFYNSRANISCVWSQDGALQDTSCQVHAWPDRRRWNQTCE LLPVSQASWACNLILGAPDSQKLTTVDIVTLRVLCREGVRWRVMAIQDFKPFENLRLMAP

SEQ ID	AMINO ACID SEQUENCE
	ISLQVVHVETHRCNISWEISQASHYFERHLEFEARTLSPGHTWEEAPLLTLKQKQEWICLE TLTPDTQYEFQVRVKPLQGEFTTWSPWSQPLAFRTKPAALGKD
642	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGAPTSSSTKKTQLQ LEHLLLDLQMILNGINNYKNPKLTAMLTAKFAMPKKATELKHLQCLEEALKPLEEVLNL AQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFAQSIISTLTGP PSGSSPMPYDLYHPSGGGAVNGTSQFTCFYNSRANISCVWSQDGALQDTSCQVHAWPDR RRWNQTCELLPVSQASWACNLILGAPDSQKLTTVDIVTLRVLCREGVRWRVMAIQDFKP FFENLRLMAPISLQVVHVETHRCNISWEISQASHYFERHLEFEARTLSPGHTWEEAPLLTLK QKQEWICLETLTPDTQYEFQVRVKPLQGEFTTWSPWSQPLAFRTKPAALGKD
643	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGAPTSSSTKKTQLQ LEHLLLDLQMILNGINNYKNPKLTAMLTAKFAMPKKATELKHLQCLEEALKPLEEVLNL AQSKNFHFDPRDVVSNINVFVLELKGSETTFMCEYADETATIVEFLNRWITFAQSIISTLTG PPSGSSPMPYDLYHPSGGGAVNGTSQFTCFYNSRANISCVWSQDGALQDTSCQVHAWPD RRRWNQTCELLPVSQASWACNLILGAPDSQKLTTVDIVTLRVLCREGVRWRVMAIQDFK PFENLRLMAPISLQVVHVETHRCNISWEISQASHYFERHLEFEARTLSPGHTWEEAPLLTL KQKQEWICLETLTPDTQYEFQVRVKPLQGEFTTWSPWSQPLAFRTKPAALGKD
644	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVCTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLVSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGPGSGSAVNGTSQ FTCFYNSRANISCVWSQDGALQDTSCQVHAWPDRRRWNQTCELLPVSQASWACNLILG APDSQKLTTVDIVTLRVLCREGVRWRVMAIQDFKPFENLRLMAPISLQVVHVETHRCNIS WEISQASHYFERHLEFEARTLSPGHTWEEAPLLTLKQKQEWICLETLTPDTQYEFQVRVK PLQ
645	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGAPTSSSTKKTQLQ LEILCLLLQMILNGILNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQ SKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
646	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGAPTSSSTKKTQLQ LEILLLLLQMILNGILNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQ SKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFIQSIISTLT
647	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGAPTSSSTKKTQLQ

SEQ ID	AMINO ACID SEQUENCE
	LEILCLFLQMILNGILNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQ SKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
648	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGAPTSSSTKKTQLQ LEILLLFLQMILNGILNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQ SKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFIQSIISTLT
649	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGAPTSSSTKKTQLQ LEHLCLLLQMILNGILNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLA QSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
650	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGAPTSSSTKKTQLQ LEHLLLLLQMILNGILNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLA QSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFIQSIISTLT
651	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGAPTSSSTKKTQLQ LEILLLLLQMILNGILNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQ SKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFAQSIISTLT
652	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGAPTSSSTKKTQLQ LEILLLFLQMILNGILNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQ SKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFAQSIISTLT
653	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGAPTSSSTKKTQLQ LEHLLLLLQMILNGILNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLA QSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFAQSIISTLT
654	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGAPTSSSTKKTQLQ LEHLCLFLQMILNGILNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLA QSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
655	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD

SEQ ID	AMINO ACID SEQUENCE
	SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGAPTSSSTKKTQLQ LEHLLLFLQMILNGILNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLA QSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFIQSIISTLT
656	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGAPTSSSTKKTQLQ LEHLLLFLQMILNGILNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLA QSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFAQSIISTLT
657	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGAPTSSSTKKTQLQ LEILCLLLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLA QSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
658	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGAPTSSSTKKTQLQ LEILLLLLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLA QSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFIQSIISTLT
659	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGAPTSSSTKKTQLQ LEILLLLLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLA QSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFAQSIISTLT
660	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGAPTSSSTKKTQLQ LEILCLFLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLA QSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
661	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGAPTSSSTKKTQLQ LEILLLFLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQ SKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFIQSIISTLT
662	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGAPTSSSTKKTQLQ LEILLLFLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQ SKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFAQSIISTLT
663	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA

SEQ ID	AMINO ACID SEQUENCE
	KGQPREPQVCTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEWESNGQPENNYDTTPPVLD SDGSFFLVSDLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGGSSPPMPYDLY HPSGPAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKH LQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEF LNRWITFAQSIISTLT
664	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPCRKELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL KSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGPGSGAVNGTSQ FTCFYNSRANISCVWSQDGALQDTSCQVHAWPDRRRWNQTCELLPVSQASWACNLILG APDSQKLTTVDIVTLRVLCREGVRWRVMAIQDFKPFENLRLMAPISLQVVHVETHRCNIS WEISQASHYFERHLEFEARTLSPGHTWEEAPLLTLKQKQEWICLETLTPDTQYEFQVRVK PLQGEFTTWSPWSQPLAFRTKPAALGKD
665	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVCTLPPSRDELTKNQVSLSCAVEGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLVSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQESLSLSPGGGSSPPMPYDLY HPSGPAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKH LQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEF LNRWITFAQSIISTLT
666	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPCRKKLTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGPGSGAVNGTSQ FTCFYNSRANISCVWSQDGALQDTSCQVHAWPDRRRWNQTCELLPVSQASWACNLILG APDSQKLTTVDIVTLRVLCREGVRWRVMAIQDFKPFENLRLMAPISLQVVHVETHRCNIS WEISQASHYFERHLEFEARTLSPGHTWEEAPLLTLKQKQEWICLETLTPDTQYEFQVRVK PLQGEFTTWSPWSQPLAFRTKPAALGKD
667	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGGSSPPMPYDL YHPSGPAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTAMLTAKFAMPKKATELK HLQCLEEALKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVE FLNRWITFAQSIISTLT
668	GGSSPPMPYDLYHPSGPGSGS
669	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGGSSPPMPYDL YHPSGPAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTAMLTAKFAMPKKATELK HLQCLEEALKPLEEVLNLAQSKNFHFDPRDVVSNINVFVLELKGSETTFMCEYADETATI VEFLNRWITFAQSIISTLT
670	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVCTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLVSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGGSSPPMPYDLY

SEQ ID	AMINO ACID SEQUENCE
	HPSGPAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKH LQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEF LNRWITFAQSIISTLT
671	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGPGSGAVNGTSQ FTCFYNSRANISCVWSQDGALQDTSCQVHAWPDRRRWNQTCELLPVSQASWACNLILG APDSQKLTTVDIVTLRVLCREGVRWRVMAIQDFKPFENLRLMAPISLQVVHVETHRCNIS WEISQASHYFERHLEFEARTLSPGHTWEEAPLLTLKQKQEWICLETLTPDTQYEFQVRVK PLQGEFTTWSPWSQPLAFRTKPAALGKD
672	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGISSGLLSGRSD NHSGPAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKH LQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEF LNRWITFAQSIISTLT
673	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGGAVGLLAPPG GLSGRSDNHSGPAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPK KATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYAD ETATIVEFLNRWITFAQSIISTLT
674	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGSPGVPLSLYSG PAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCL EEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRW ITFAQSIISTLT
675	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGGSSPPVPLSLY SGPAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQ CLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLN RWITFAQSIISTLT
676	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGGSPGGVPLSL YSGPAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTAMLTAKFAMPKKATELKHL QCLEEALKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFL NRWITFAQSIISTLT

SEQ ID	AMINO ACID SEQUENCE
677	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGGSSPPRAAAV KSPSGPAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELK HLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVE FLNRWITFAQSIISTLT
678	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGGPGGPRAAAV KSPSGPAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELK HLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVE FLNRWITFAQSIISTLT
679	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGGSGRAAAVKS PSGPAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTAMLTAKFAMPKKATELKHL QCLEEALKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFL NRWITFAQSIISTLT
680	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGGSSPPRAAAV KSPSGPAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTAMLTAKFAMPKKATELK HLQCLEEALKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVE FLNRWITFAQSIISTLT
681	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGGPGGPRAAAV KSPSGPAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTAMLTAKFAMPKKATELK HLQCLEEALKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVE FLNRWITFAQSIISTLT
682	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGGSGHEQLTVS GPAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQC LEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNR WITFAQSIISTLT
683	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGGSSPPHEQLT VSGPAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHL

SEQ ID	AMINO ACID SEQUENCE
	QCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFL NRWITFAQSIISTLT
684	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGSPPGGHEQLT VSGPAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHL QCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFL NRWITFAQSIISTLT
685	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGGSGHEQLTVS GPAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTAMLTAKFAMPKKATELKHLQ CLEEALKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLN RWITFAQSIISTLT
686	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGGSSPPHEQLT VSGPAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTAMLTAKFAMPKKATELKHL QCLEEALKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFL NRWITFAQSIISTLT
687	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGSPPGGHEQLT VSGPAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTAMLTAKFAMPKKATELKHL QCLEEALKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFL NRWITFAQSIISTLT
688	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGSGPDSGGFML TSGPAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHL QCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFL NRWITFAQSIISTLT
689	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGPGSPGDSGGF MLTSGPAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELK HLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVE FLNRWITFAQSIISTLT
690	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL

SEQ ID	AMINO ACID SEQUENCE
	DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGSSPPGDSGGF MLTSGPAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELK HLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVE FLNRWITFAQSIISTLT
691	GISSGLLSGRSDNHGGP
692	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGPGSPGDSGGF MLTSGPAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTAMLTAKFAMPKKATELK HLQCLEEALKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVE FLNRWITFAQSIISTLT
693	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGSSPPGDSGGF MLTSGPAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTAMLTAKFAMPKKATELK HLQCLEEALKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVE FLNRWITFAQSIISTLT
694	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGISSGLLSGRSD NHSGPAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTAMLTAKFAMPKKATELK HLQCLEEALKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVE FLNRWITFAQSIISTLT
695	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGGAVGLLAPPG GLSGRSDNHSGPAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTAMLTAKFAMPK KATELKHLQCLEEALKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYAD ETATIVEFLNRWITFAQSIISTLT
696	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGGSPGGVPLSL YSGPAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHL QCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFL NRWITFAQSIISTLT
697	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGSPGVPLSLYSG PAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTAMLTAKFAMPKKATELKHLQCL EEALKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNR WITFAQSIISTLT

SEQ ID	AMINO ACID SEQUENCE
698	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGGSGRAAAVKS PSGPAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHL QCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFL NRWITFAQSIISTLT
699	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGGSSPPGGGSS GGGSGPAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTAMLTAKFAMPKKATEL KHLQCLEEALKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATI VEFLNRWITFAQSIISTLT
700	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGGSSPPGGGSS GGGSGPAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELK HLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVE FLNRWITFAQSIISTLT
701	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGGSSPPMPYDL YHPSGPAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELK HLQCLEERLKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVE FLNRWITFAQSIISTLT
702	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGGSSPPMPYDL YHPSGPAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTEKFYMPKKATELK HLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVE FLNRWITFAQSIISTLT
703	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGGSSPPMPYDL YHPSGPAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFNMPKKATELK HLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVE FLNRWITFAQSIISTLT
704	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGGSSPPMPYDL YHPSGPAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELK

SEQ ID	AMINO ACID SEQUENCE
	HLQCLEESLKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVE FLNRWITFAQSIISTLT
705	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGGSSPPMPYDL YHPSGPAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTAKFYMPKKATELK HLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVE FLNRWITFAQSIISTLT
706	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGGSSPPMPYDL YHPSGPAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFRMPKKATELK HLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVE FLNRWITFAQSIISTLT
707	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGGSSPPMPYDL YHPSGPAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFAFYMPKKATELK HLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVE FLNRWITFAQSIISTLT
708	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGGSSPPMPYDL YHPSGPAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFAMPKKATELK HLQCLEESLKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVE FLNRWITFAQSIISTLT
709	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGGSSPPMPYDL YHPSGPAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTSKFYMPKKATELK HLQCLEESLKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVE FLNRWITFAQSIISTLT
710	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGGSSPPMPYDL YHPSGPAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTGMLTFKFAMPKKATELK HLQCLEESLKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVE FLNRWITFAQSIISTLT
711	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL

SEQ ID	AMINO ACID SEQUENCE
	DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGGSSPPVPLSLY SGPAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTAMLTAKFAMPKKATELKHLQ CLEEALKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLN RWITFAQSIISTLT
712	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVCTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLVSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGPGSGAVNGTSQF TCFYNSRANISCVWSQDGALQDTSCQVHAWPDRRRWNQTCELLPVSQASWACNLILGA PDSQKLTTVDIVTLRVLCREGVRWRVMAIQDFKPFENLRLMAPISLQVVHVETHRCNISW EISQASHYFERHLEFEARTLSPGHTWEEAPLLTLKQKQEWICLETLTPDTQYEFQVRVKPL QGEFTTWSPWSQPLAFRTKPAALGKD
713	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGISSGLLSGRSD NHGGPAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKH LQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEF LNRWITFAQSIISTLT
714	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGISSGLLSGRSD NHGGPAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTAMLTAKFAMPKKATELK HLQCLEEALKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVE FLNRWITFAQSIISTLT
715	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGGSSPPMPYDL YHPSGPGSGSNWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVIS LESGDASIHDTVENLIILANNSLSSNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS
716	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVCTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLVSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGPPSGSSPMPYDL YHPSGGGAVNGTSQFTCFYNSRANISCVWSQDGALQDTSCQVHAWPDRRRWNQTCELL PVSQASWACNLILGAPDSQKLTTVDIVTLRVLCREGVRWRVMAIQDFKPFENLRLMAPIS LQVVHVETHRCNISWEISQASHYFERHLEFEARTLSPGHTWEEAPLLTLKQKQEWICLETL TPDTQYEFQVRVKPLQGEFTTWSPWSQPLAFRTKPAALGKD
717	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGSPGVPLSLYSG PAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCL EERLKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNR WITFAQSIISTLT

SEQ ID	AMINO ACID SEQUENCE
718	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGSPGVPLSLYSG PAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTEKFYMPKKATELKHLQCL EEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRW ITFAQSIISTLT
719	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGSPGVPLSLYSG PAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCL EESLKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRW ITFAQSIISTLT
720	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGSPGVPLSLYSG PAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTAKFYMPKKATELKHLQCL EEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRW ITFAQSIISTLT
721	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVCTLPPSRDELTKNQVSLTCLVEGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQESLSLSPG
722	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGSPGVPLSLYSG PAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFRMPKKATELKHLQCL EEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRW ITFAQSIISTLT
723	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGSPGVPLSLYSG PAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTSKFYMPKKATELKHLQCL EESLKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRW ITFAQSIISTLT
724	GISSGLLSGRSDNPSGP
725	GGSGISSGLLSGRSDNPSGP
726	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGSPGVPLSLYSG PAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTAMLTAKFAMPKKATELKHLQCL

SEQ ID	AMINO ACID SEQUENCE
	EEALKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNR WITFAQSIISTLT
727	SGS
728	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGGSGRAAAVKS PSGPAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTSKFYMPKKATELKHL QCLEESLKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFL NRWITFAQSIISTLT
729	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGISSGLLSGRSS GPAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTSKFYMPKKATELKHLQC LEESLKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNR WITFAQSIISTLT
730	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGGSGISSGLLSG RSSGPAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTSKFYMPKKATELKH LQCLEESLKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEF LNRWITFAQSIISTLT
731	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGISSGLLSGRSD NPSGPAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTSKFYMPKKATELKH LQCLEESLKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEF LNRWITFAQSIISTLT
732	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGGSGISSGLLSG RSDNPSGPAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTSKFYMPKKATE LKHLQCLEESLKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATI VEFLNRWITFAQSIISTLT
733	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGISSGLLSGRSD QPSGPAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTSKFYMPKKATELKH LQCLEESLKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEF LNRWITFAQSIISTLT
734	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA

SEQ ID	AMINO ACID SEQUENCE
	KGQPREPQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGGSGISSGLLSG RSDQPSGPAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTSKFYMPKKATE LKHLQCLEESLKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATI VEFLNRWITFAQSIISTLT
735	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGKQLRVVNEYS SMDNMLLGGPAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTSKFYMPKK ATELKHLQCLEESLKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADE TATIVEFLNRWITFAQSIISTLT
736	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGKQLRVVNEYS SEDNMLLGGPAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTSKFYMPKKA TELKHLQCLEESLKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADET ATIVEFLNRWITFAQSIISTLT
737	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGKQLRVVNGYS SEDNMLLGGPAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTSKFYMPKKA TELKHLQCLEESLKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADET ATIVEFLNRWITFAQSIISTLT
738	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGKQLRVVGGL VHLKNTMETGPAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTSKFYMPK KATELKHLQCLEESLKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYAD ETATIVEFLNRWITFAQSIISTLT
739	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGTRDRLDEVNF KQLRVVNGGPAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTSKFYMPKK ATELKHLQCLEESLKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADE TATIVEFLNRWITFAQSIISTLT
740	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGTRDRLDEVNF KLLRVVNGGPAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTSKFYMPKK ATELKHLQCLEESLKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADE TATIVEFLNRWITFAQSIISTLT

SEQ ID	AMINO ACID SEQUENCE
741	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGTRDRLDPVNF KQLRVVNGGPAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTSKFYMPKK ATELKHLQCLEESLKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADE TATIVEFLNRWITFAQSIISTLT
742	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGTRDRLDPVNF KLLRVVNGGPAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTSKFYMPKK ATELKHLQCLEESLKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADE TATIVEFLNRWITFAQSIISTLT
743	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGNPMGSEPVNF KQLRVVNGGPAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTSKFYMPKK ATELKHLQCLEESLKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADE TATIVEFLNRWITFAQSIISTLT
744	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGNPMGSEPVNF KLLRVVNGGPAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTSKFYMPKK ATELKHLQCLEESLKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADE TATIVEFLNRWITFAQSIISTLT
745	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGNPMGSDPVNF KQLRVVNGGPAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTSKFYMPKK ATELKHLQCLEESLKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADE TATIVEFLNRWITFAQSIISTLT
746	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGNPMGSDPVNF KLLRVVNGGPAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTSKFYMPKK ATELKHLQCLEESLKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADE TATIVEFLNRWITFAQSIISTLT
747	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGGSSPPMPYDL YHPSGPSGSPGNWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVI

SEQ ID	AMINO ACID SEQUENCE
	SLESGDASIHDTVENLIILANNSLSSNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINT S
748	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGGSSPPGGGSS GGGSGPSGSPGNWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVI SLESGDASIHDTVENLIILANNSLSSNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINT S
749	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGGSSPPMPYDL YHPSGPSGSPGNWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVI SLESGDASIHDTVENLIILANNSLSSNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINT SGGGGSGGGGSGGGGSGGGGSITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGT SSLTECVLNKATNVAHWTTPSLKCIRDPALVHQRPAPPSTVTTAGVTPQPESLSPSGKEPA ASSPSSNNTAATTAAIVPGSQLMPSKSPSTGTTEISSHESSHGTPSQTTAKNWELTASASHQ PPGVYPQGHSDTT
750	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGGSSPPMPYDL YHPSGPSGSPGNWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVI SLESGDASIHDTVENLIILANNSLSSNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINT SGGGGSGGGGSGGGGSGGGGSITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGT SSLTECVLNKATNVAHWTTPSLKCIRDPALVHQRPAPPSTVTTAGVTPQPESLSPSGKEPA AS
751	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGGSSPPGGGSS GGGSGPGSGSNWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVIS LESGDASIHDTVENLIILANNSLSSNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS
752	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGGSSPPMPYDL YHPSGPGSGSNWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVIS LESGDASIHDTVENLIILANNSLSSNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS GGGGSGGGGSGGGGSGGGGSITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTS SLTECVLNKATNVAHWTTPSLKCIRDPALVHQRPAPPSTVTTAGVTPQPESLSPSGKEPAA SSPSSNNTAATTAAIVPGSQLMPSKSPSTGTTEISSHESSHGTPSQTTAKNWELTASASHQP PGVYPQGHSDTT
753	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL

SEQ ID	AMINO ACID SEQUENCE
	DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGGSSPPMPYDL YHPSGPGSGSNWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVIS LESGDASIHDTVENLIILANNSLSSNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS GGGGSGGGGSGGGGSGGGGSITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTS SLTECVLNKATNVAHWTTPSLKCIRDPALVHQRPAPPSTVTTAGVTPQPESLSPSGKEPAA S
754	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGGSSPPVPLSLY SGPGSGSNWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLES GDASIHDTVENLIILANNSLSSNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS
755	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVCTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLVSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGPGSGSAVNGTSQ FTCFYNSRANISCVWSQDGALQDTSCQVHAWPDRRRWNQTCELLPVSQASWACNLILG APDSQKLTTVDIVTLRVLCREGVRWRVMAIQDFKPFENLRLMAPISLQVVHVETHRCNIS WEISQASHYFERHLEFEARTLSPGHTWEEAPLLTLKQKQEWICLETLTPDTQYEFQVRVK PLQGEFTTWSPWSQPLAFRTKPAALGKDPGGPSPVPLSLYSGGPITCPPPMSVEHADIWVK SYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIRDPALVHQRPAPPS GGGGSGGGGSGGGGSGGGGSNWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTA MKCFLLELQVISLESGDASIHDTVENLIILANNSLSSNGNVTESGCKECEELEEKNIKEFLQ SFVHIVQMFINTS
756	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVCTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLVSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGPGSGSAVNGTSQ FTCFYNSRANISCVWSQDGALQDTSCQVHAWPDRRRWNQTCELLPVSQASWACNLILG APDSQKLTTVDIVTLRVLCREGVRWRVMAIQDFKPFENLRLMAPISLQVVHVETHRCNIS WEISQASHYFERHLEFEARTLSPGHTWEEAPLLTLKQKQEWICLETLTPDTQYEFQVRVK PLQGEFTTWSPWSQPLAFRTKPAALGKDSGSGGSPVPLSLYSGGPITCPPPMSVEHADIWV KSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIRDPALVHQRPAP PSGGGGSGGGGSGGGGSGGGGSNWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVT AMKCFLLELQVISLESGDASIHDTVENLIILANNSLSSNGNVTESGCKECEELEEKNIKEFL QSFVHIVQMFINTS
757	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVCTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLVSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGPGSGSAVNGTSQ FTCFYNSRANISCVWSQDGALQDTSCQVHAWPDRRRWNQTCELLPVSQASWACNLILG APDSQKLTTVDIVTLRVLCREGVRWRVMAIQDFKPFENLRLMAPISLQVVHVETHRCNIS WEISQASHYFERHLEFEARTLSPGHTWEEAPLLTLKQKQEWICLETLTPDTQYEFQVRVK PLQGEFTTWSPWSQPLAFRTKPAALGKDGGGSSPVPLSLYSGGPITCPPPMSVEHADIWV KSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIRDPALVHQRPAP PSGGGGSGGGGSGGGGSGGGGSNWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVT

SEQ ID	AMINO ACID SEQUENCE
	AMKCFLLELQVISLESGDASIHDTVENLIILANNSLSSNGNVTESGCKECEELEEKNIKEFL QSFVHIVQMFINTS
758	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGGSSPPVPLSLY SGPSGSPGNWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLE SGDASIHDTVENLIILANNSLSSNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTSG GSGGGSGGGSGGGSGGGSGITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSS LTECVLNKATNVAHWTTPSLKCIRDPALVHQRPAPPSTVTTAGVTPQPESLSPSGKEPAAS SPSSNNTAATTAAIVPGSQLMPSKSPSTGTTEISSHESSHGTPSQTTAKNWELTASASHQPP GVYPQGHSDTT
759	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGGSSPPVPLSLY SGPSGSPGNWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLE SGDASIHDTVENLIILANNSLSSNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTSG GSGGGSGGGSGGGSGGGSGGGSGITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKA GTSSLTECVLNKATNVAHWTTPSLKCIRDPALVHQRPAPPSTVTTAGVTPQPESLSPSGKE PAASSPSSNNTAATTAAIVPGSQLMPSKSPSTGTTEISSHESSHGTPSQTTAKNWELTASAS HQPPGVYPQGHSDTT
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SEQ ID	AMINO ACID SEQUENCE
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784	APTSSSTKKTQLQLEHLCLFLQMILNGILNYKNPKLTRMLTFKFYMPKKATELKHLQCLE EELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWI TFCQSIISTLT

SEQ ID	AMINO ACID SEQUENCE
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794	SG
795	PGSG
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804	GGSPGGVPLSLYSGP
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SEQ ID	AMINO ACID SEQUENCE
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2019347751 27 Mar 2025

CLAIMS

What is claimed is:

1. A masked cytokine comprising:

a) a first half-life extension domain and a second half-life extension domain, wherein the first half-life extension domain is a first Fc domain or fragment thereof, and the second half-life extension domain is a second Fc domain or fragment thereof;

b) a masking moiety comprising an amino acid sequence having at least about 98% sequence identity to the amino acid sequence of SEQ ID NO: 10; and

c) a cytokine wherein the cytokine is an IL-2 polypeptide, wherein the IL-2 polypeptide comprises the amino acid sequence of SEQ ID NO: 3,

wherein the masking moiety is linked to the first half-life extension domain via a first linker, wherein the first linker comprises a cleavable peptide;

wherein the cytokine is linked to the second half-life extension domain via a second linker; and

wherein the first half-life extension domain and the second half-life extension domain contain modifications promoting the association of the first and the second half-life extension domain.

2. A masked cytokine comprising:

a) a first polypeptide comprising a first half-life extension domain and a masking moiety and

b) a second polypeptide comprising a second half-life extension domain and a cytokine;

wherein the first half-life extension domain is a first Fc domain or fragment thereof, and the second half-life extension domain is a second Fc domain or fragment thereof;

wherein the masking moiety comprises an amino acid sequence of SEQ ID NO: 826

wherein the cytokine is an IL-2 polypeptide comprising the amino acid sequence of SEQ ID NO: 3;

wherein the masking moiety is linked to the C-terminus of the first half-life extension domain via a first linker;

wherein the cytokine is linked to the C-terminus of the second half-life extension domain via a second linker, wherein the second linker comprises a cleavable peptide; and

wherein the first half-life extension domain and the second half-life extension domain contain modifications promoting the association of the first and the second half-life extension domain.

3. The masked cytokine of claim 1, wherein the masking moiety comprises an amino acid sequence of SEQ ID NO: 826.

4. The masked cytokine of any one of claims 1-3, wherein the first Fc domain or fragment thereof comprises an amino acid sequence of SEQ ID NO: 155, and the second Fc domain or fragment thereof comprises an amino acid sequence of SEQ ID NO: 156.

5. The masked cytokine of any one of claims 1-3, wherein the cleavable peptide comprises an amino acid sequence of SEQ ID NO: 96.

6. The masked cytokine of claim 1 or claim 3, wherein the first linker comprises an amino acid sequence of SEQ ID NO: 15, and the second linker comprises an amino acid sequence of SEQ ID NO: 339.

7. The masked cytokine of claim 2, wherein the cleavable peptide comprises an amino acid sequence of SEQ ID NO: 135.

8. The masked cytokine of claim 2, wherein the first linker comprises an amino acid sequence of SEQ ID NO: 28, and the second linker comprises an amino acid sequence of SEQ ID NO: 35.

9. The masked cytokine of claim 1, wherein the masking moiety comprises an amino acid sequence of SEQ ID NO: 826; wherein the first Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 155, and the second Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 156; and wherein the first linker comprises an amino acid sequence of SEQ ID NO: 15, and the second linker comprises an amino acid sequence of SEQ ID NO: 339.

10. The masked cytokine of claim 2, wherein the first Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 155, and the second Fc domain or fragment thereof comprises the amino acid sequence of SEQ ID NO: 156; and
wherein the first linker comprises an amino acid sequence of SEQ ID NO: 28, and the second linker comprises an amino acid sequence of SEQ ID NO: 35.

11. A pharmaceutical composition comprising the masked cytokine of any one of claims 1-10, and a pharmaceutically acceptable carrier.

12. A kit comprising the masked cytokine of any one of claims 1-10.

13. A nucleic acid encoding a masked cytokine of any one of claims 1-10.

14. A vector comprising the nucleic acid of claim 13.

15. An isolated host cell comprising the nucleic acid of claim 13.

16. A method of producing a masked cytokine comprising culturing the isolated host cell of claim 15 under a condition that produces the masked cytokine.

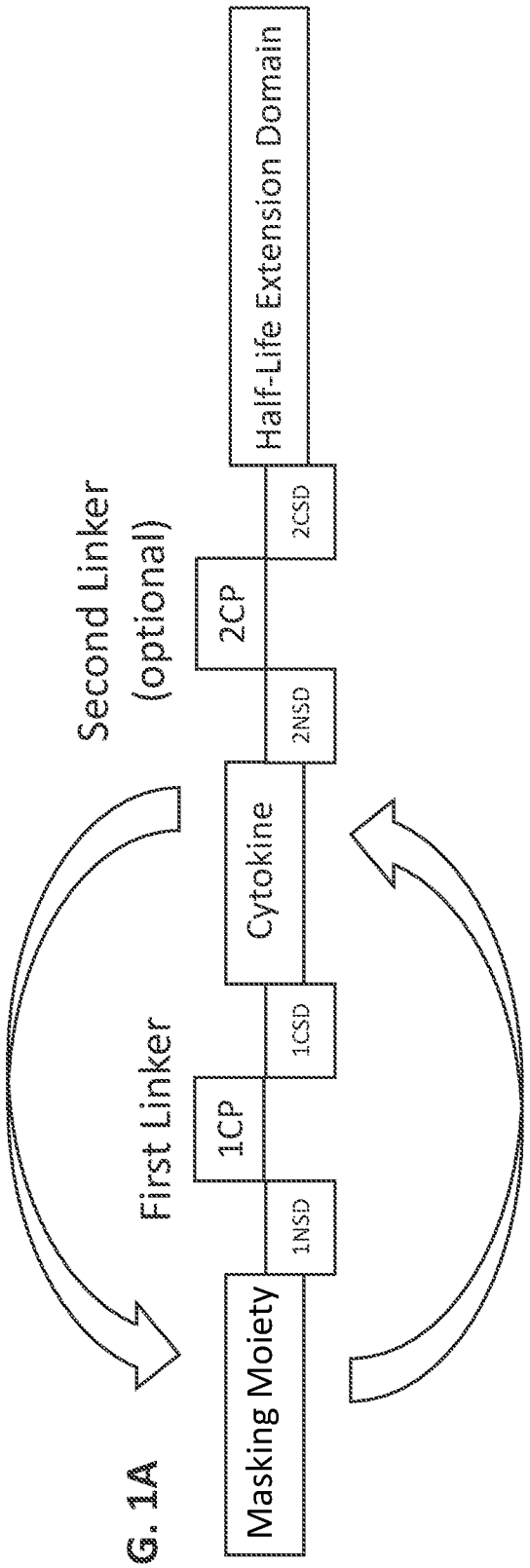

Masking Moiety
1NSD
1CP
1CSD
Cytokine
2NSD
2CP
2CSD
Half-Life Extension Domain
First Linker
Second Linker
(optional)

FIG. 1A

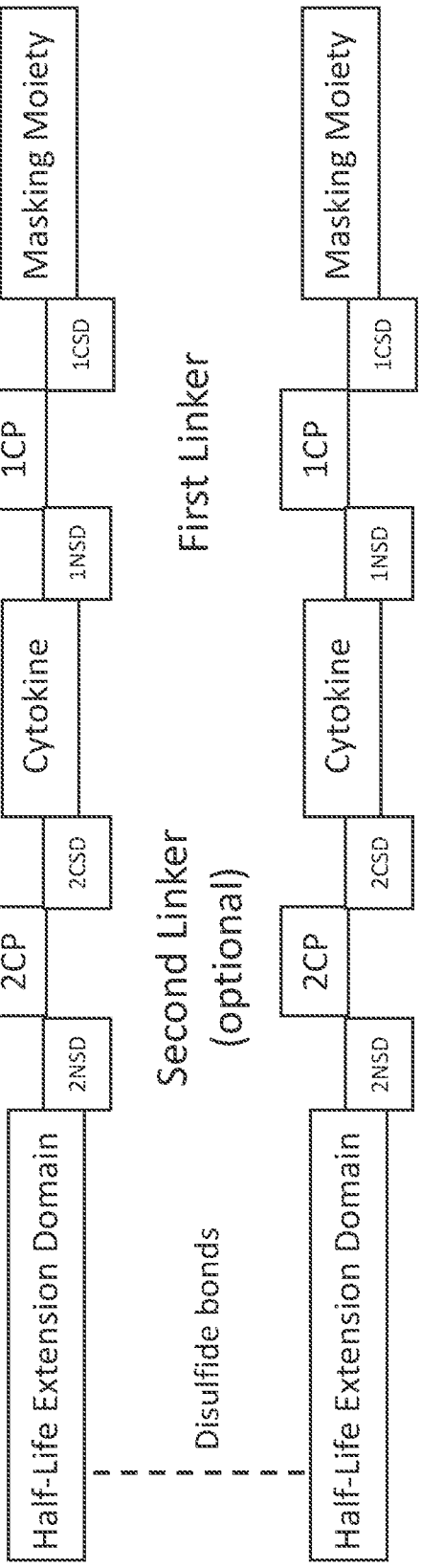

Half-Life Extension Domain
2NSD
2CP
2CSD
Cytokine
1NSD
1CP
1CSD
Masking Moiety
Disulfide bonds
First Linker
Second Linker
(optional)

FIG. 1B

FIG. 2A

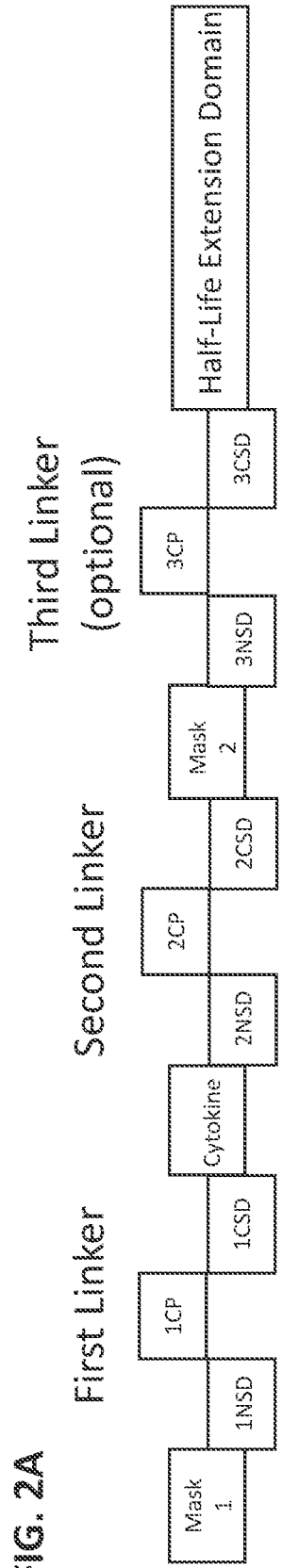
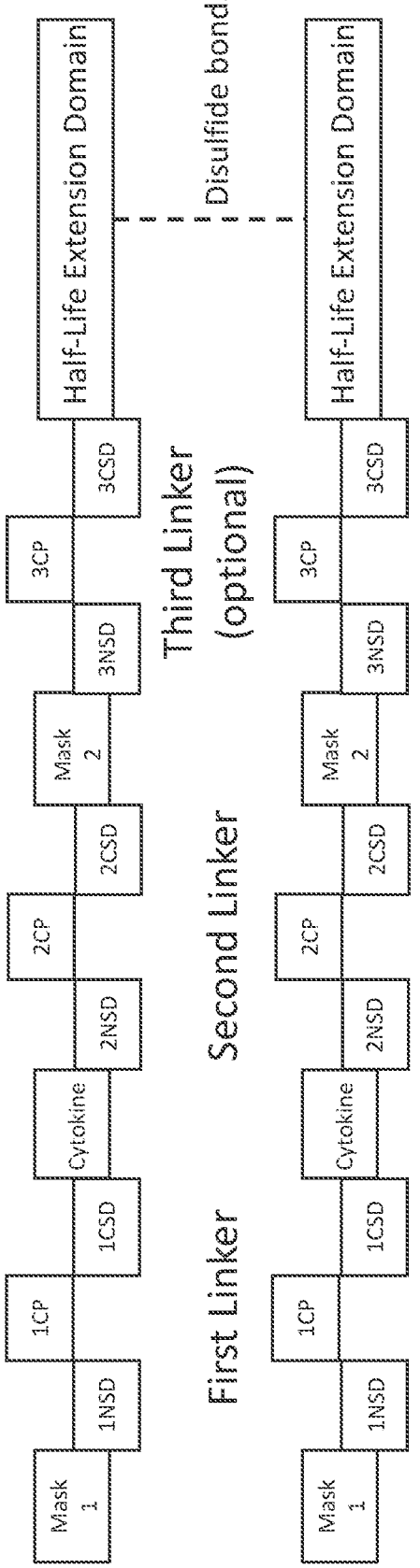

First Linker
Second Linker
Third Linker
(optional)
Mask 1
1NSD
1CP
1CSD
Cytokine
2NSD
2CP
2CSD
Mask 2
3NSD
3CP
3CSD
Half-Life Extension Domain

FIG. 2B


First Linker
Second Linker
Third Linker
(optional)
Disulfide bonds
Mask 1
1NSD
1CP
1CSD
Cytokine
2NSD
2CP
2CSD
Mask 2
3NSD
3CP
3CSD
Half-Life Extension Domain

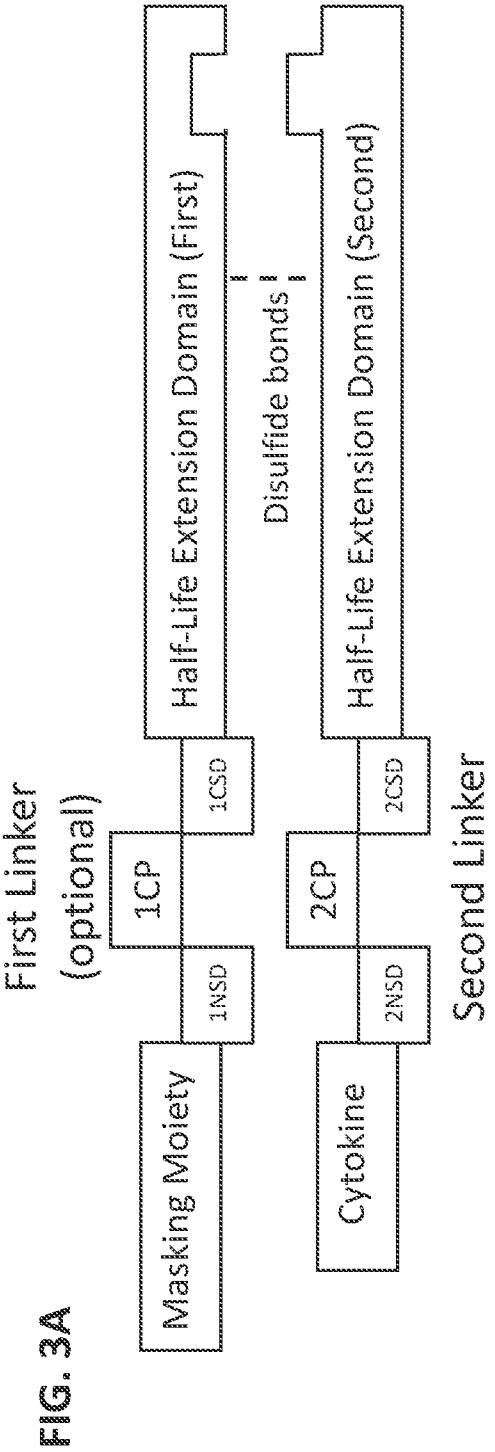

First Linker
(optional)
1CP
1CSD
Half-Life Extension Domain (First)
Masking Moiety
1NSD
Disulfide bonds
2CP
2CSD
Half-Life Extension Domain (Second)
Cytokine
2NSD
Second Linker
(optional)

FIG. 3A

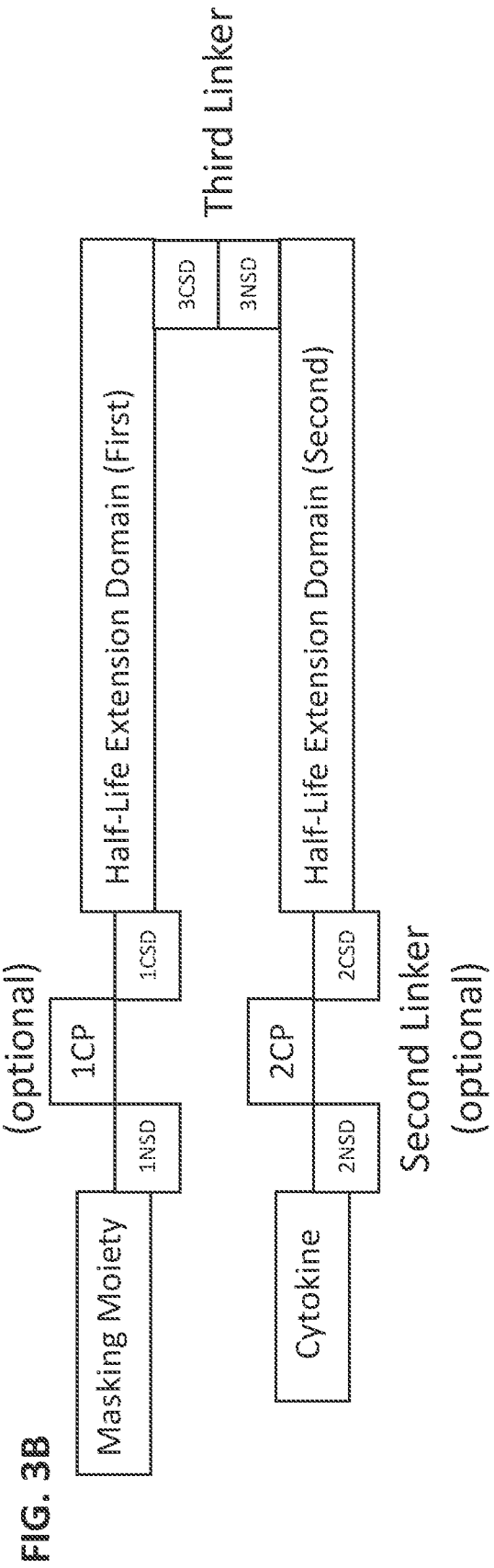

Third Linker
3CSD
3NSD
First Linker
(optional)
1CP
1CSD
Half-Life Extension Domain (First)
Masking Moiety
1NSD
2CP
2CSD
Half-Life Extension Domain (Second)
Cytokine
2NSD
Second Linker
(optional)

FIG. 3B

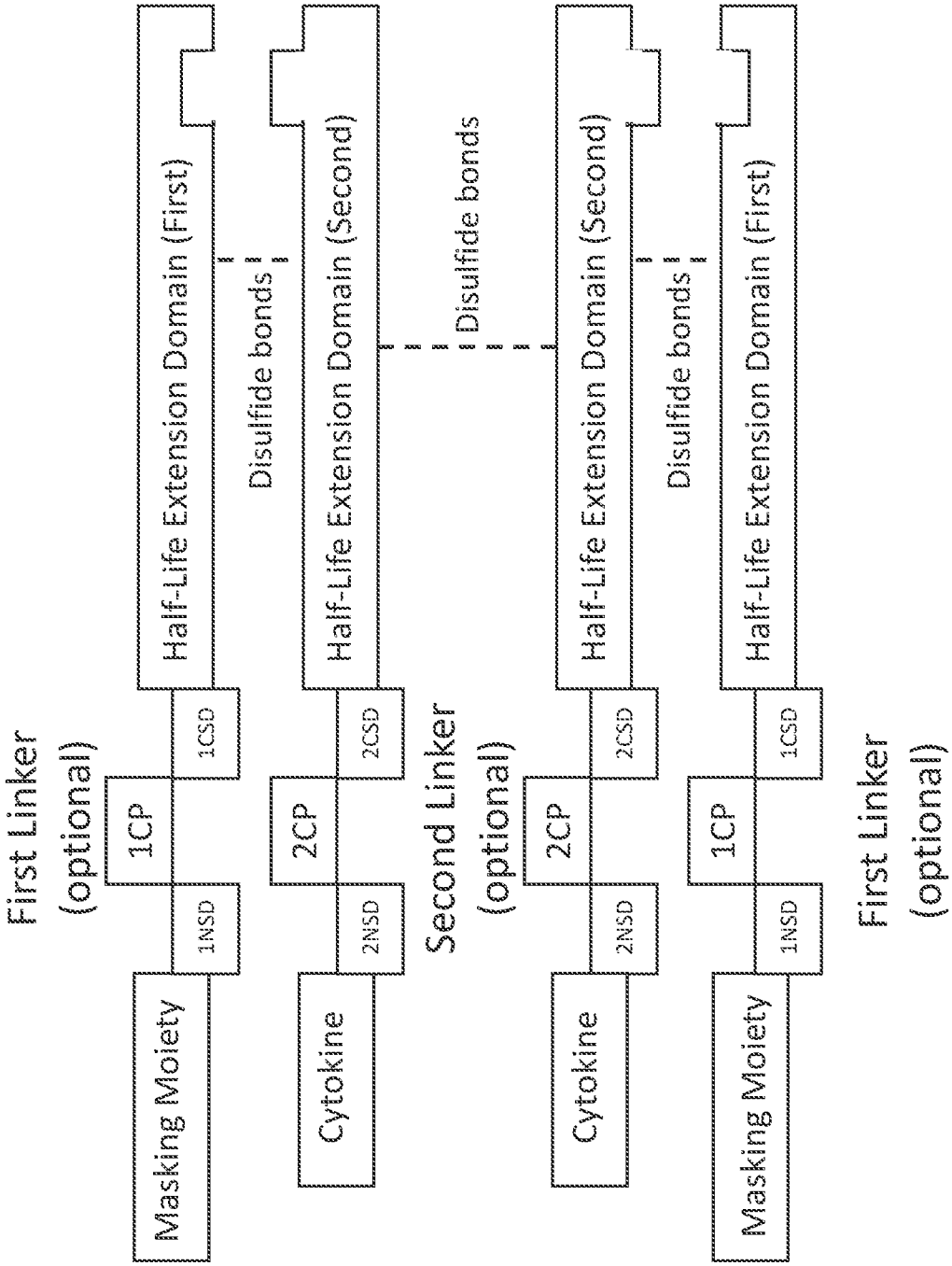

Masking Moiety
1NSD
1CP
1CSD
Half-Life Extension Domain (First)
First Linker (optional)
Disulfide bonds
Cytokine
2NSD
2CP
2CSD
Half-Life Extension Domain (Second)
Second Linker (optional)
Disulfide bonds
Cytokine
2NSD
2CP
2CSD
Half-Life Extension Domain (Second)
Disulfide bonds
Masking Moiety
1NSD
1CP
1CSD
Half-Life Extension Domain (First)
First Linker (optional)

Figure 4

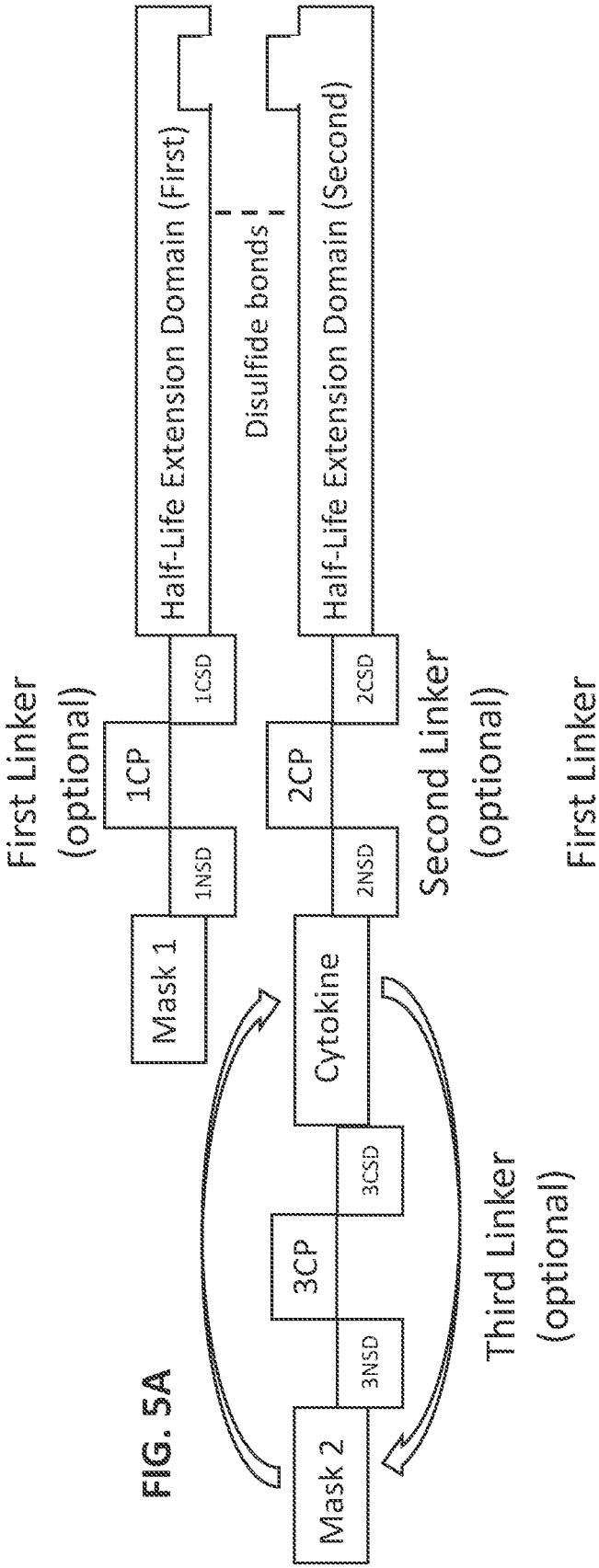

First Linker
(optional)
Mask 1
1NSD
1CP
1CSD
Half-Life Extension Domain (First)
Disulfide bonds
Half-Life Extension Domain (Second)
2CSD
2CP
2NSD
Second Linker
(optional)
Cytokine
3CSD
3CP
3NSD
Mask 2
Third Linker
(optional)

FIG. 5A

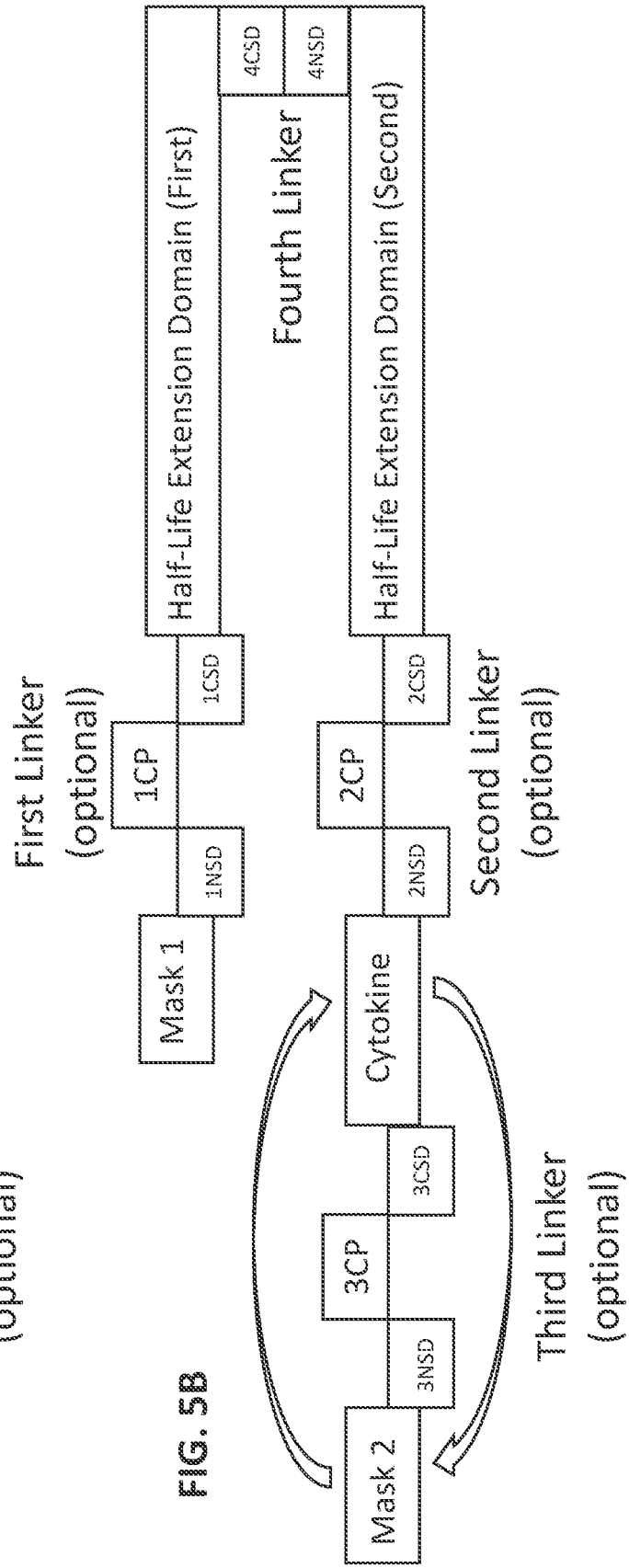

First Linker
(optional)
Mask 1
1NSD
1CP
1CSD
Half-Life Extension Domain (First)
Fourth Linker
4CSD
4NSD
Half-Life Extension Domain (Second)
2CSD
2CP
2NSD
Second Linker
(optional)
Cytokine
3CSD
3CP
3NSD
Mask 2
Third Linker
(optional)

FIG. 5B

Figure 6

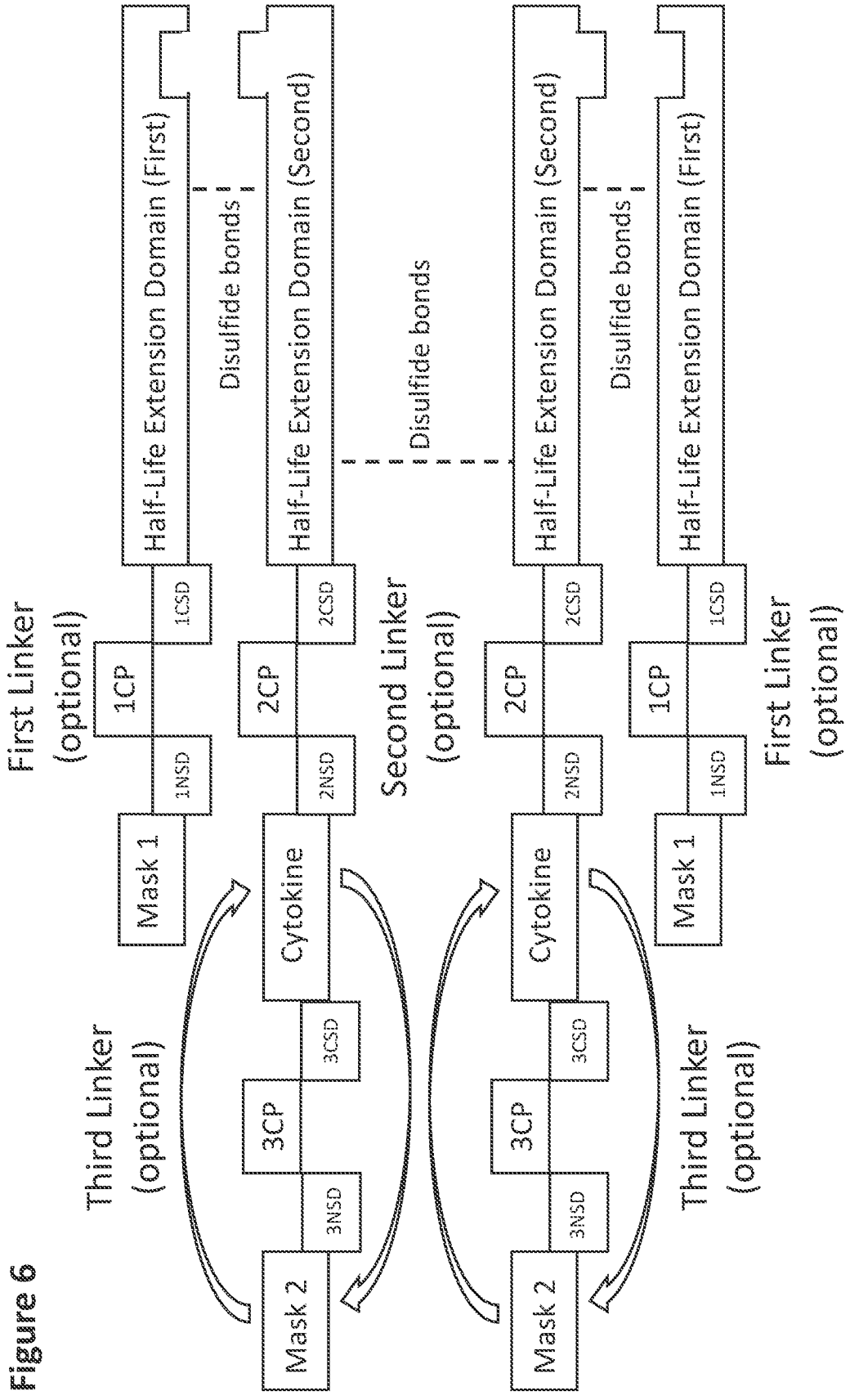

Half-Life Extension Domain (First)
Disulfide bonds
Half-Life Extension Domain (Second)
Disulfide bonds
Half-Life Extension Domain (Second)
Disulfide bonds
Half-Life Extension Domain (First)
First Linker (optional)
1CP
1CSD
2CP
2CSD
Second Linker (optional)
2CP
2CSD
1CP
1CSD
First Linker (optional)
Mask 1
1NSD
Cytokine
2NSD
Cytokine
2NSD
Mask 1
1NSD
Third Linker (optional)
3CP
3CSD
3CP
3CSD
Third Linker (optional)
Mask 2
3NSD
Mask 2
3NSD

FIG. 7A

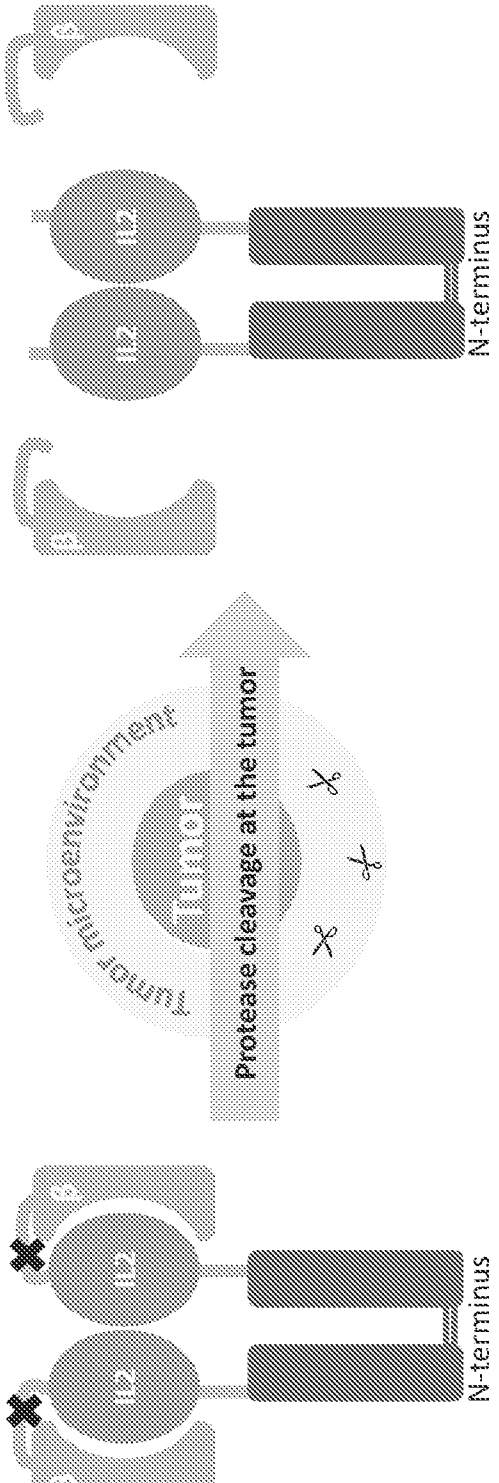

Tumor microenvironment
Tumor
Protease cleavage at the tumor
N-terminus

FIG. 7B

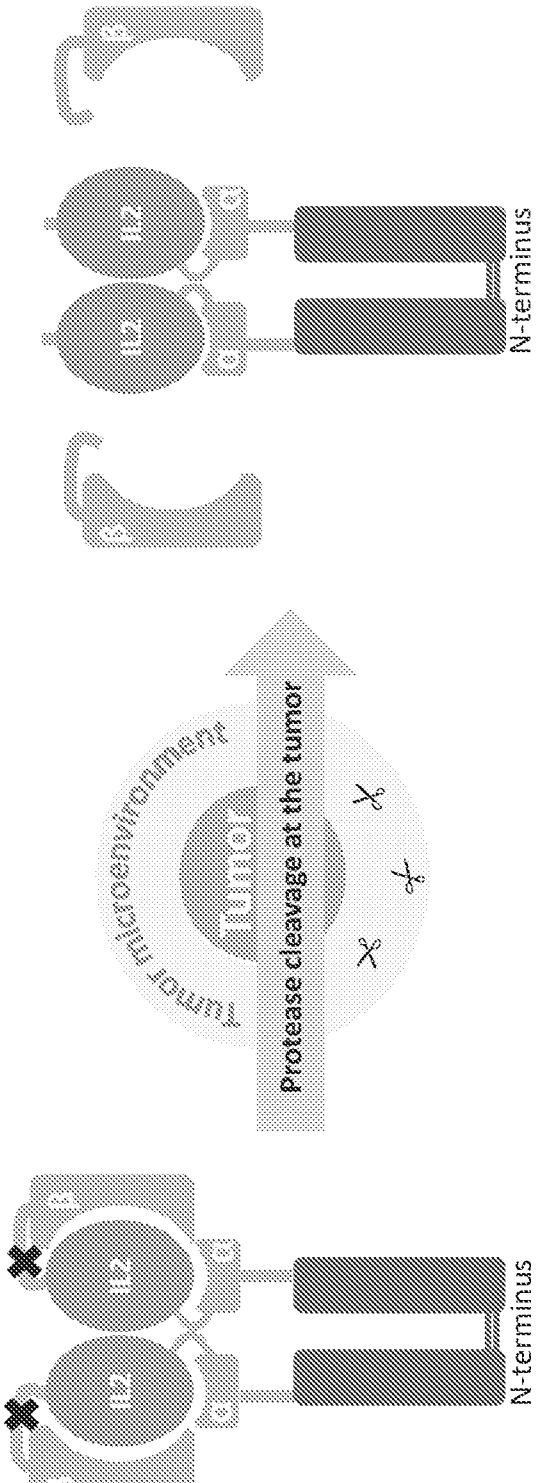

Tumor microenvironment
Tumor
Protease cleavage at the tumor
N-terminus

FIG. 7C

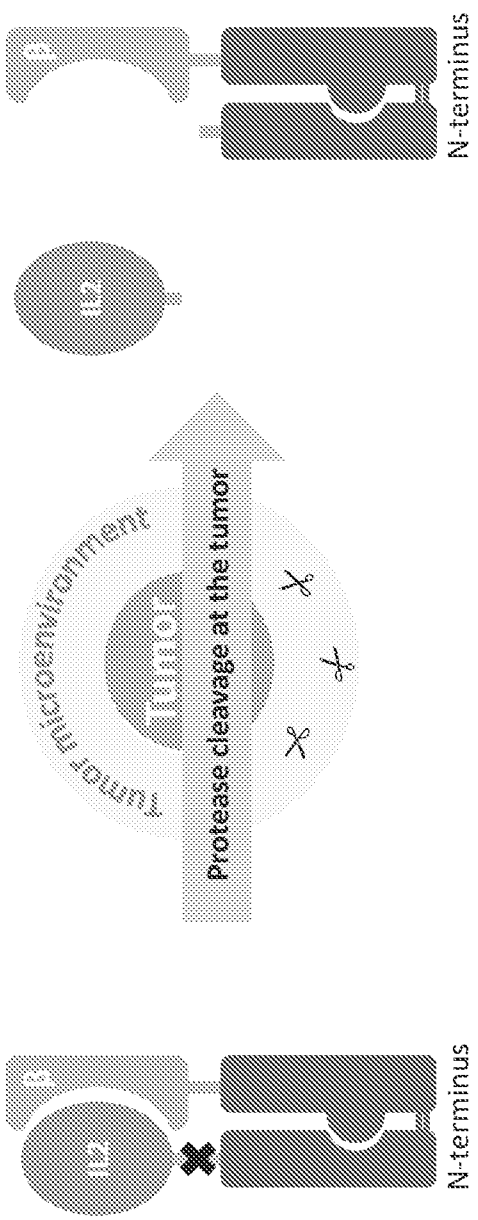
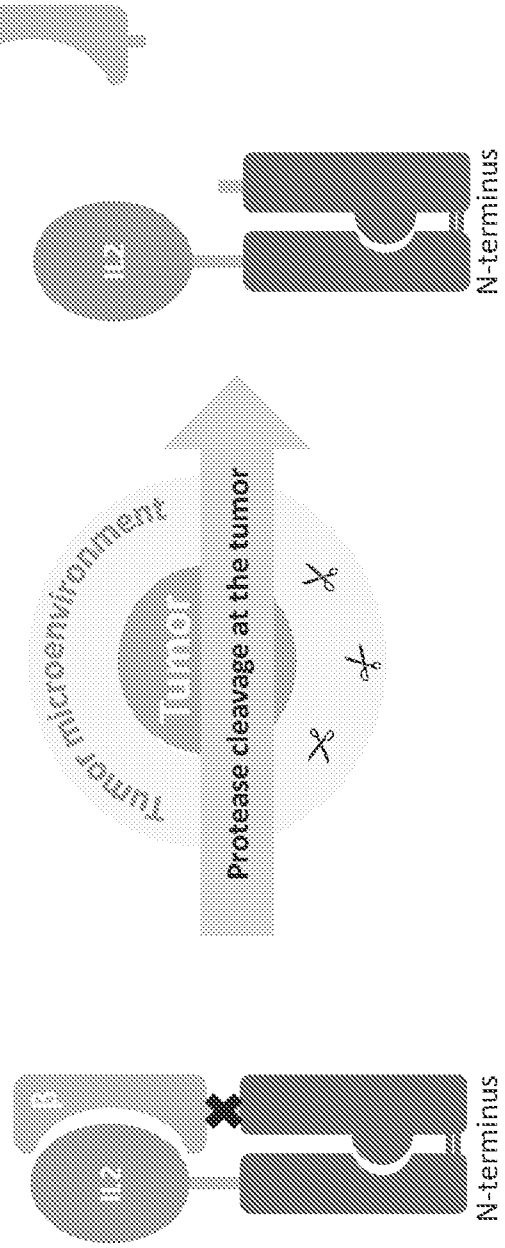

B
IL2
N-terminus
Protease cleavage at the tumor
Tumor microenvironment
Tumor
B
IL2
N-terminus

FIG. 7D


B
IL2
N-terminus
Protease cleavage at the tumor
Tumor microenvironment
Tumor
B
IL2
N-terminus

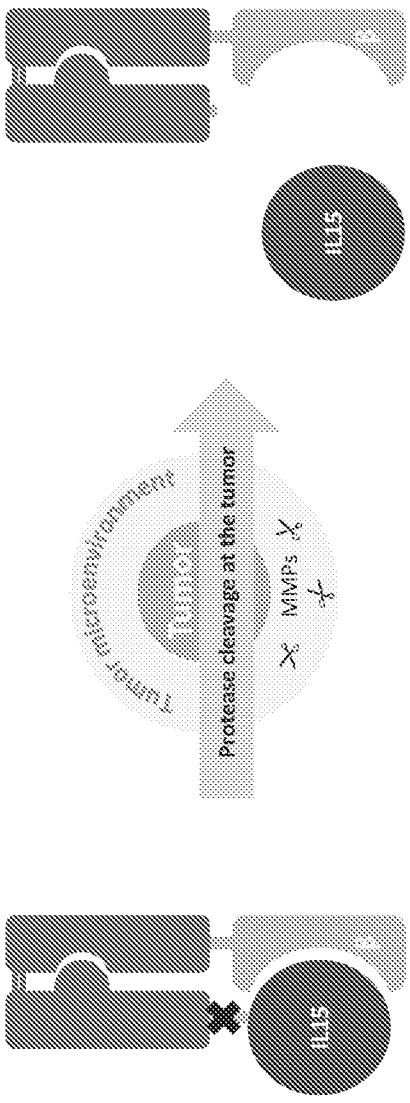

IL15
IL15
Protease cleavage at the tumor
MMPs
Tumor microenvironment
Tumor
IL15

FIG. 7E

Figure 8

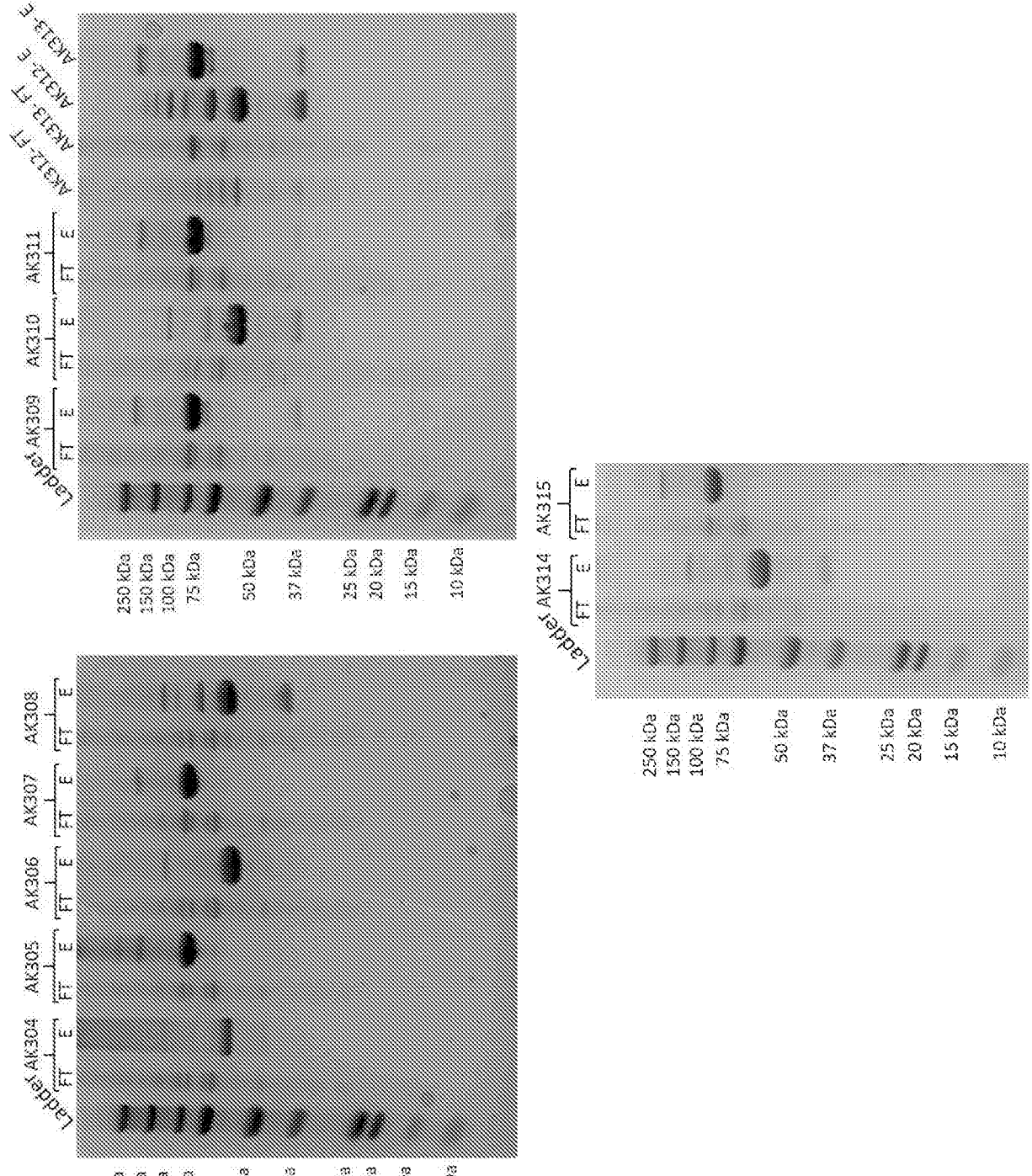

Ladder
AK304
FT
E
AK305
FT
E
AK306
FT
E
AK307
FT
E
AK308
FT
E
250 kDa
150 kDa
100 kDa
75 kDa
50 kDa
37 kDa
25 kDa
20 kDa
15 kDa
10 kDa
Ladder
AK309
FT
E
AK310
FT
E
AK311
FT
E
AK312-FT
AK313-FT
AK312-E
AK313-E
Ladder
AK314
FT
E
AK315
FT
E

FIG. 9A

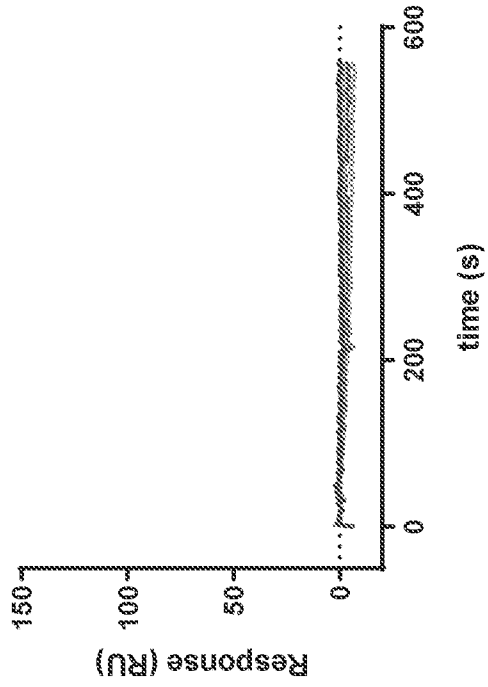


FIG. 9B

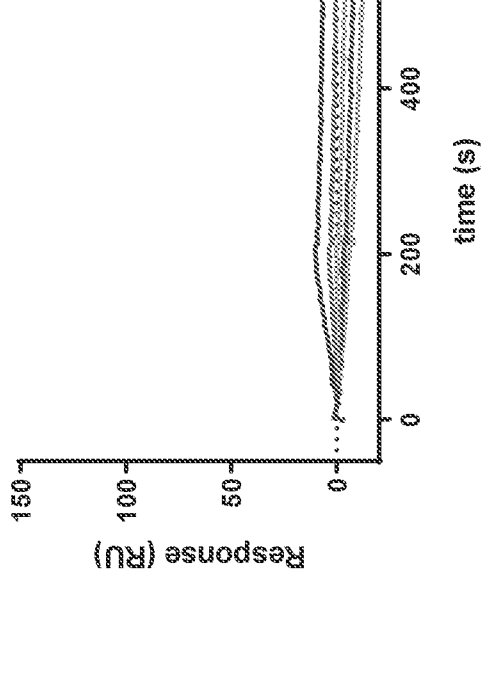


FIG. 9C

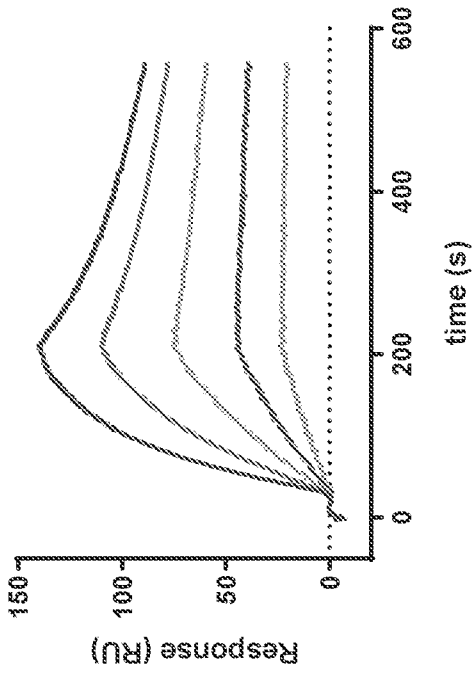


FIG. 9D

Sample	ka (1/(M*s))	kd (1/s)	KD	Chi2	U-value: kd (%)
AK215	ND	ND	ND	ND	ND
AK216	ND	ND	ND	ND	ND
rhIL2	8.61e+5	1.04e-3	1.21 nM	4.86	1.2

FIG. 10A

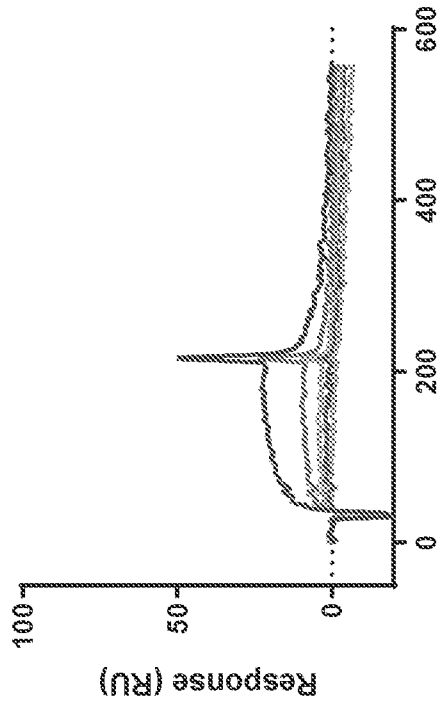


FIG. 10B

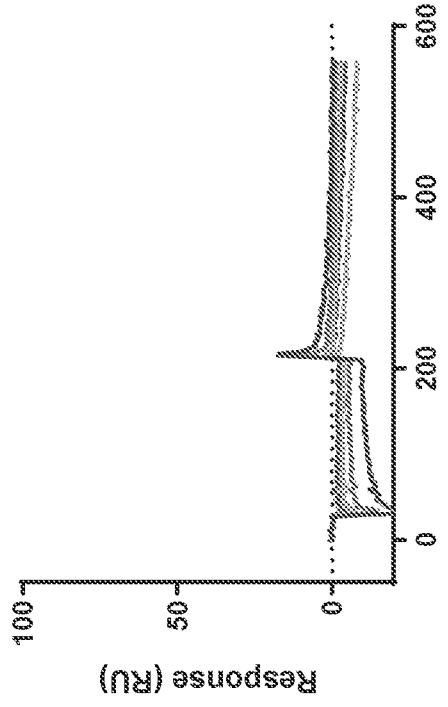


FIG. 10C

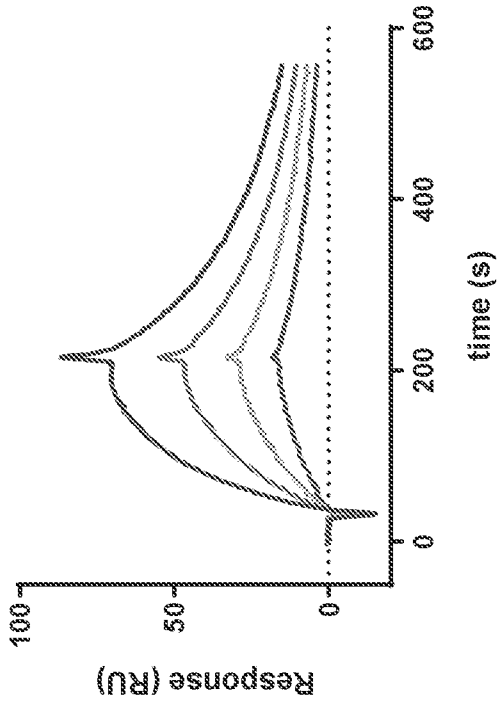


FIG. 10D

Sample	ka (1/(M*s))	kd (1/s)	KD	Chi2	U-value: kd (%)
AK216	ND	ND	ND	ND	ND
AK218	ND	ND	ND	ND	ND
rhIL2	3.95e+4	4.83e-3	122 nM	2.06	1.00

FIG. 11A

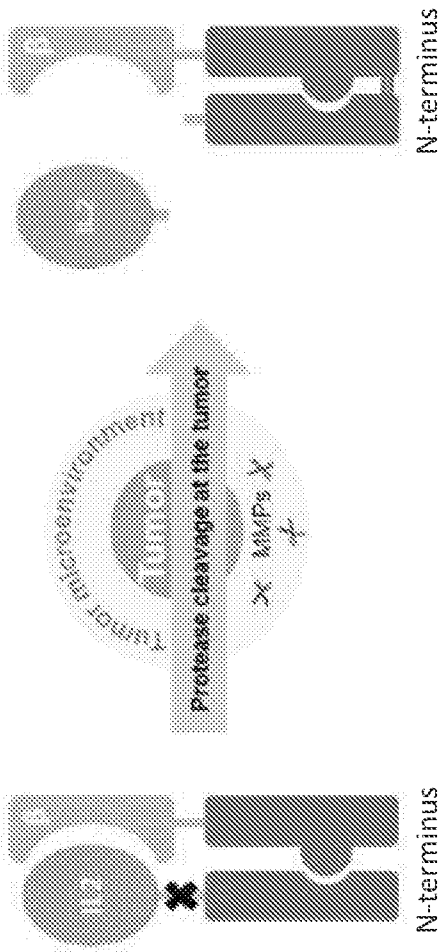
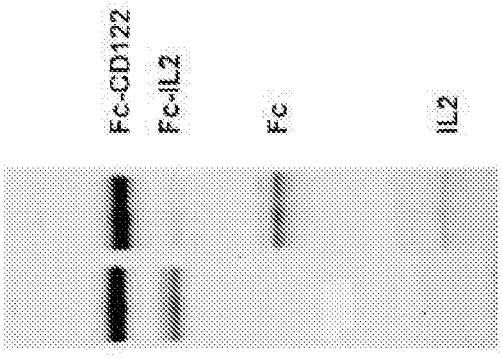


FIG. 11B



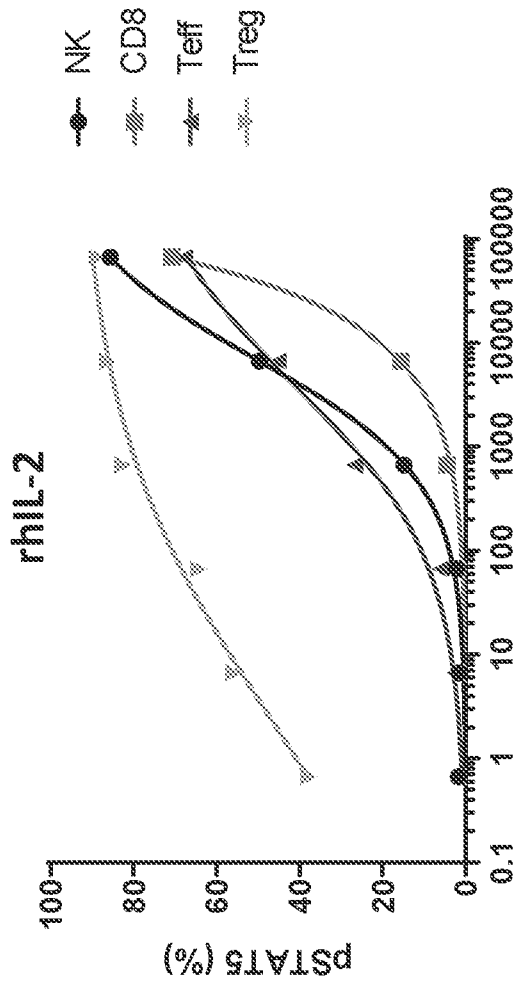


FIG. 12A

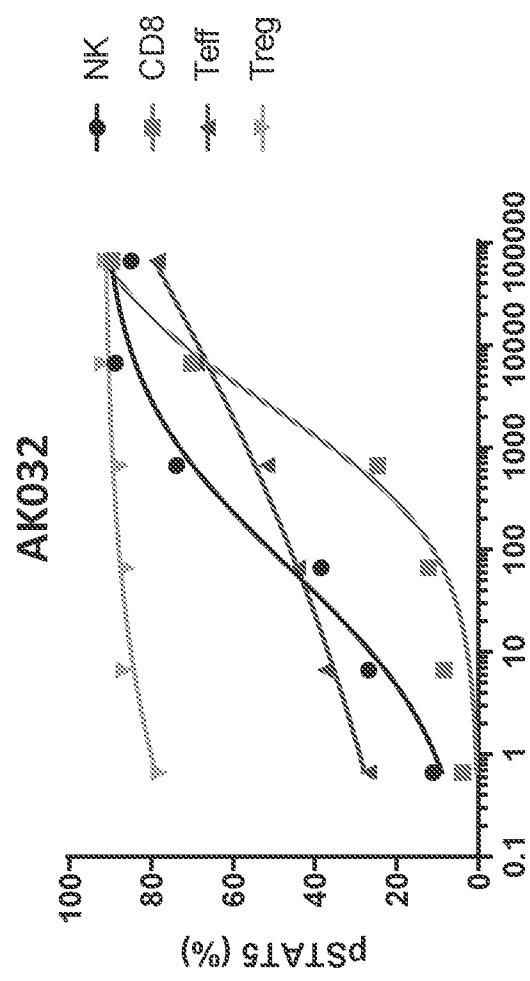


FIG. 12B

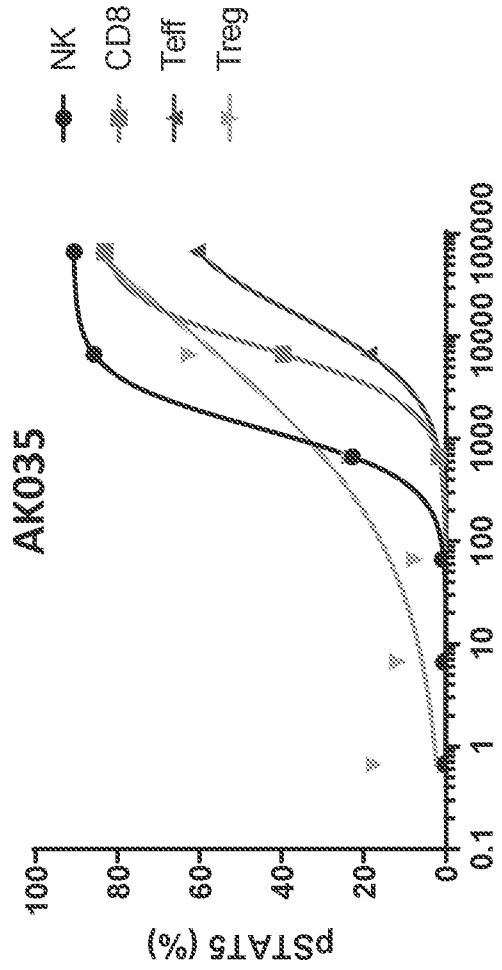


FIG. 12C

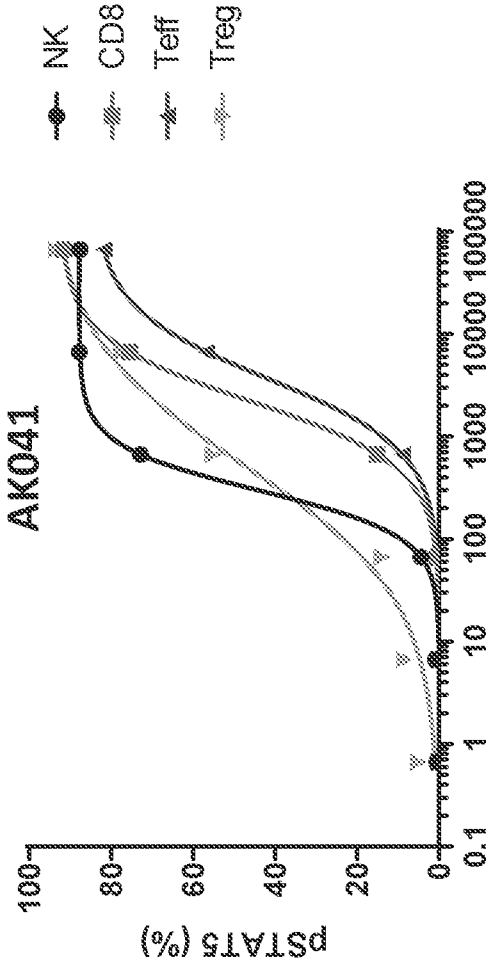


FIG. 12D

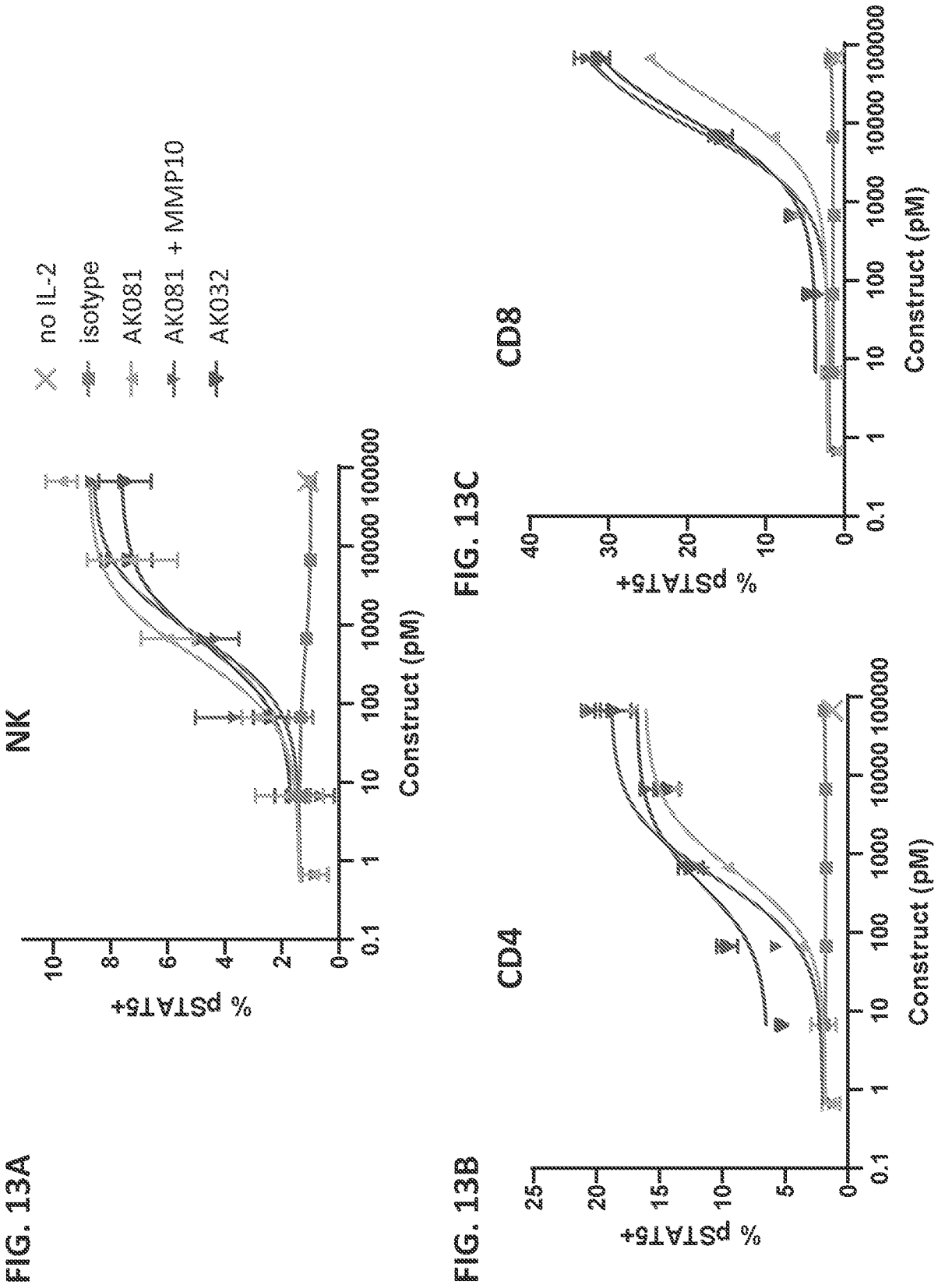


FIG. 13A

FIG. 13B

FIG. 13C

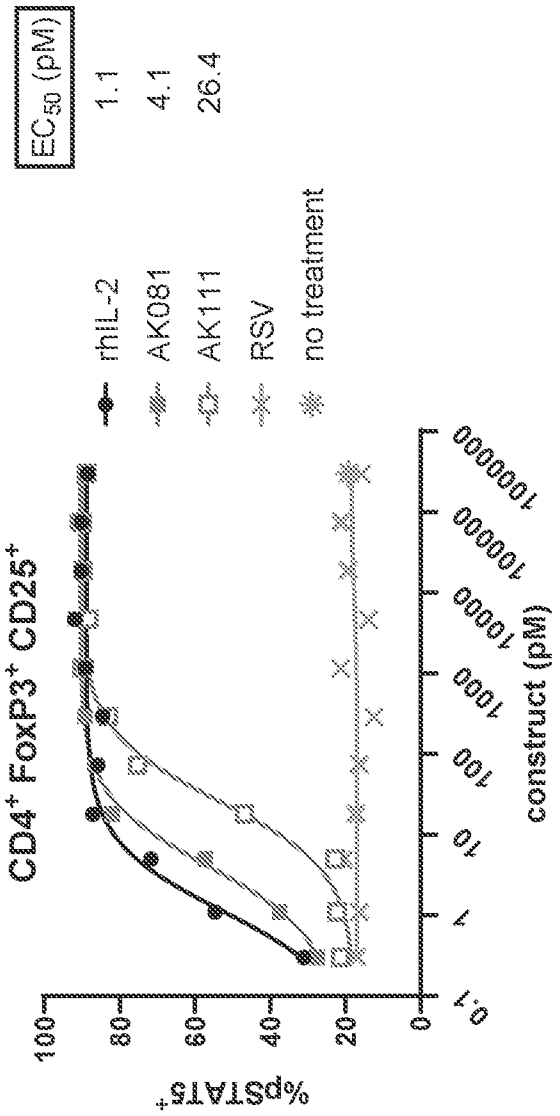


FIG. 14A

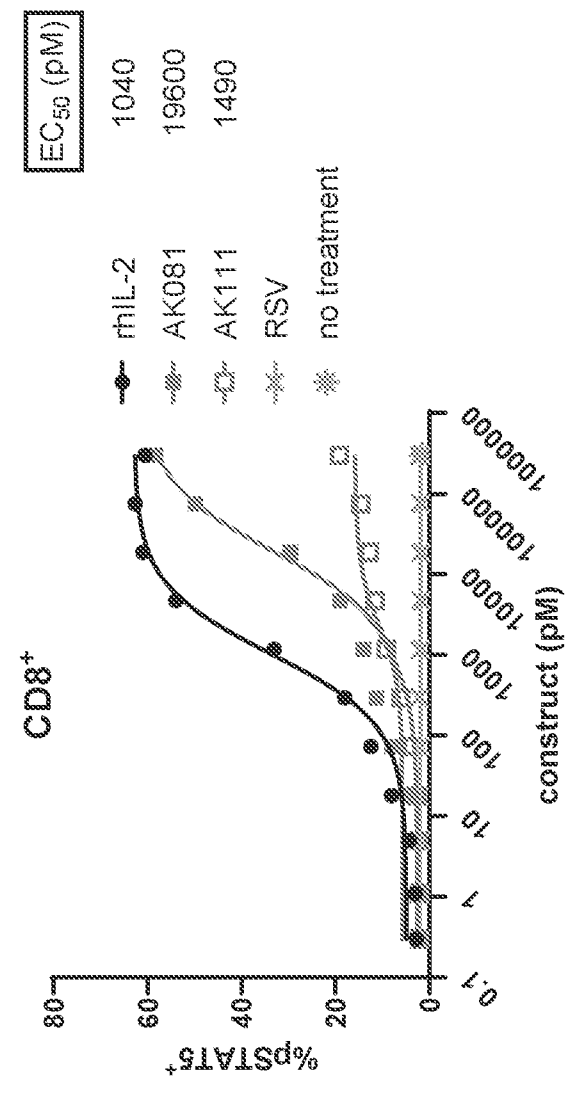


FIG. 14B

FIG. 14C

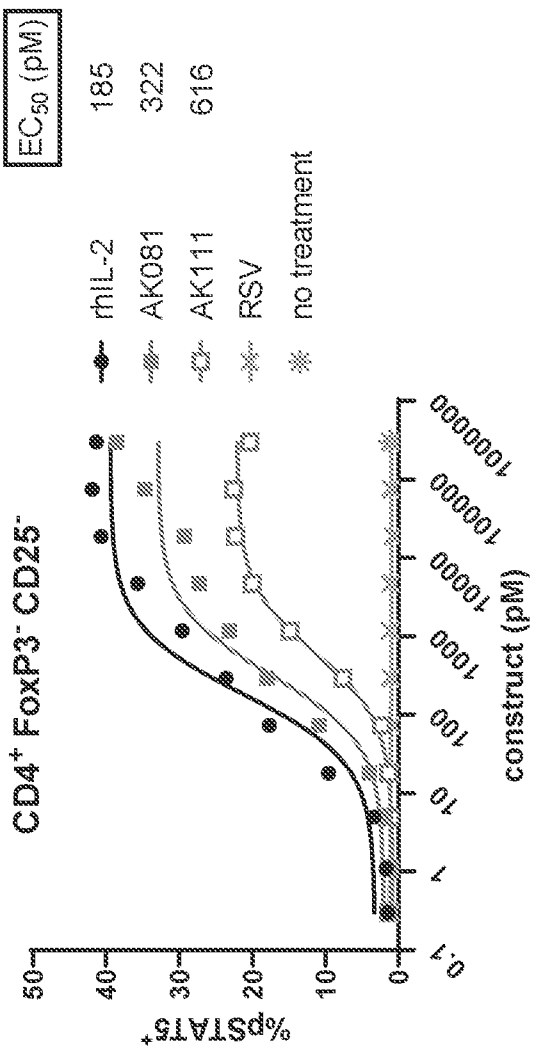


FIG. 14D

Construct	FoxP3+ T_{reg}		CD4+ T_{help}		CD8+ T_{cyto}	
	EC_{50} (pM)	Fold-change	EC_{50} (pM)	Fold-change	EC_{50} (pM)	Fold-change
rhIL-2	1.1		1040		185	
AK081	4.1	3.7	19600	18.8	322	1.7
AK111	26.4	24.0	1490*	1.4*	616	3.3

**Prism was able to find a best-fit value, but was unable to calculate a complete confidence interval. This best-fit value should be interpreted with caution.*

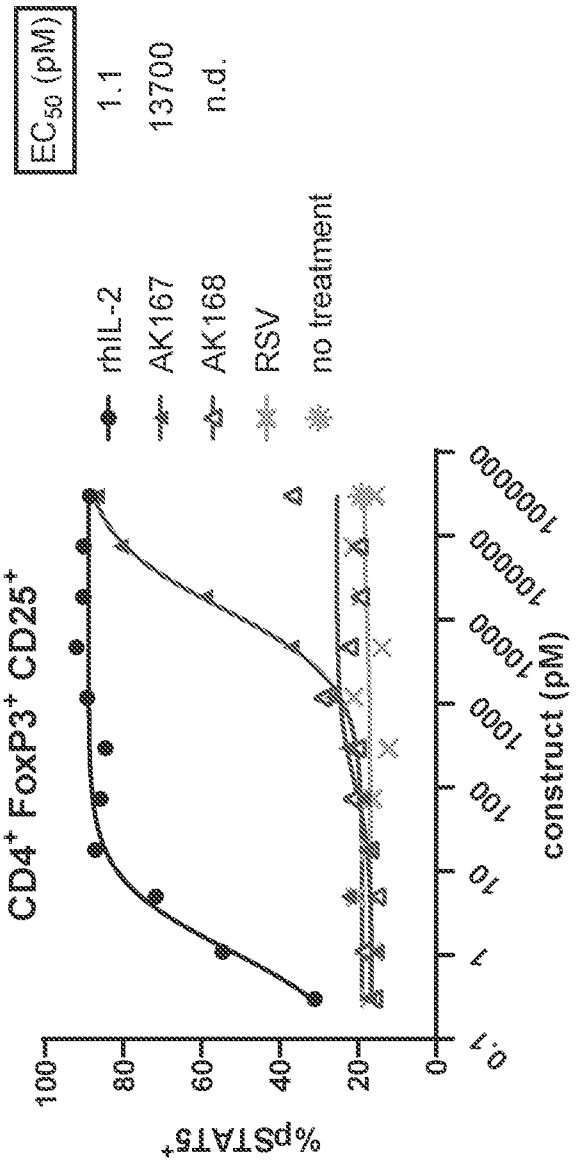


FIG. 15A

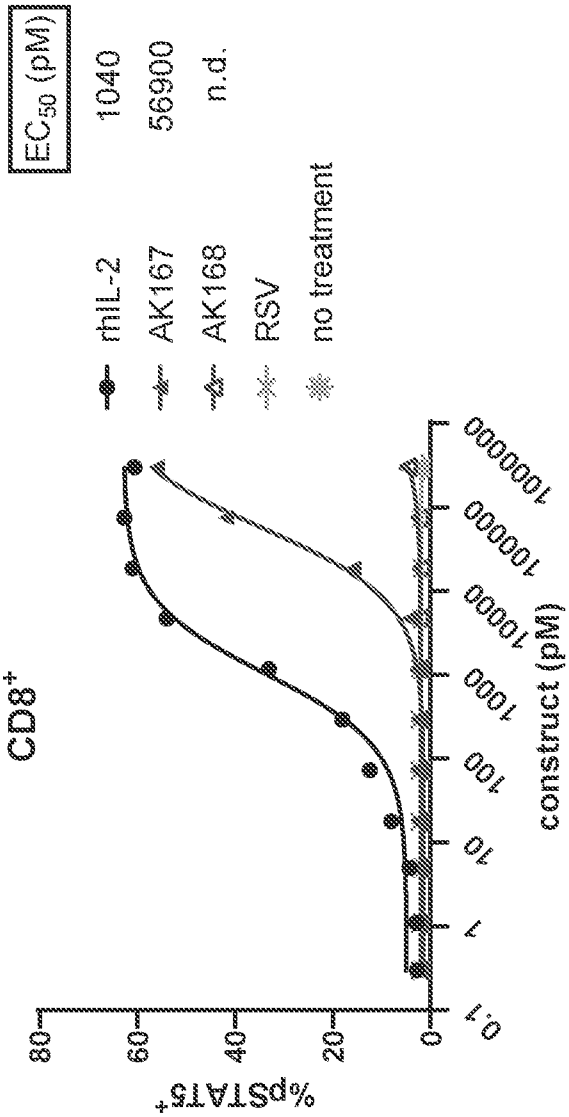


FIG. 15B

FIG. 15C

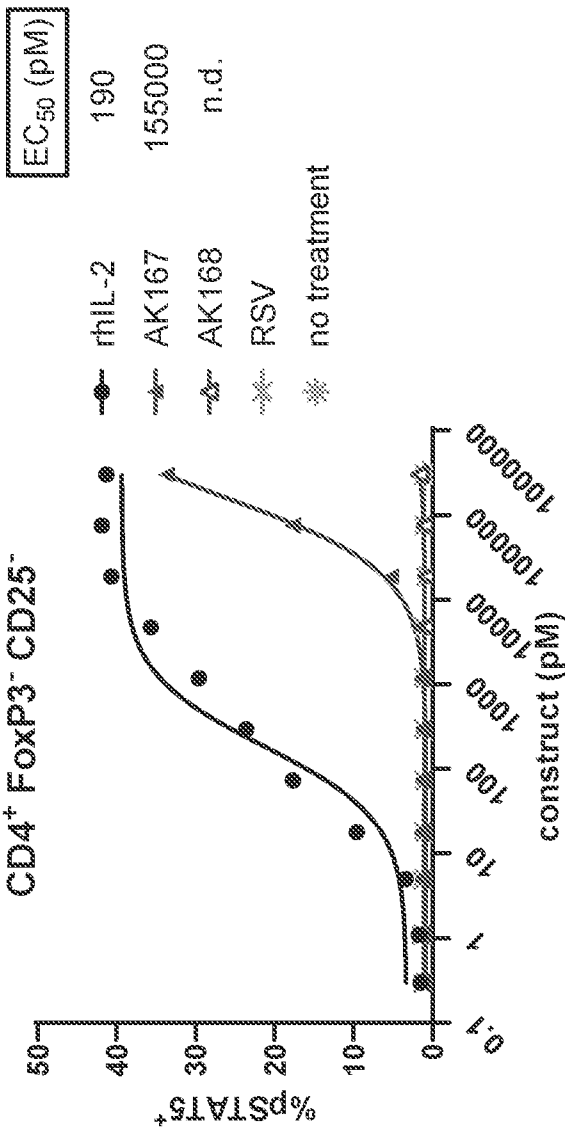


FIG. 15D

Construct	FoxP3+ Treg		CD4+ Thelp		CD8+ Tcyto	
	EC50 (pM)	*Fold-change*	*EC50 (pM)*	*Fold-change*	*EC50 (pM)*	*Fold-change*
rhIL-2	1.1		1040		190	
AK167	13700	12455	56900	55	155000	816
AK168	*n.d.*		*n.d.*		*n.d.*	

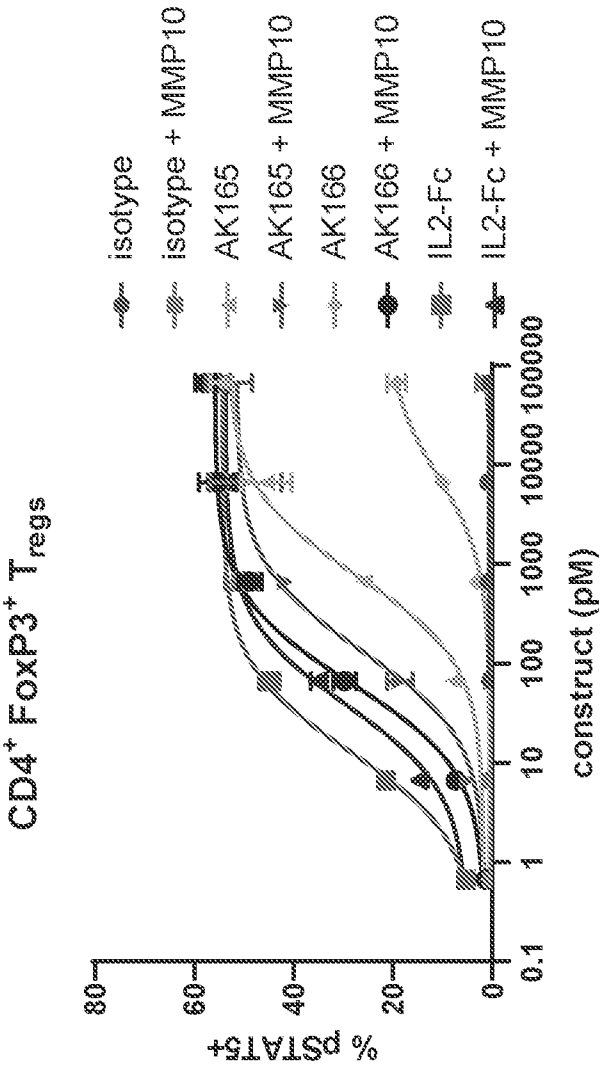


FIG. 16A

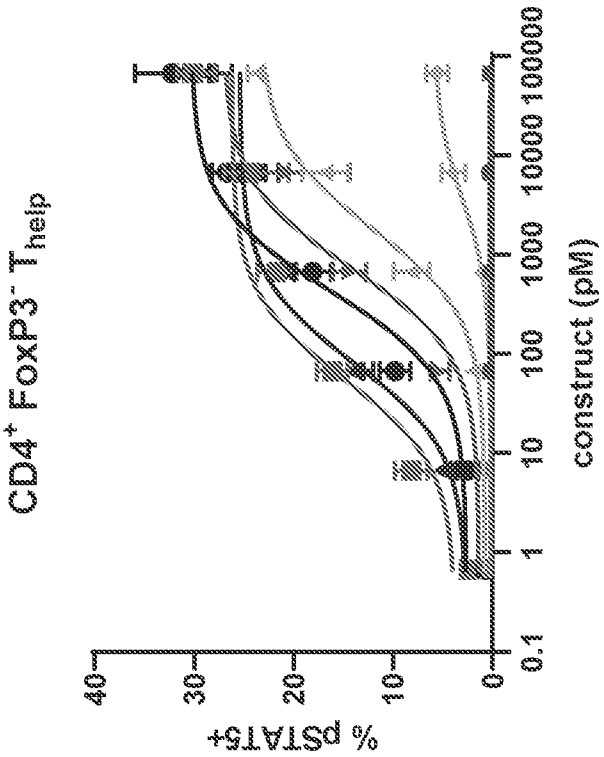


FIG. 16B

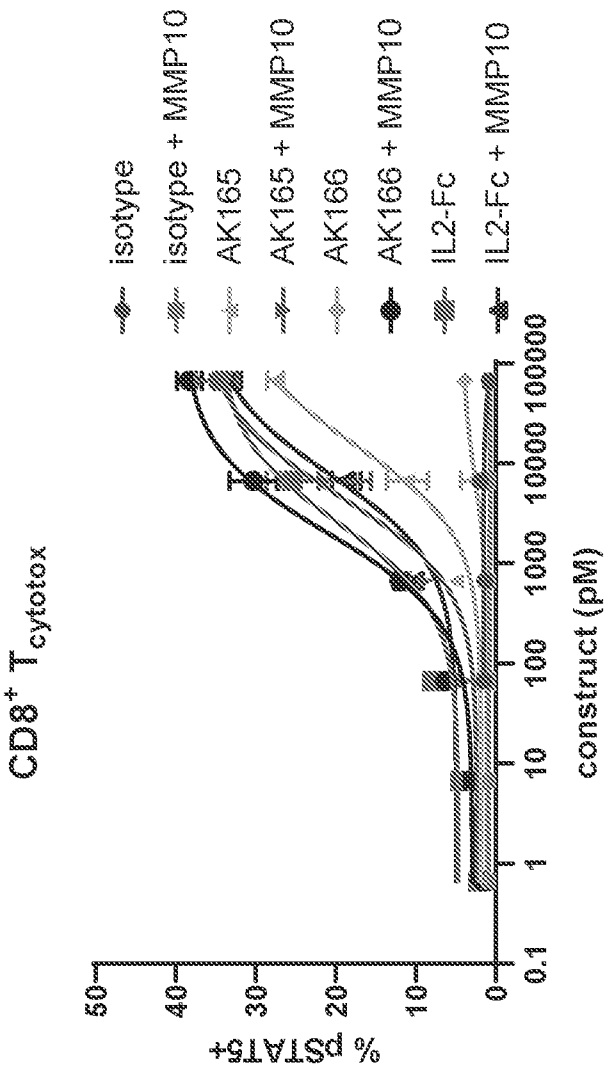


FIG. 16C

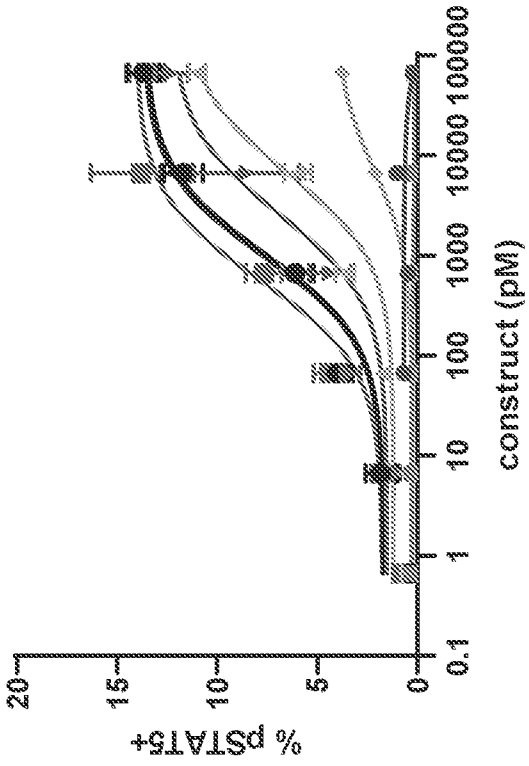


FIG. 16D

FIG. 17A

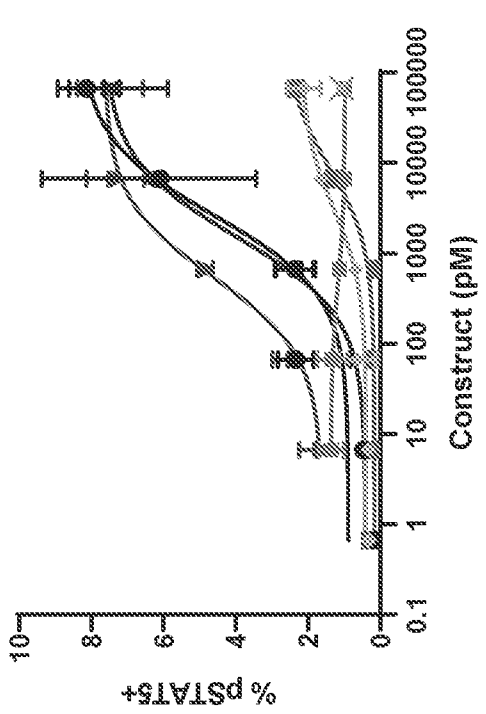


FIG. 17B

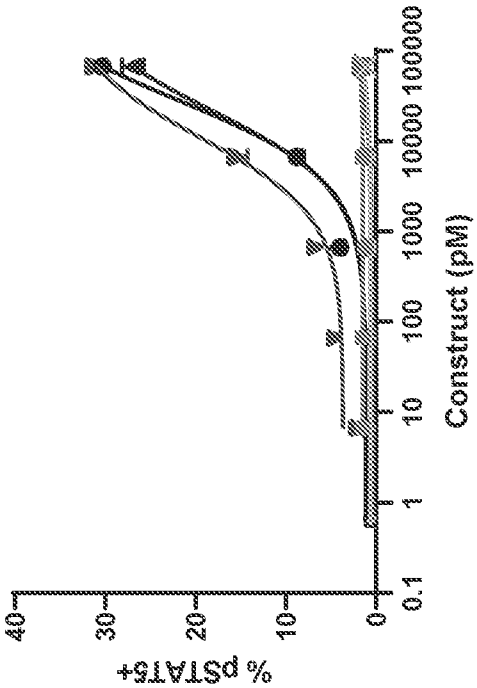
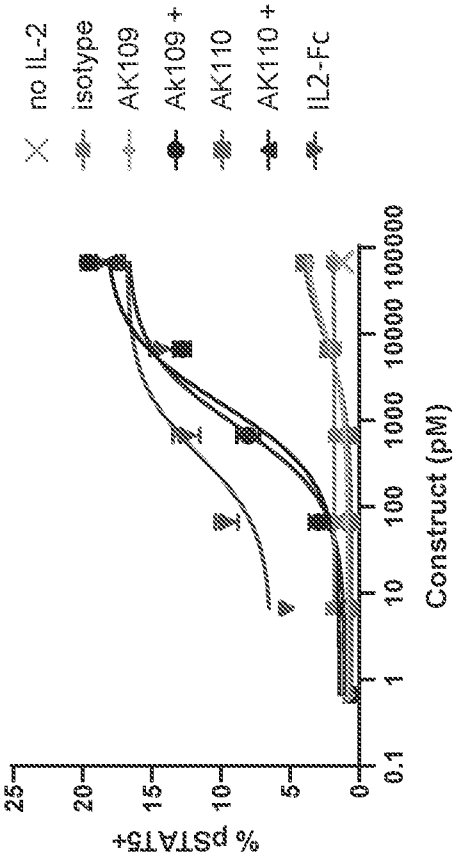


FIG. 17C



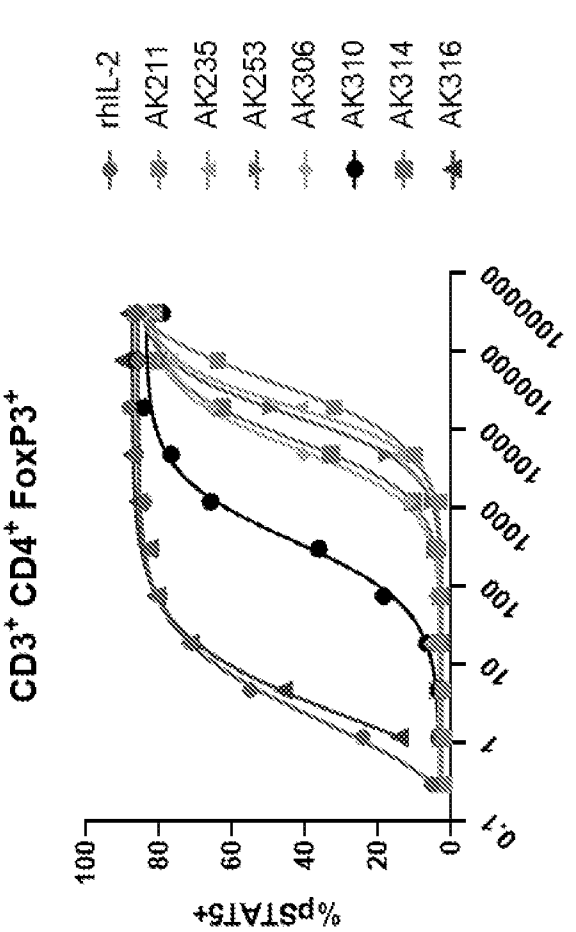


FIG. 18A

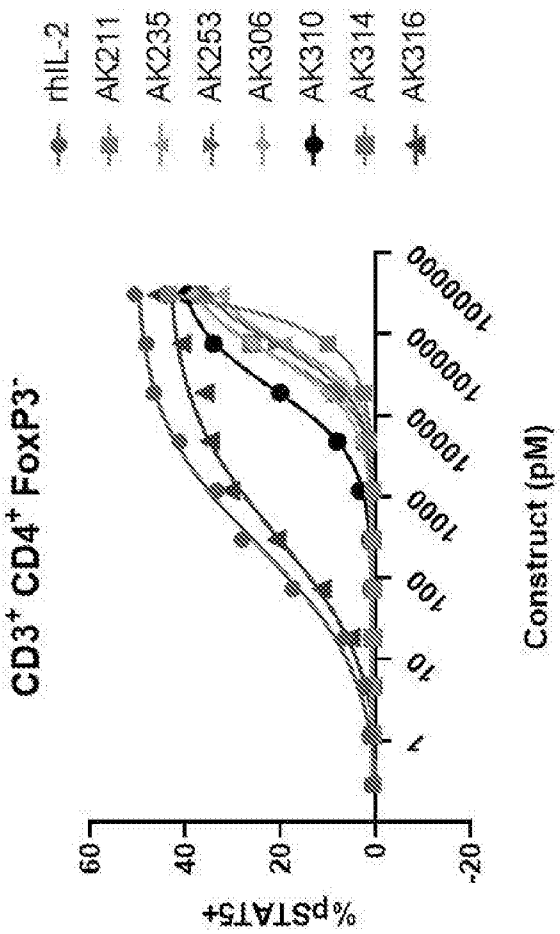


FIG. 18B

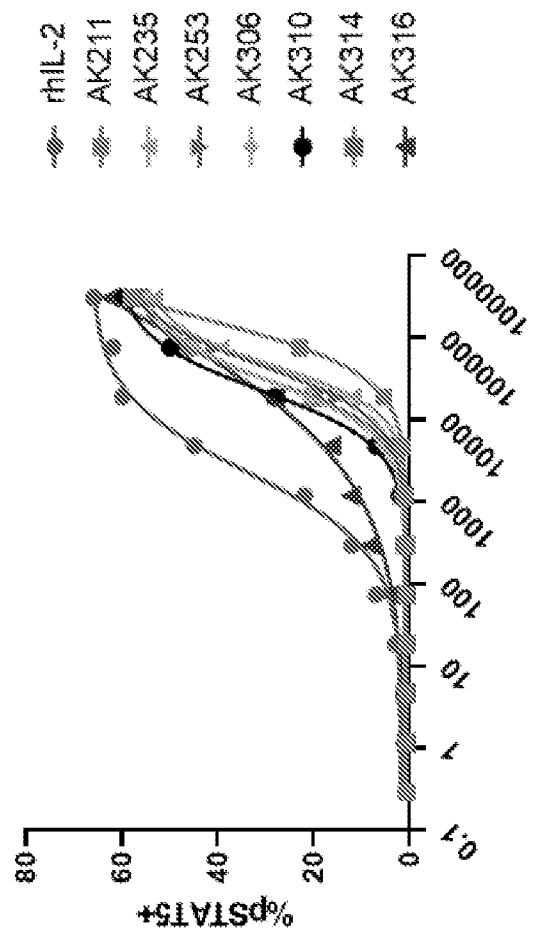


FIG. 18C

FIG. 18D

	CD3+ CD4+ FoxP3+	CD3+ CD4+ FoxP3-	CD3+ CD8+
Construct	EC_{50} (pM)	EC_{50} (pM)	EC_{50} (pM)
rhIL-2	1.94	247	2300
AK211	39500	*	164000
AK253	15400	75100	46400
AK235	19200	69500	44100
AK314	7250	49400	29500
AK306	5680	56300	28800
AK310	373	20800	22300
AK316	1.73	331	167000**

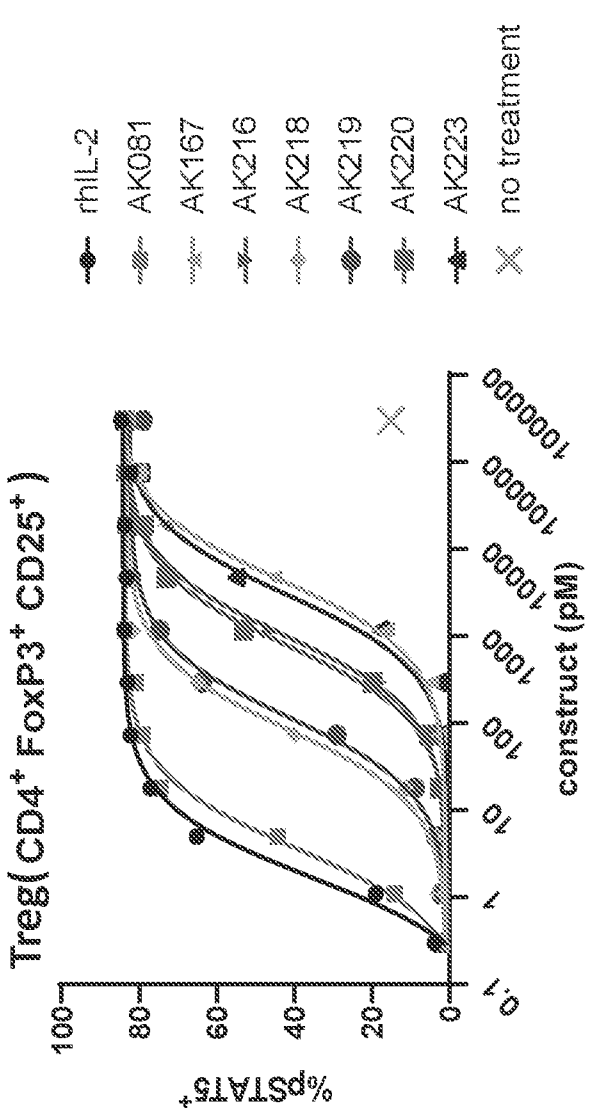


FIG. 19A

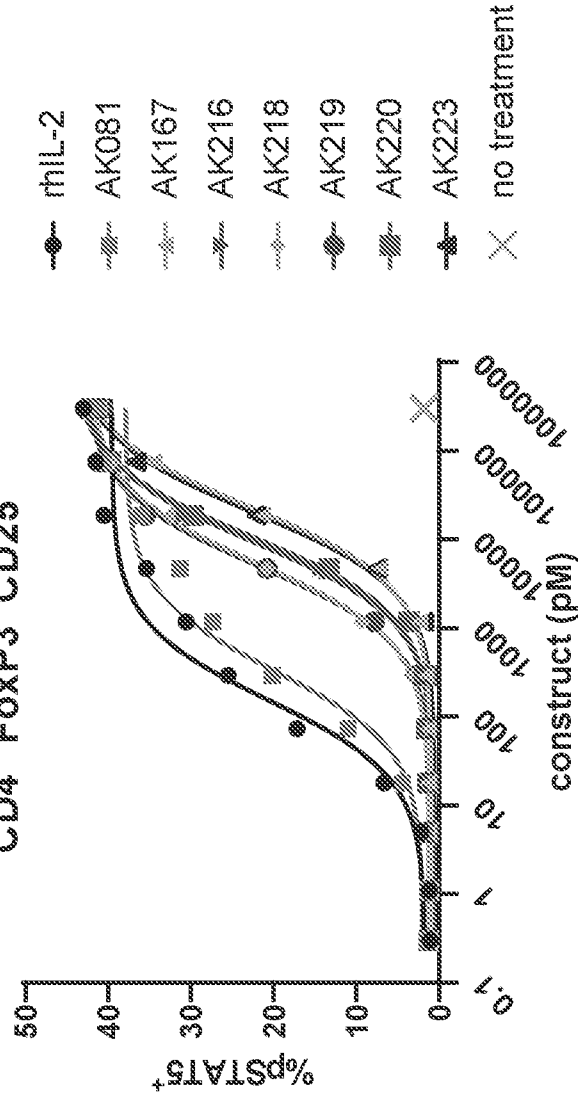


FIG. 19B

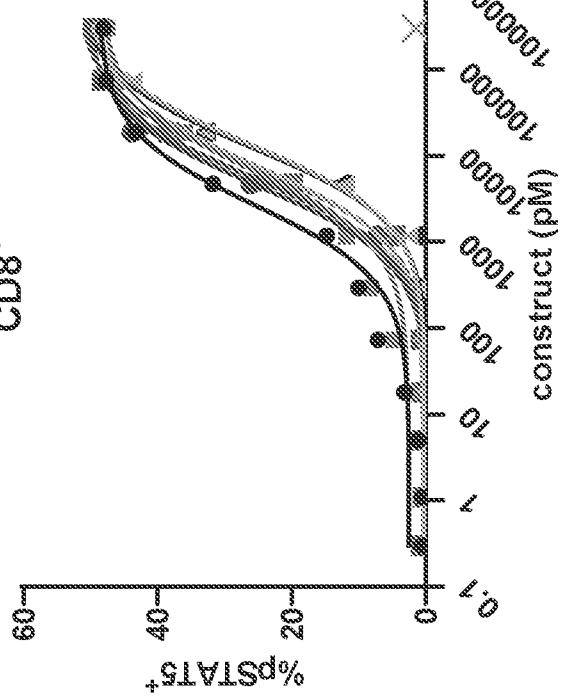


FIG. 19C

Construct	FoxP3$^+$ T_{reg}	CD4$^+$ T_{help}	CD8$^+$ T_{cyto}
	EC_{50} (pM)	EC_{50} (pM)	EC_{50} (pM)
rhIL-2	1.67	154	2710
AK081	3.59	332	6700
AK167	4390	22900	13200
AK216	1020	9200	5490
AK218	86.7	5270	7550
AK219	117	5030	4570
AK220	782	10900	7650
AK223	3040	20200	12600

FIG. 19D

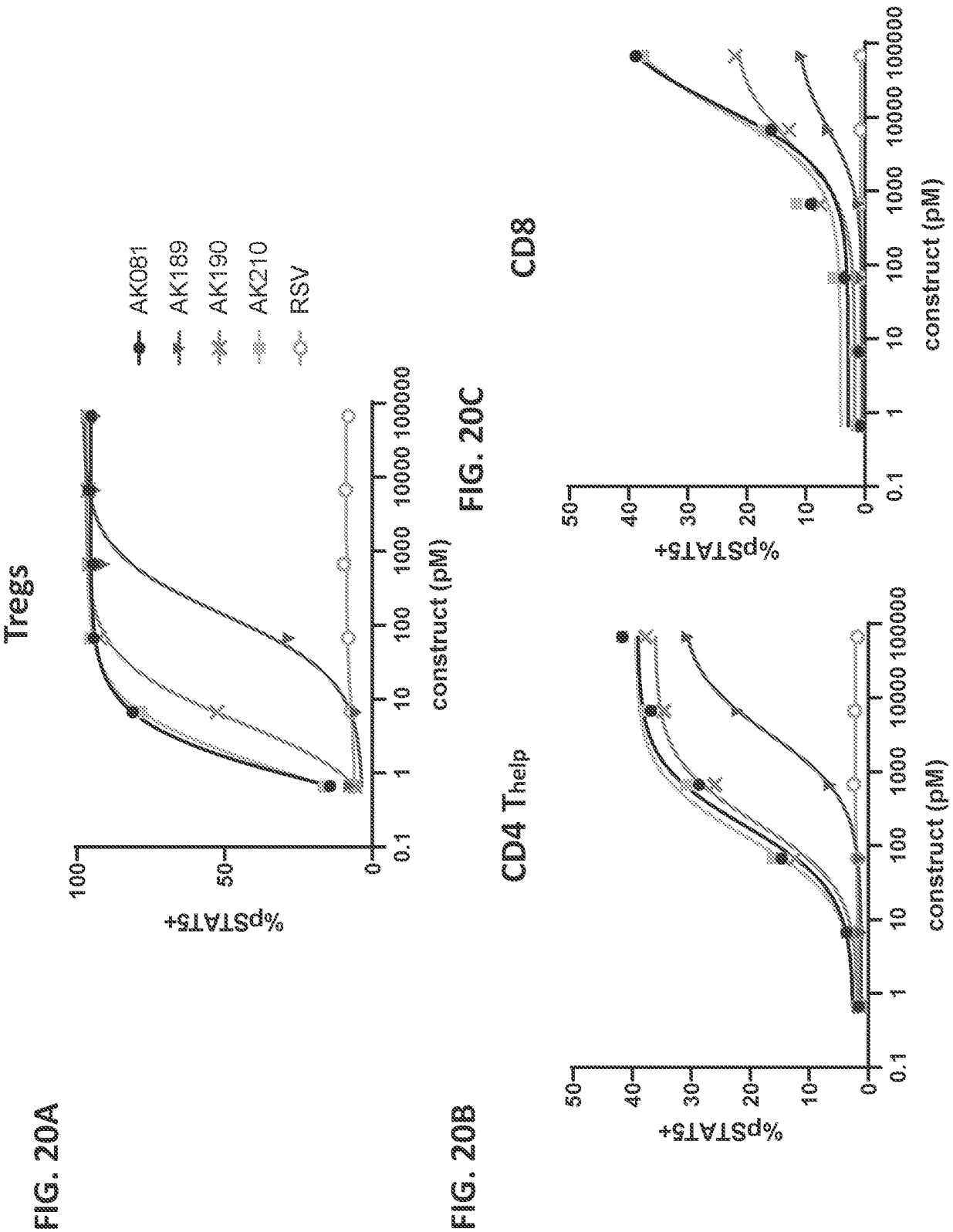


FIG. 20A

FIG. 20B

FIG. 20C

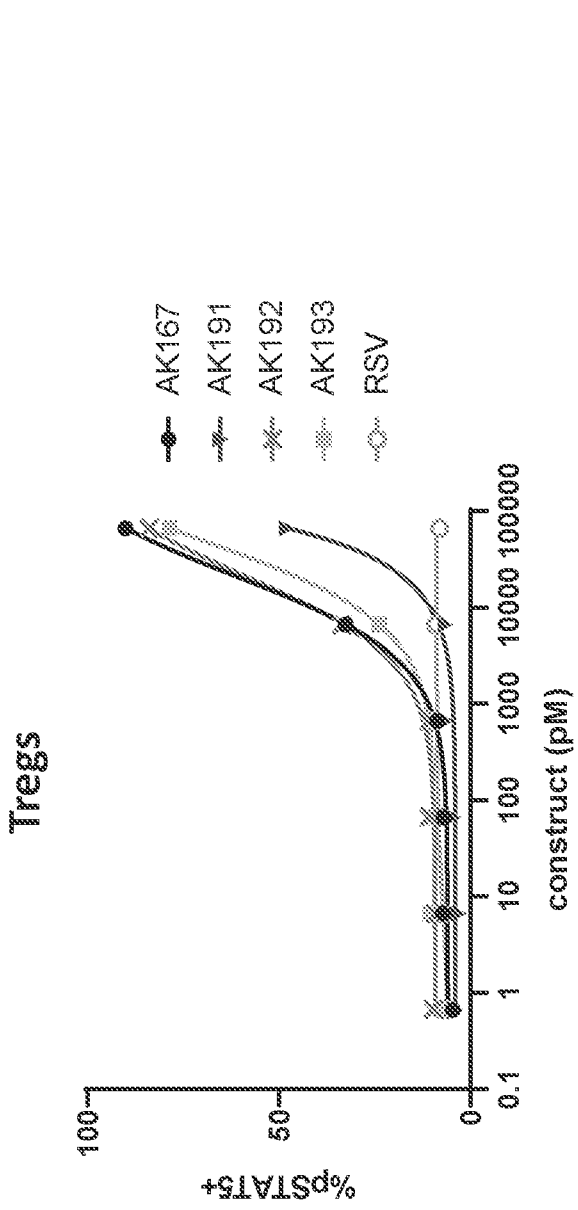


FIG. 21A

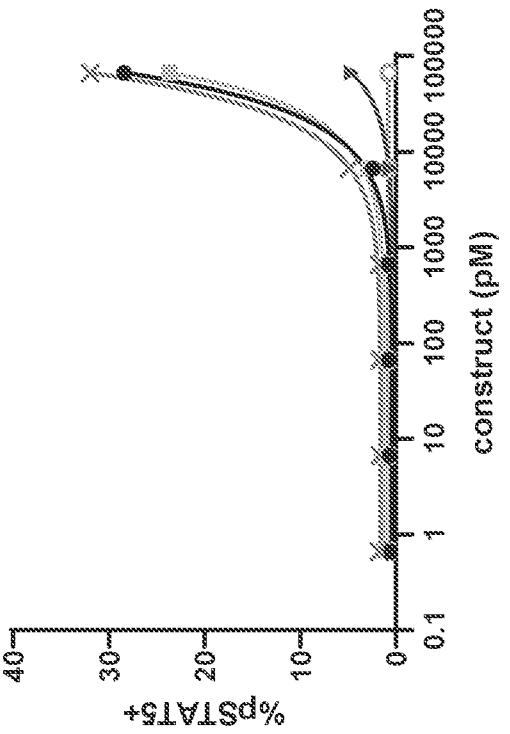


FIG. 21C

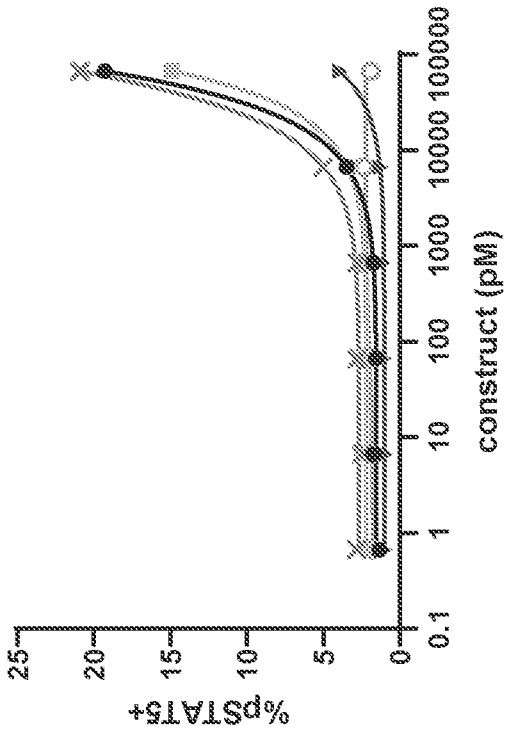


FIG. 21B

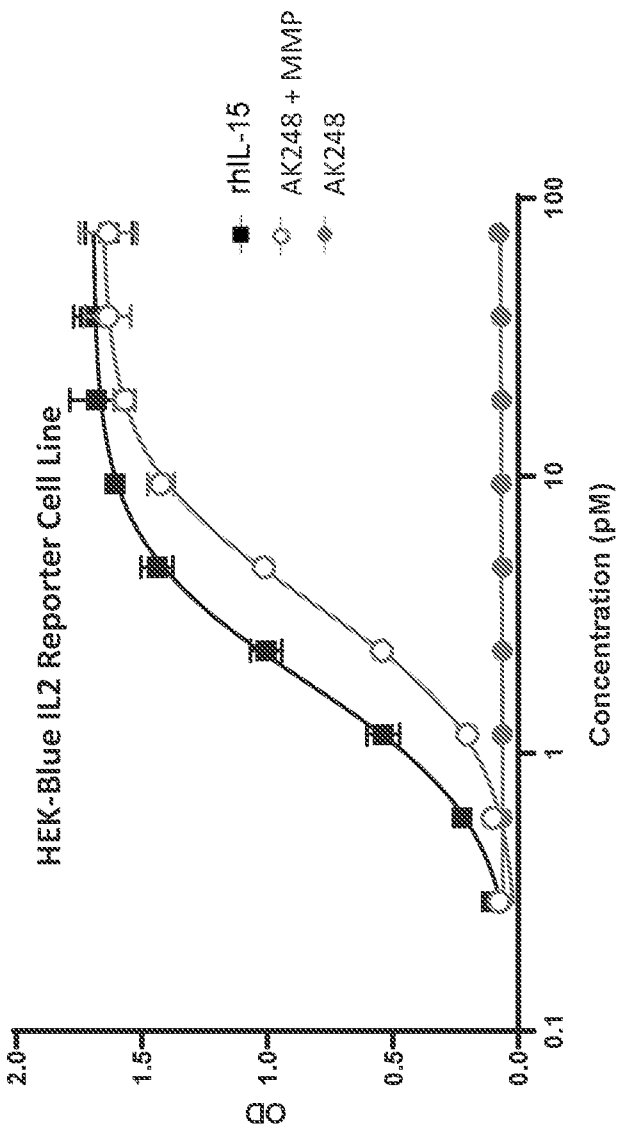


FIG. 22A

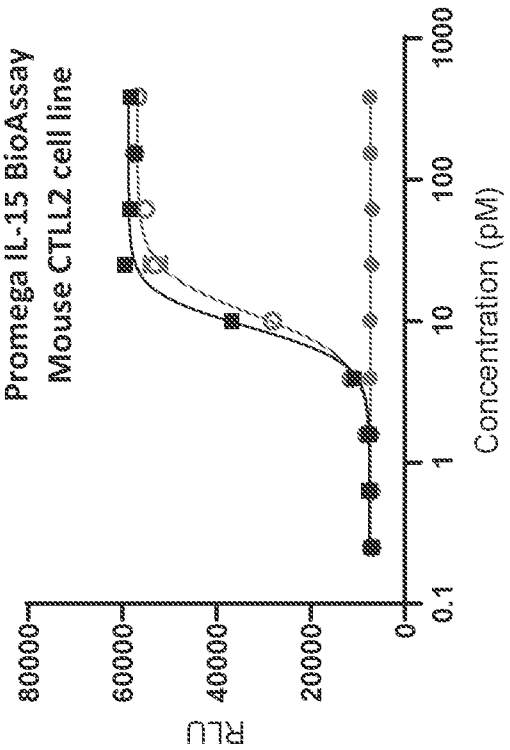


FIG. 22B

FIG. 23A

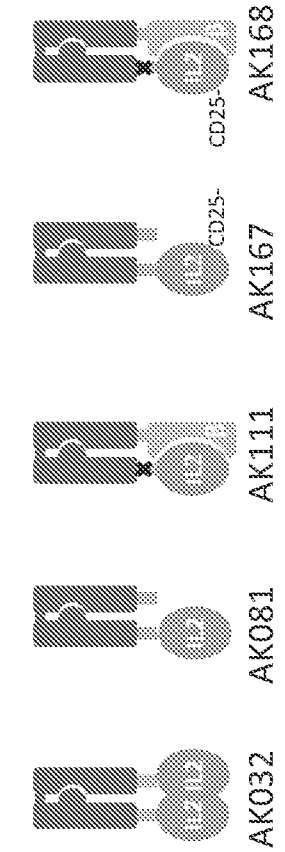


FIG. 23B

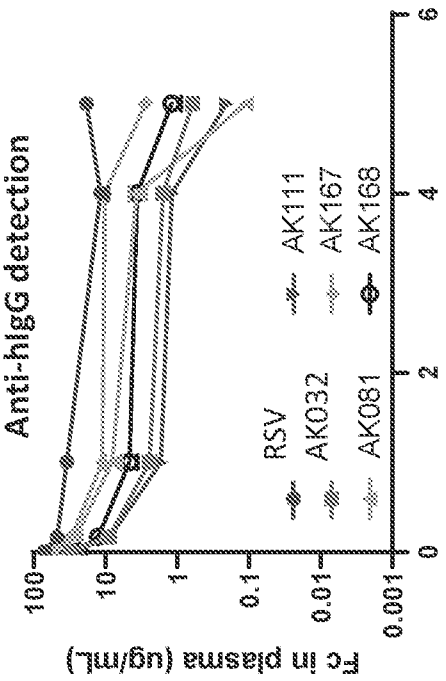


FIG. 23C

FIG. 23D

FIG. 24A

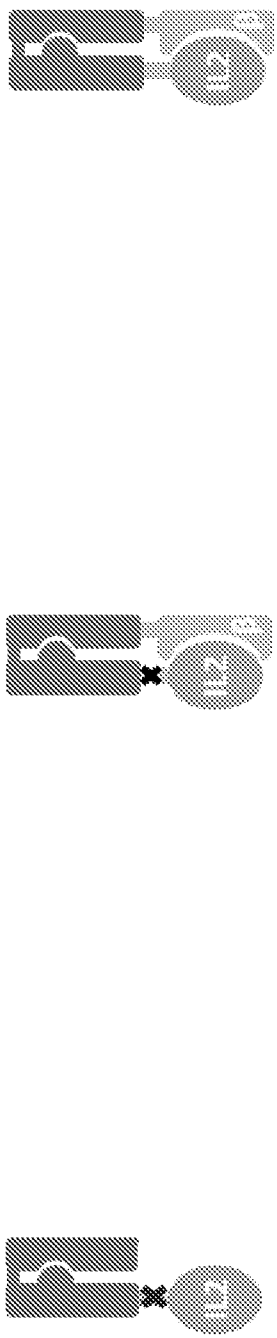
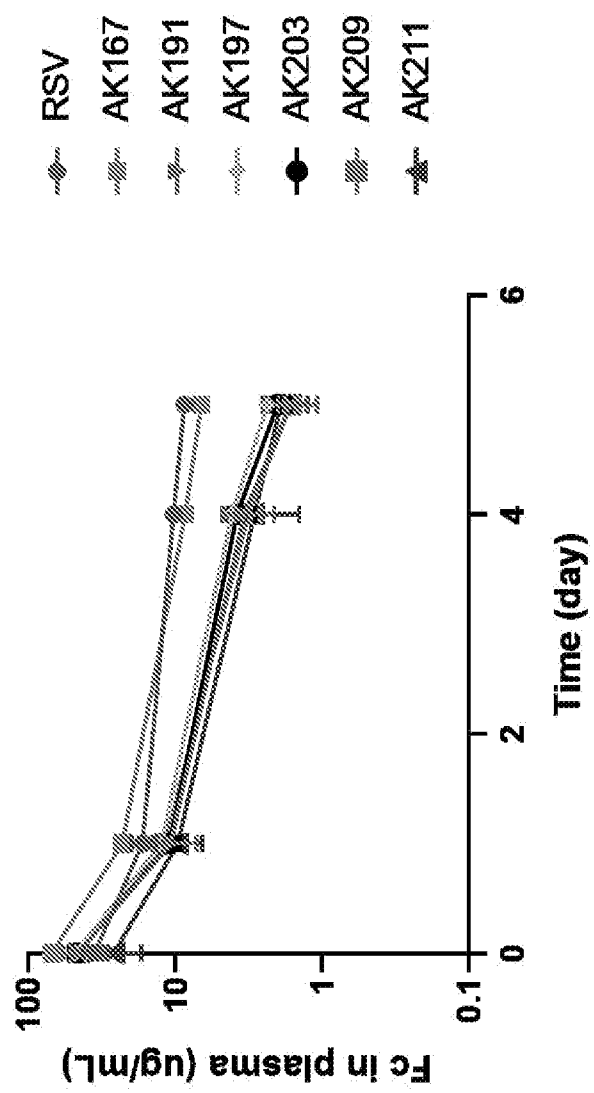


FIG. 24B



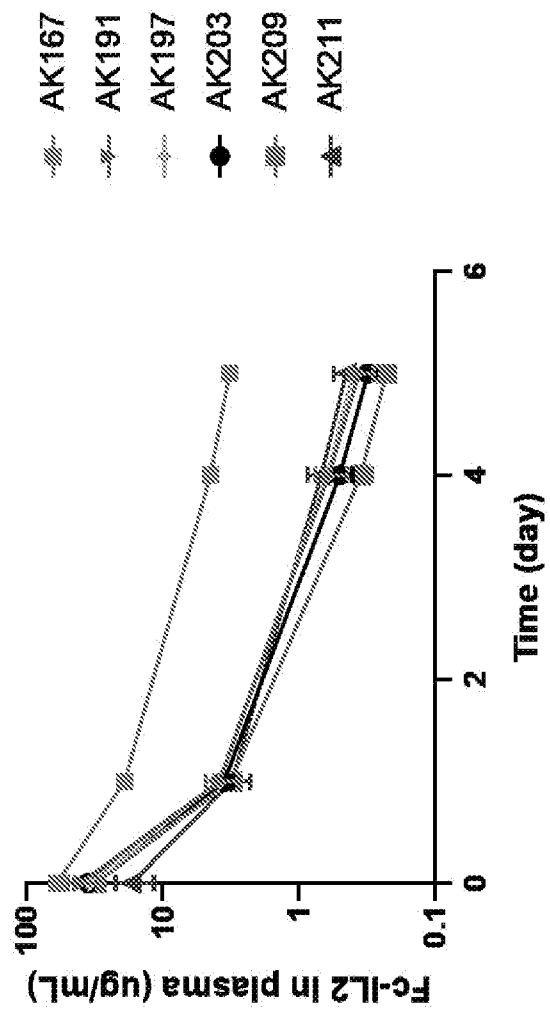


FIG. 24C

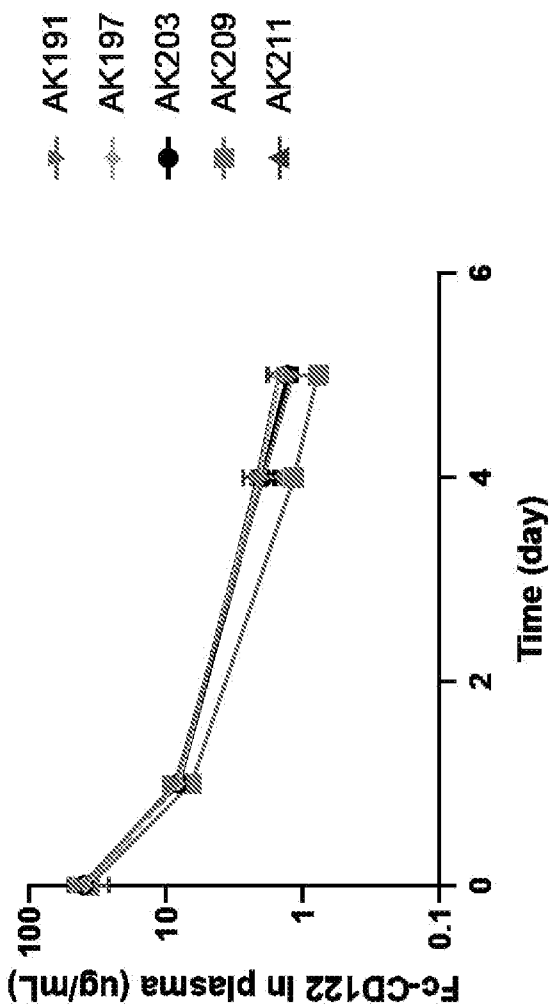


FIG. 24D

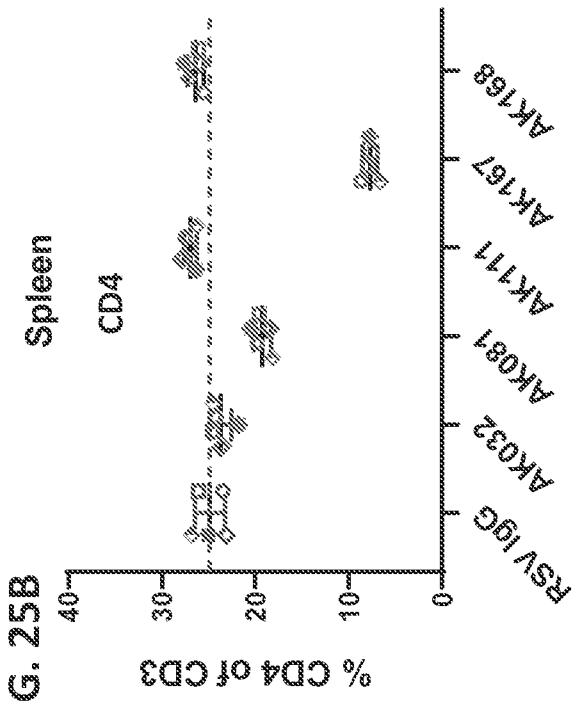


FIG. 25B

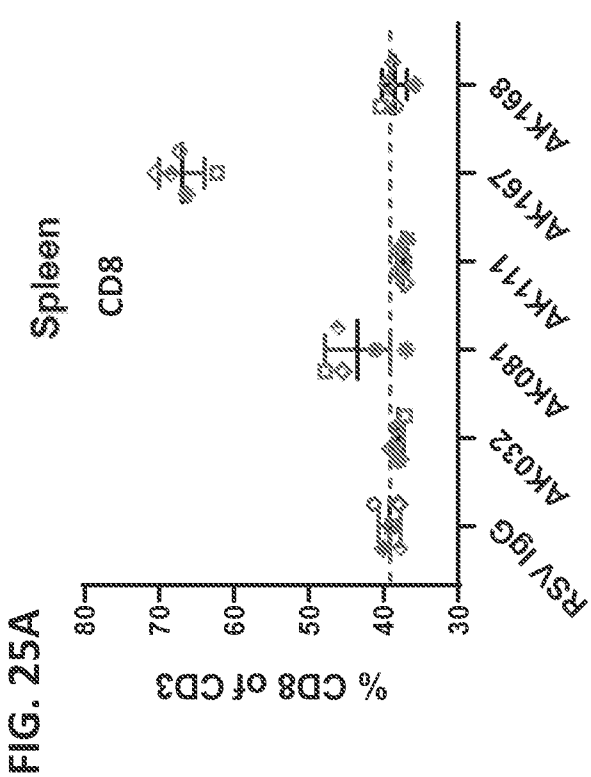


FIG. 25A

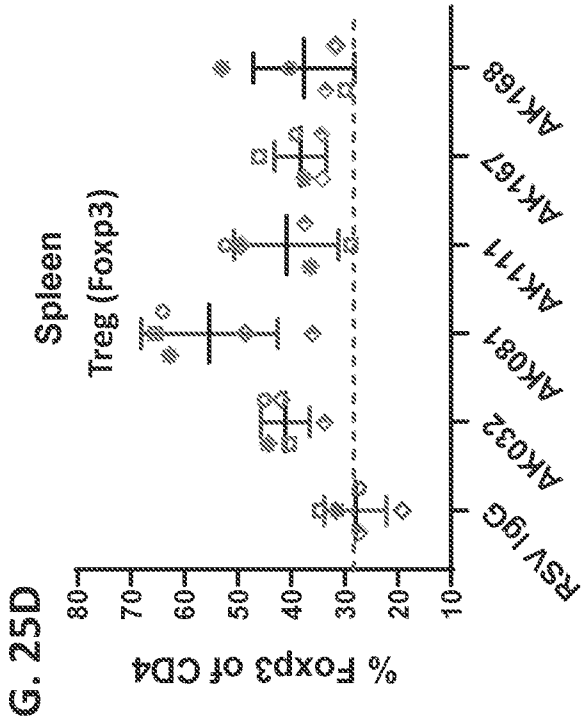


FIG. 25D

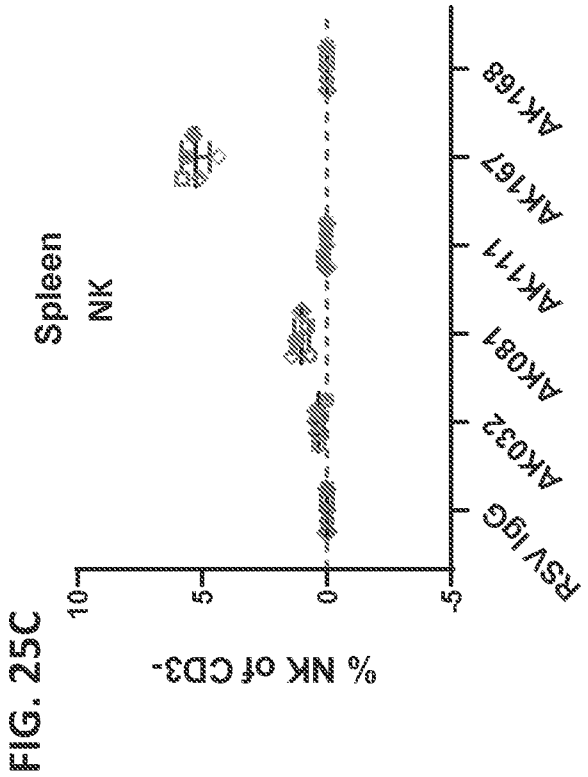


FIG. 25C

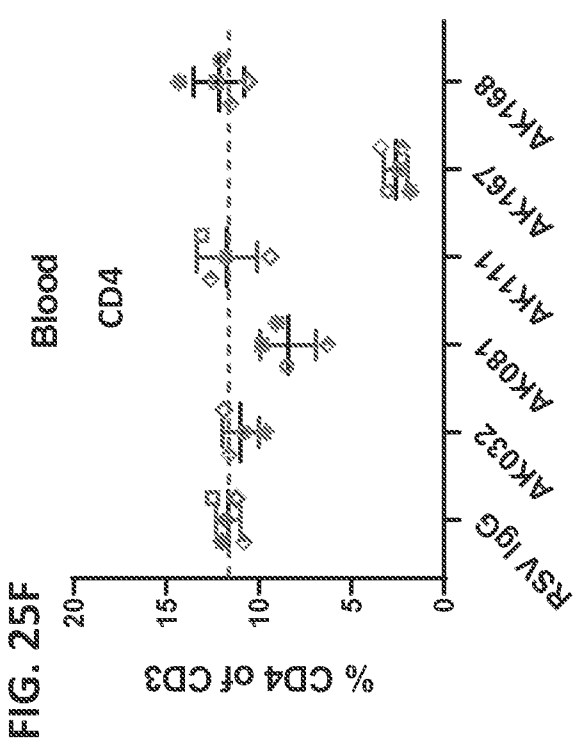


FIG. 25F

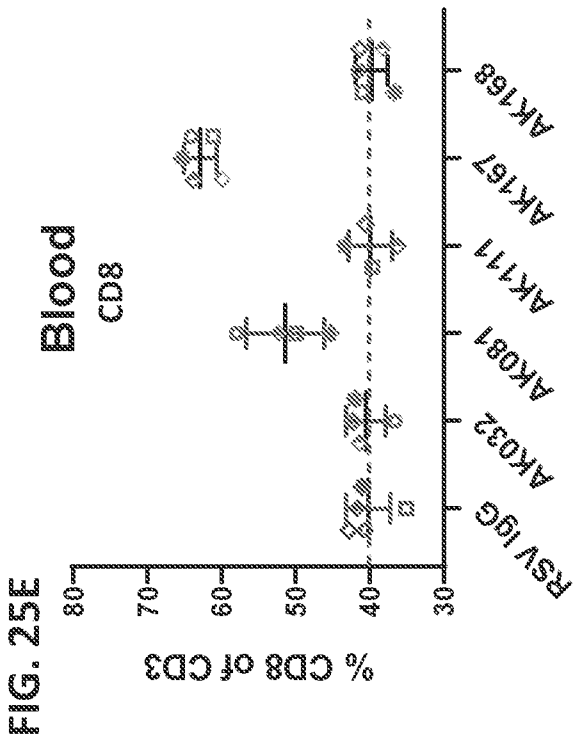


FIG. 25E

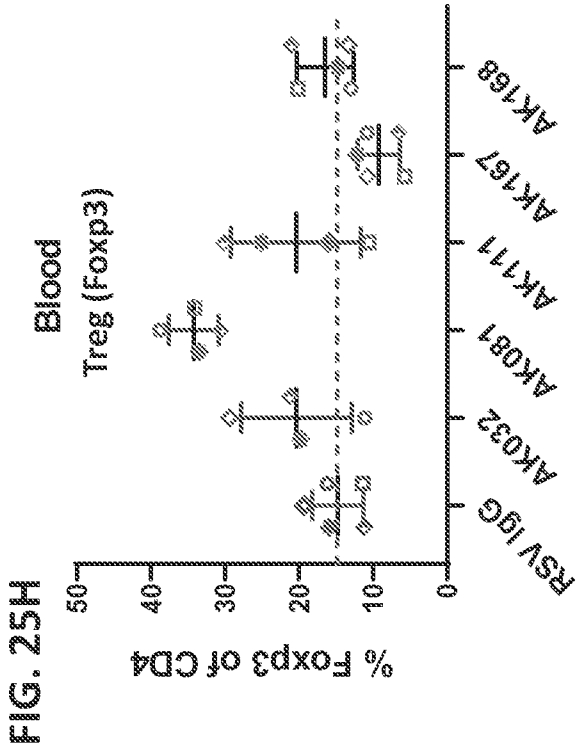


FIG. 25H

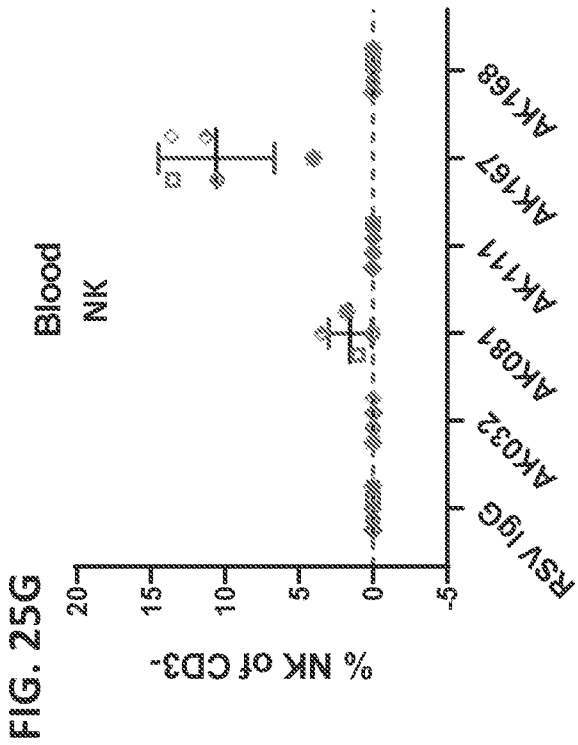


FIG. 25G

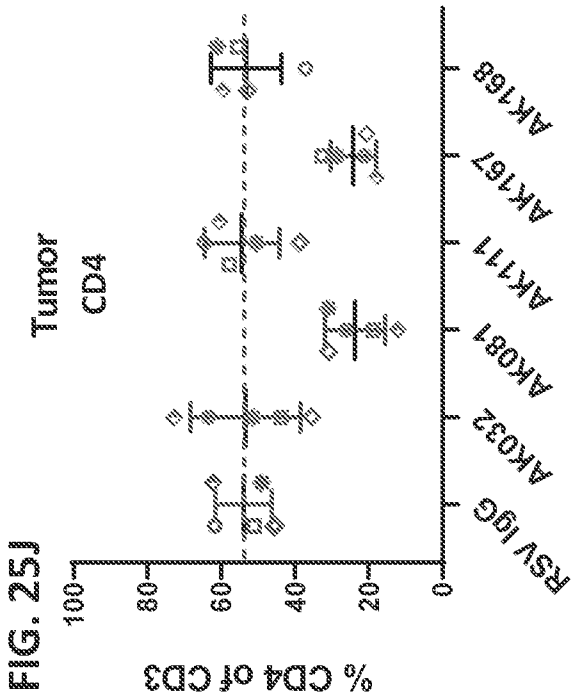


FIG. 25J

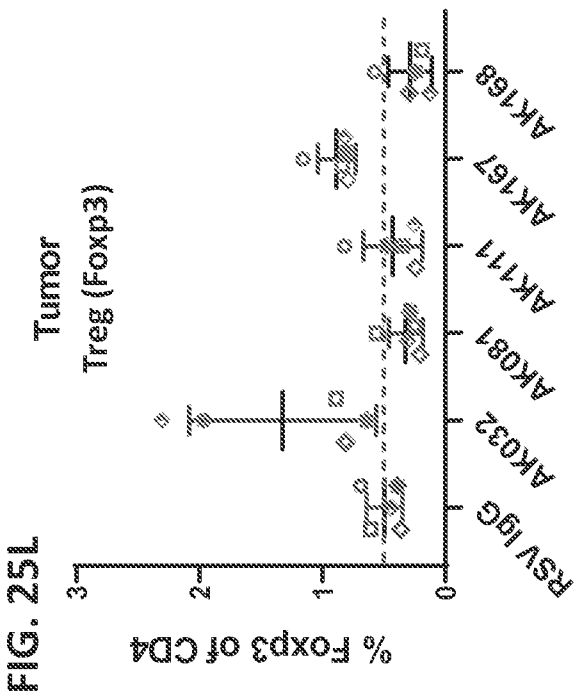


FIG. 25L

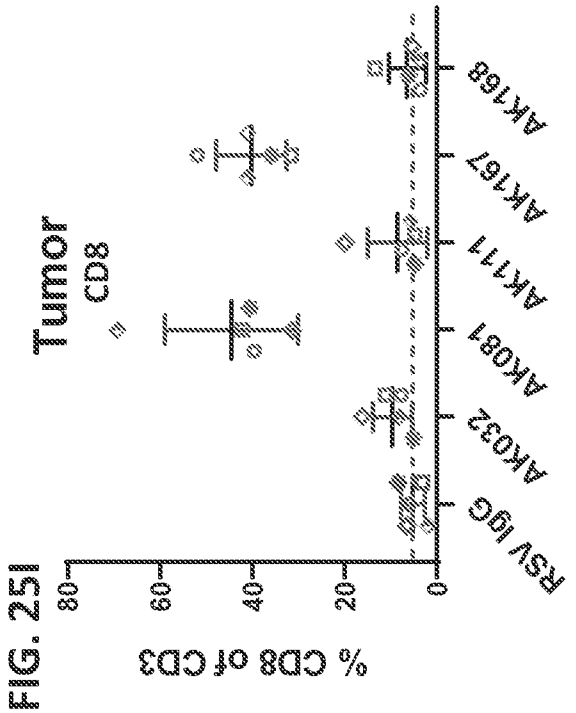


FIG. 25I

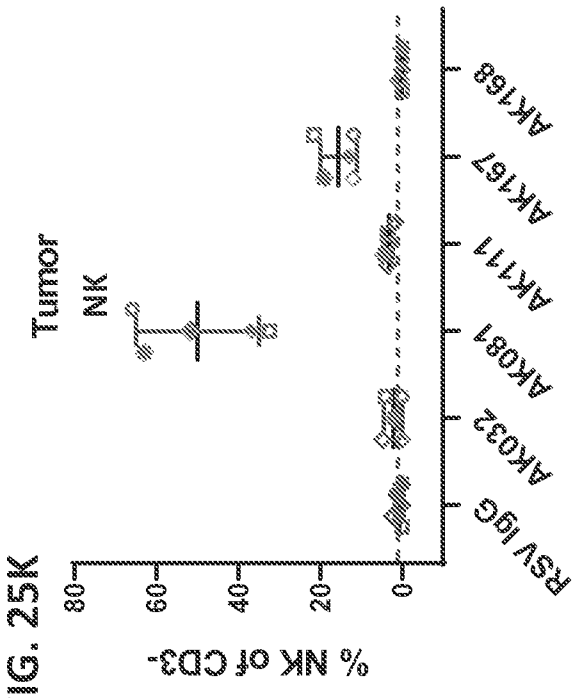


FIG. 25K

FIG. 26A

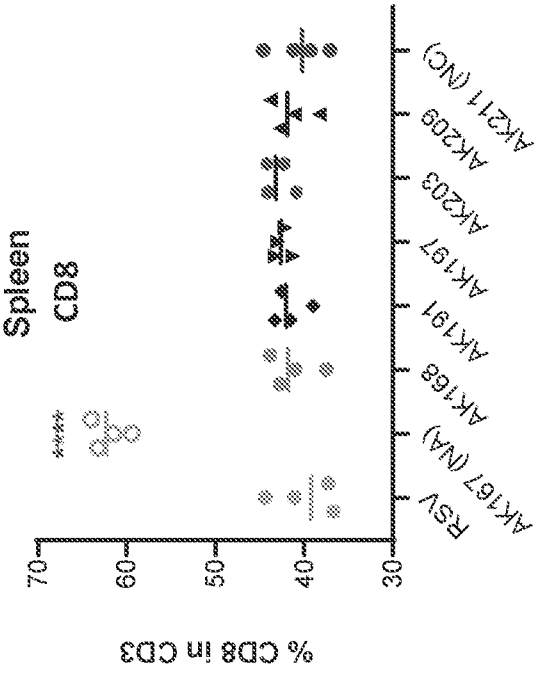


FIG. 26B

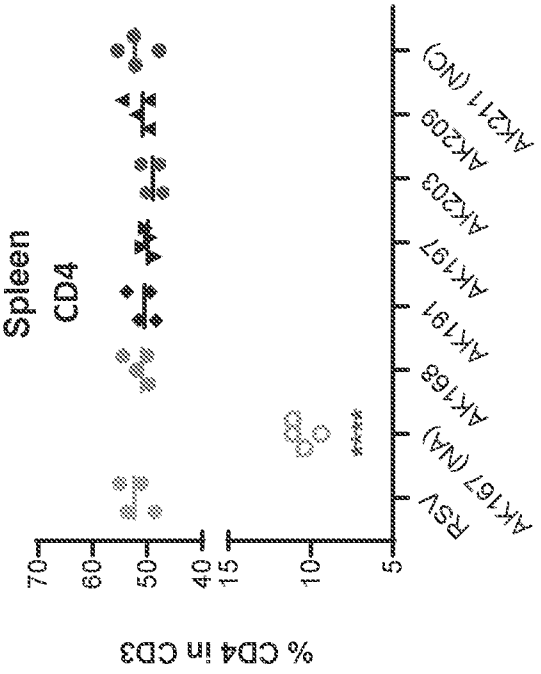


FIG. 26C

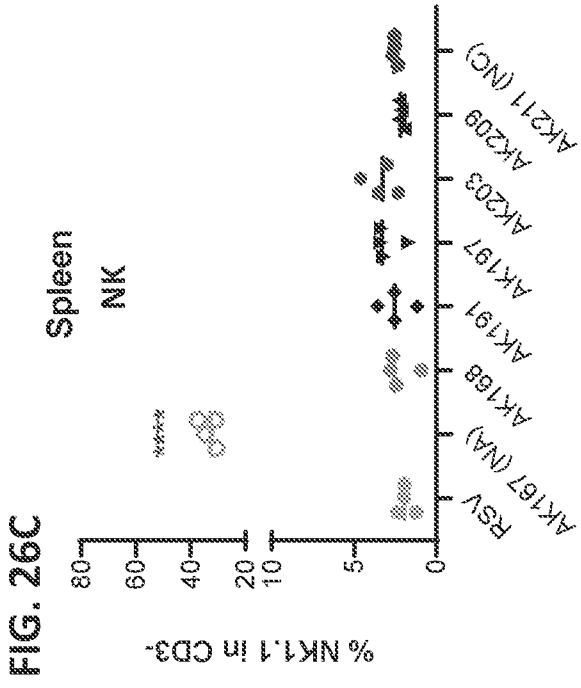
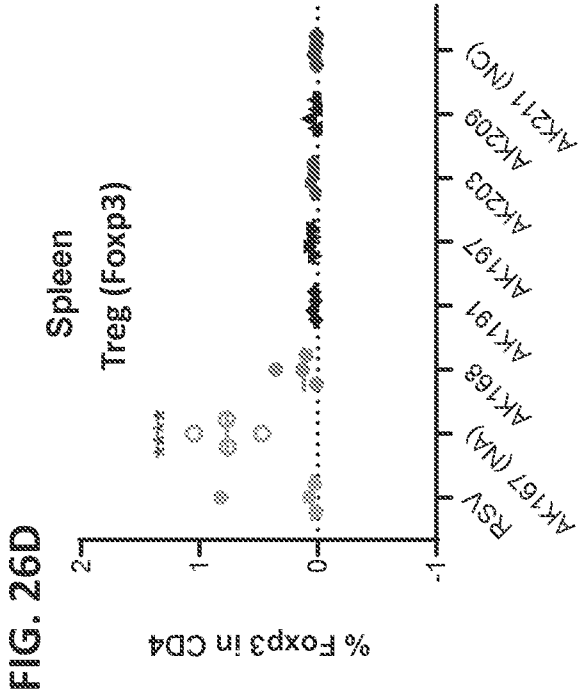


FIG. 26D



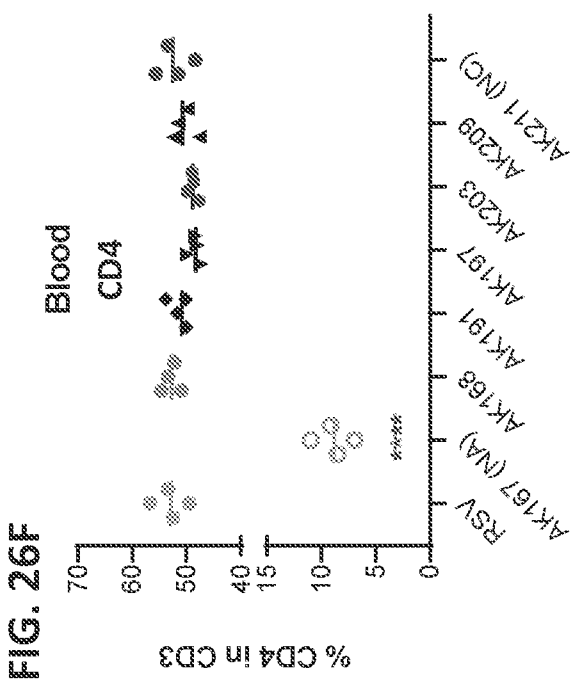


FIG. 26F

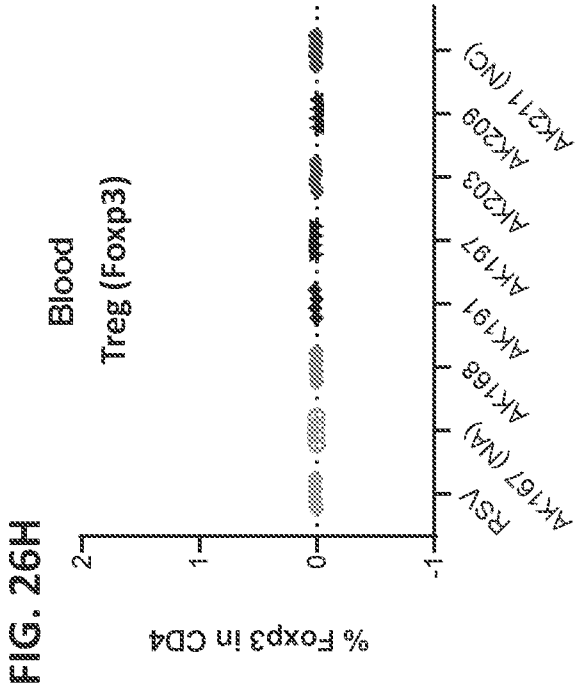


FIG. 26H

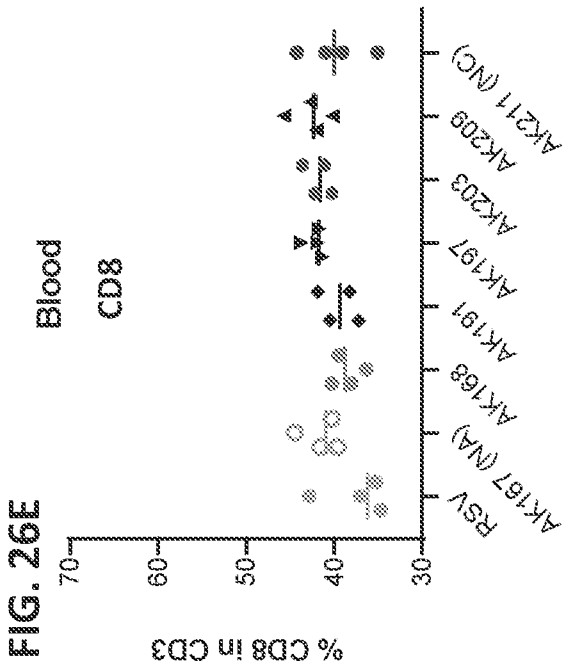


FIG. 26E

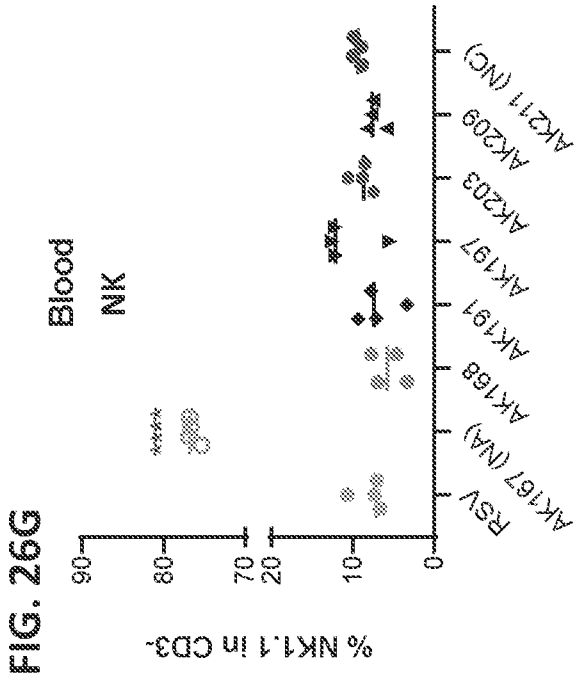


FIG. 26G

FIG. 26J

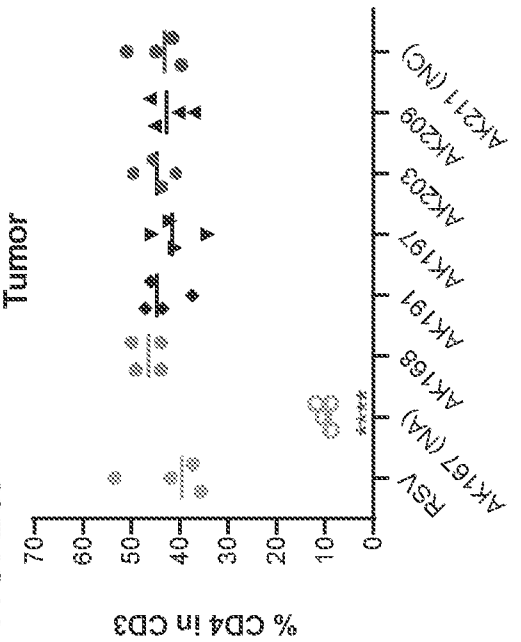


FIG. 26L

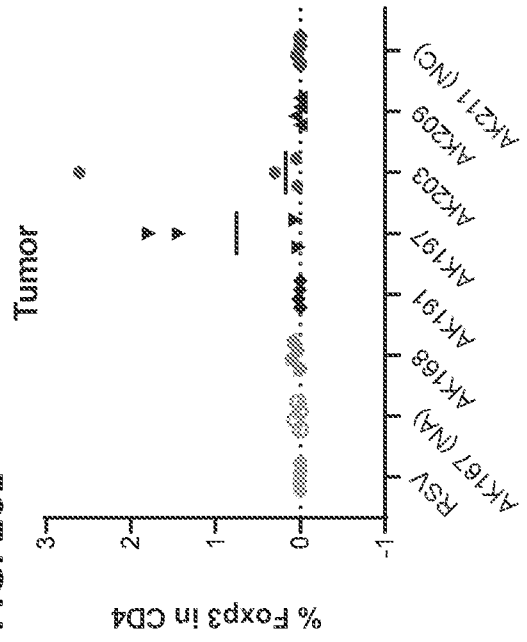


FIG. 26I

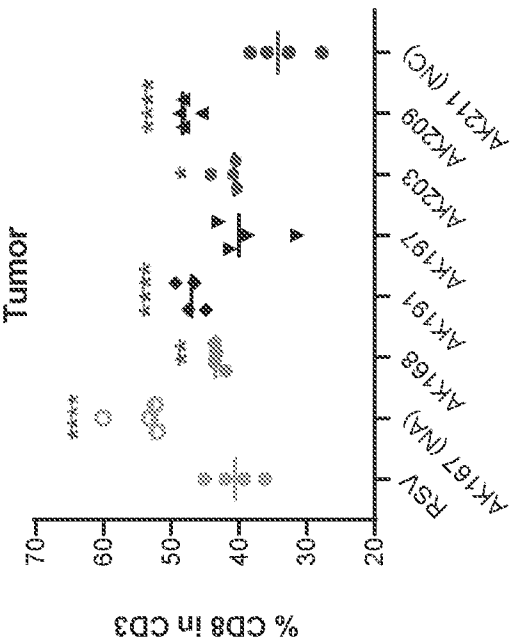


FIG. 26K

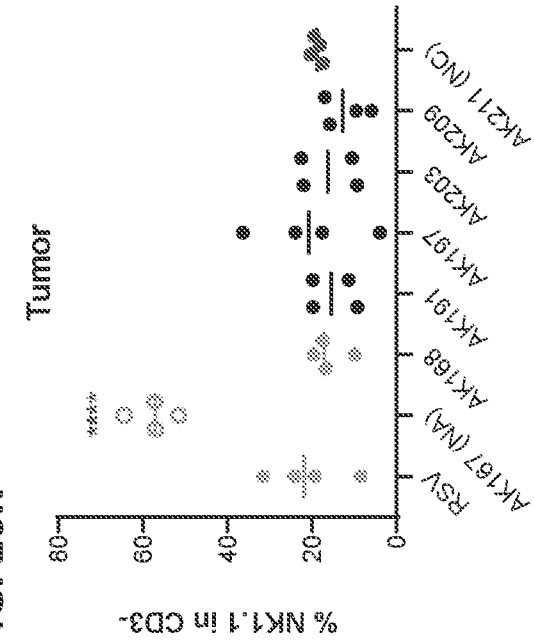


FIG. 27A

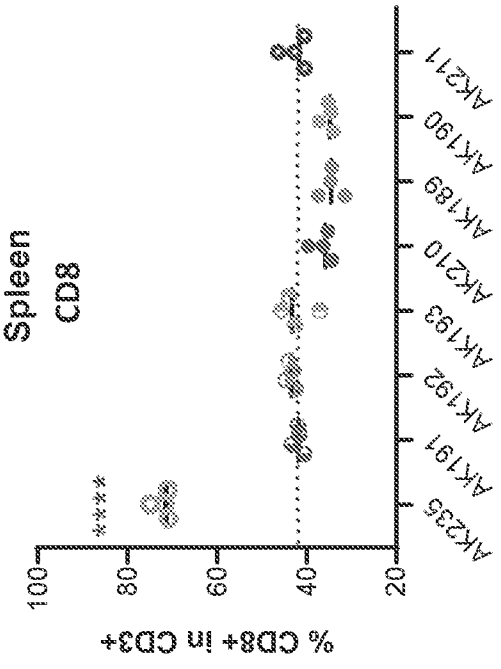


FIG. 27B

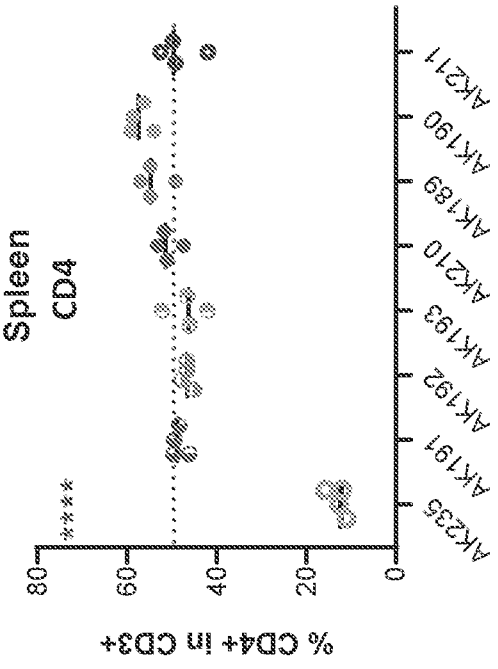


FIG. 27C

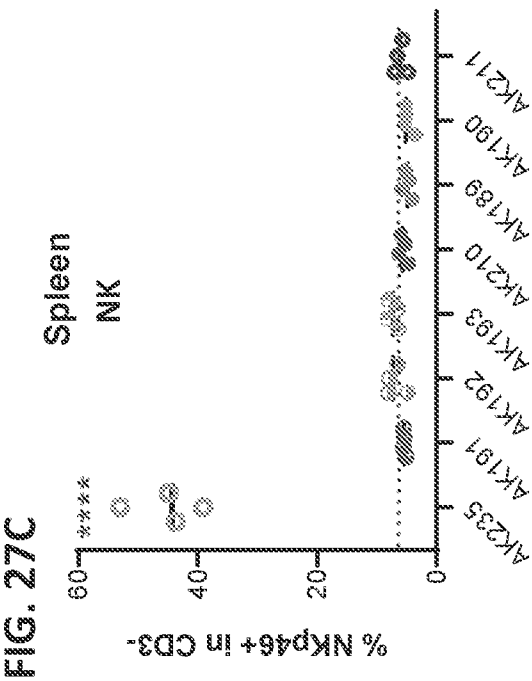
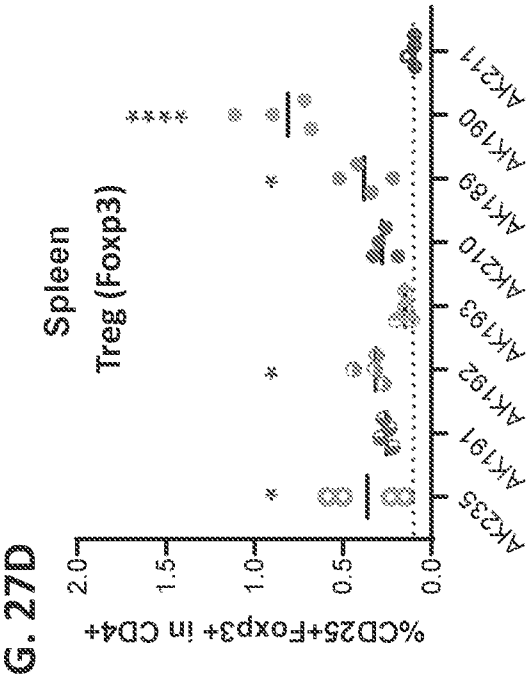


FIG. 27D



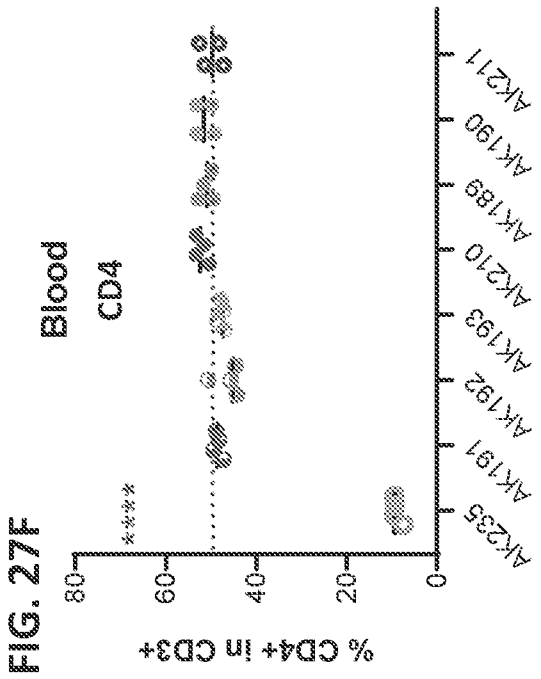


FIG. 27F

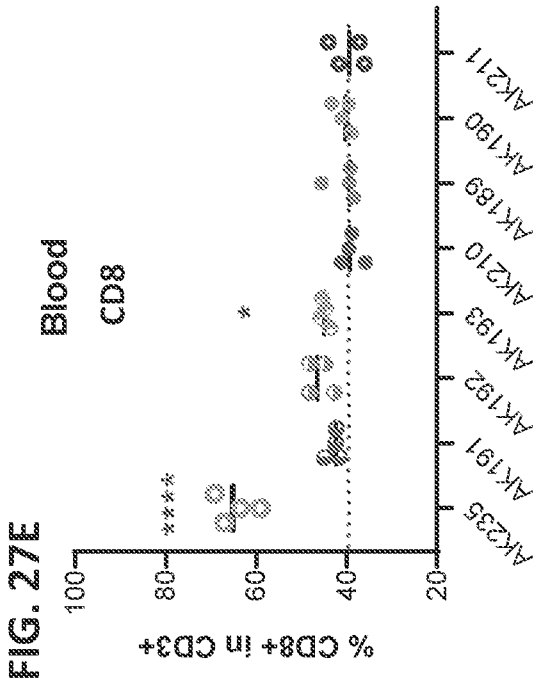


FIG. 27E

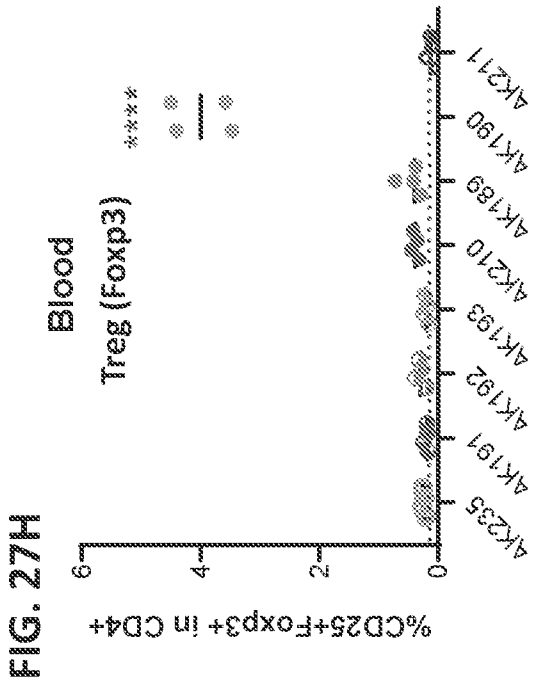


FIG. 27H

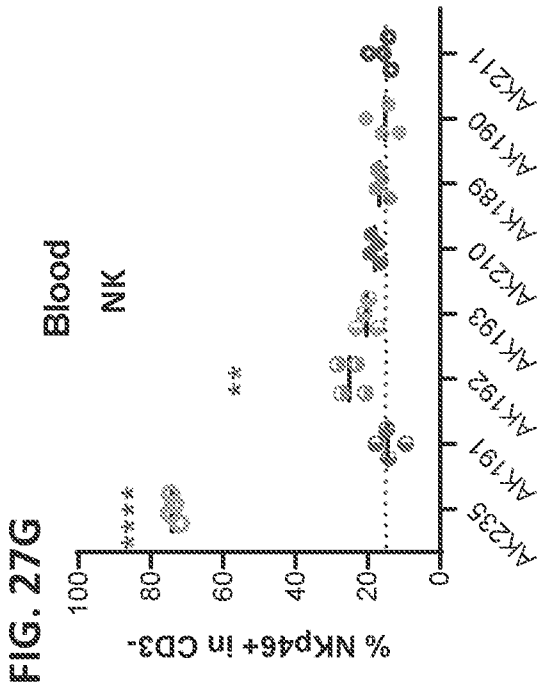


FIG. 27G

FIG. 27I

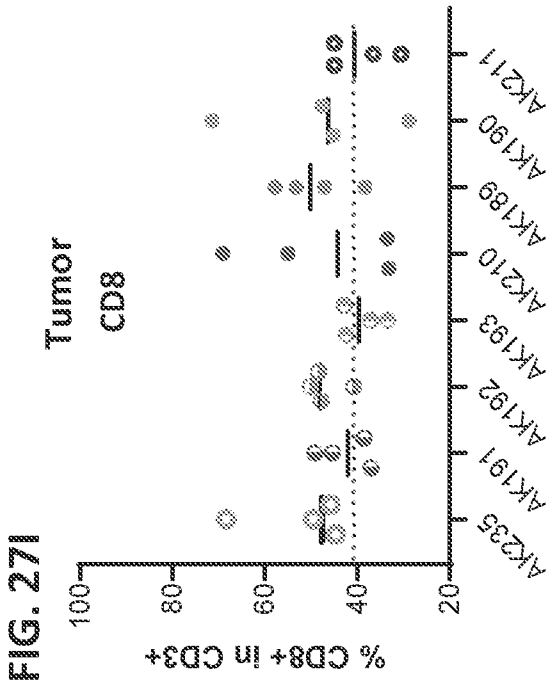


FIG. 27J

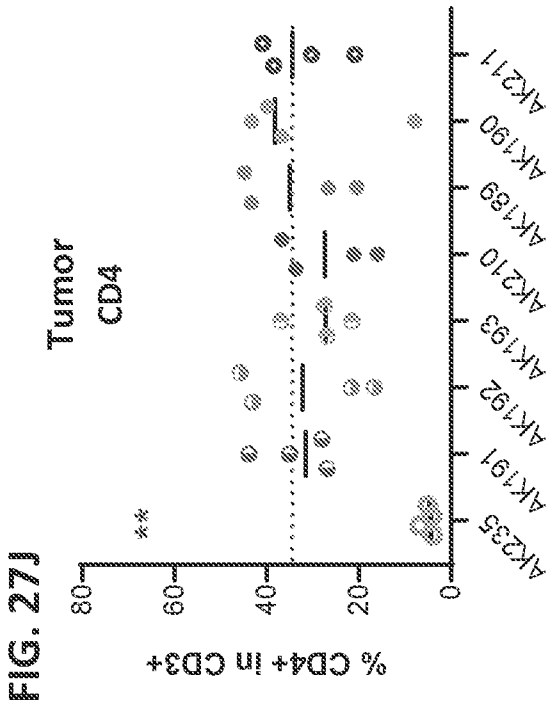


FIG. 27K

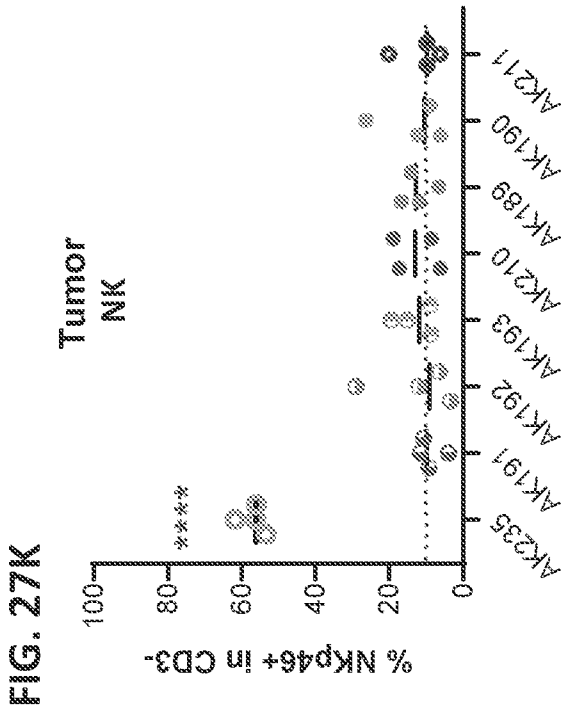


FIG. 27L

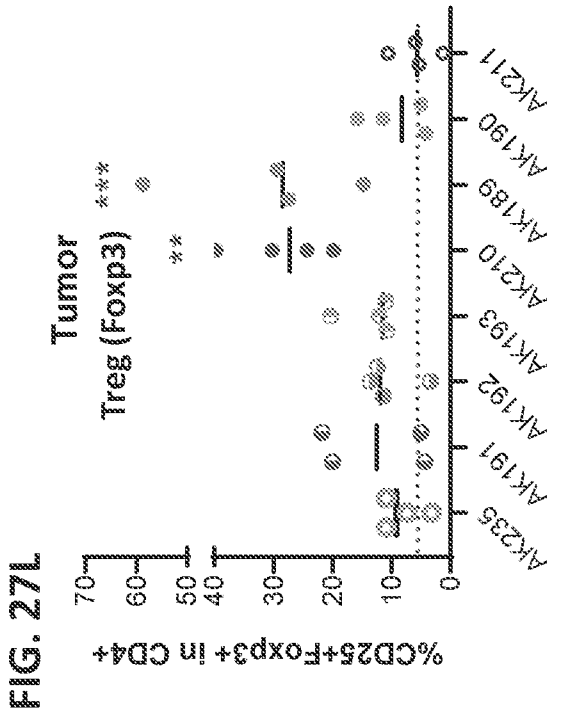


FIG. 28A

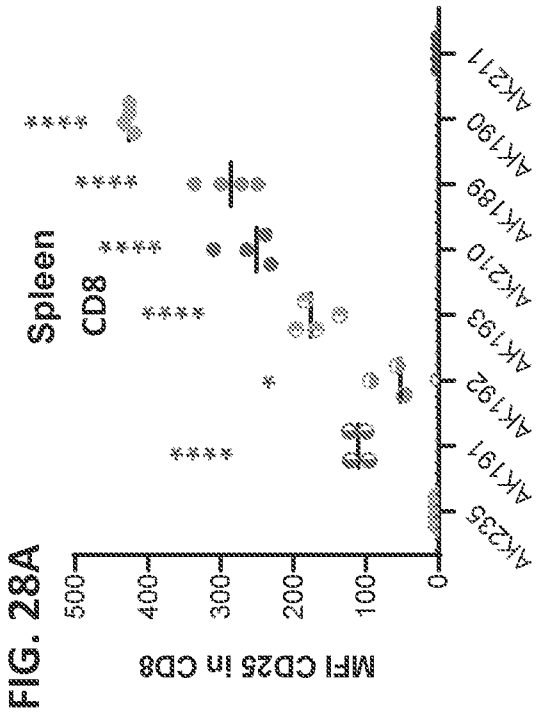


FIG. 28B

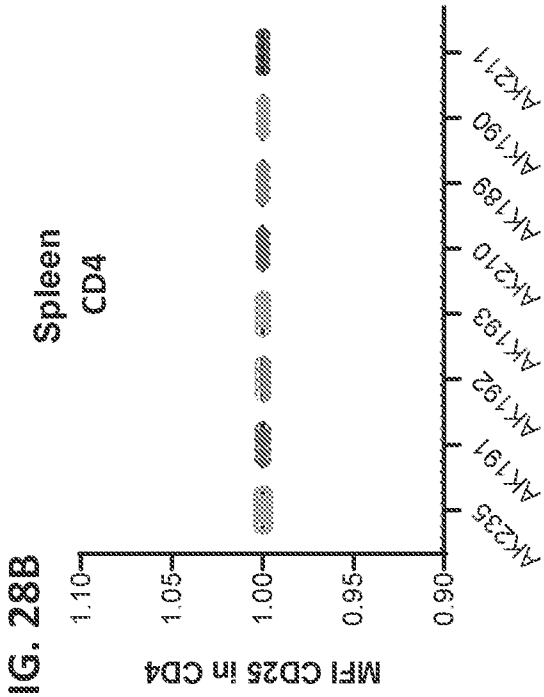


FIG. 28C

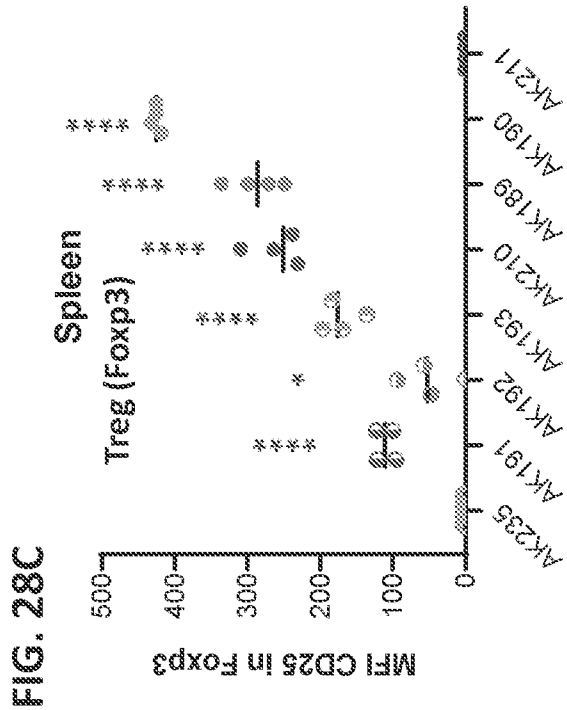


FIG. 28E

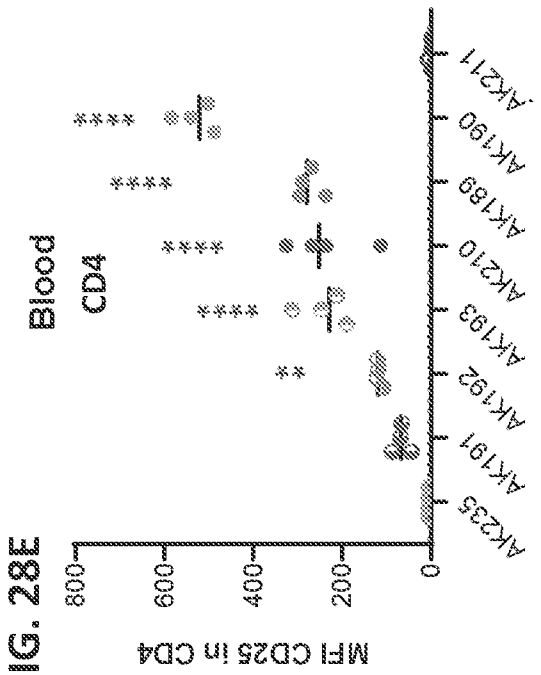


FIG. 28D

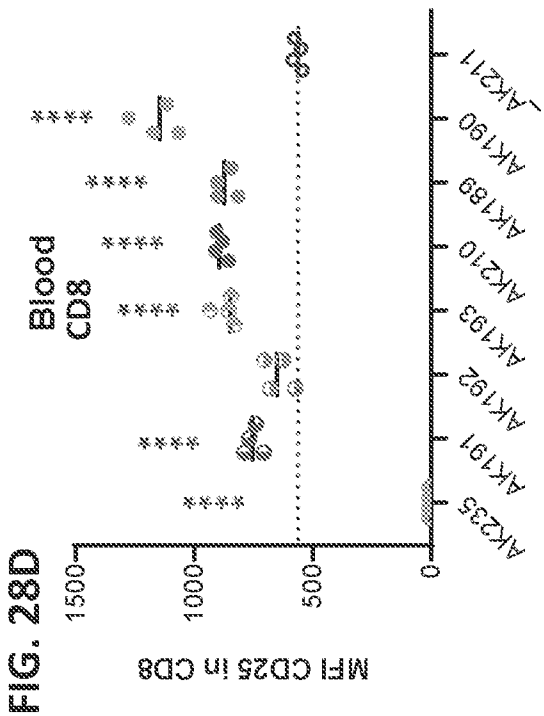


FIG. 28F

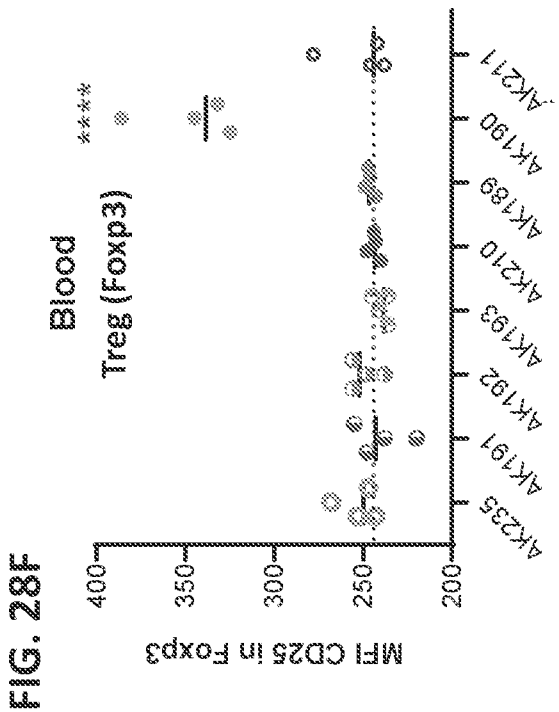


FIG. 28H

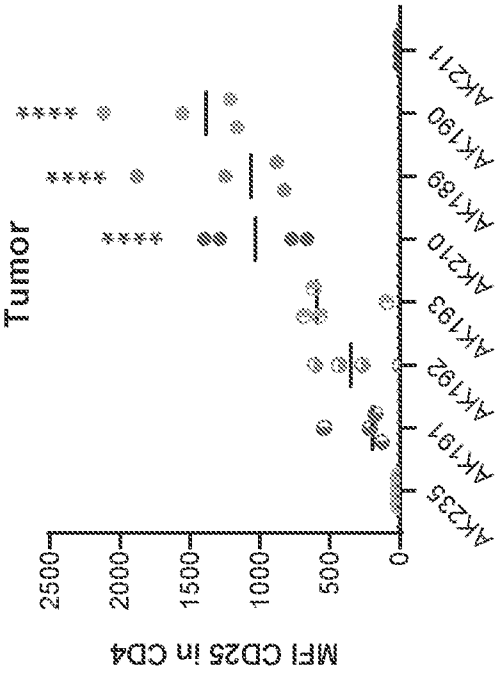


FIG. 28G

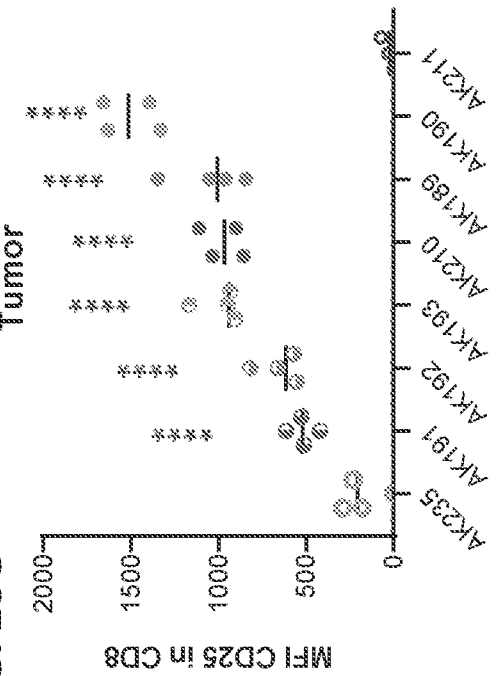
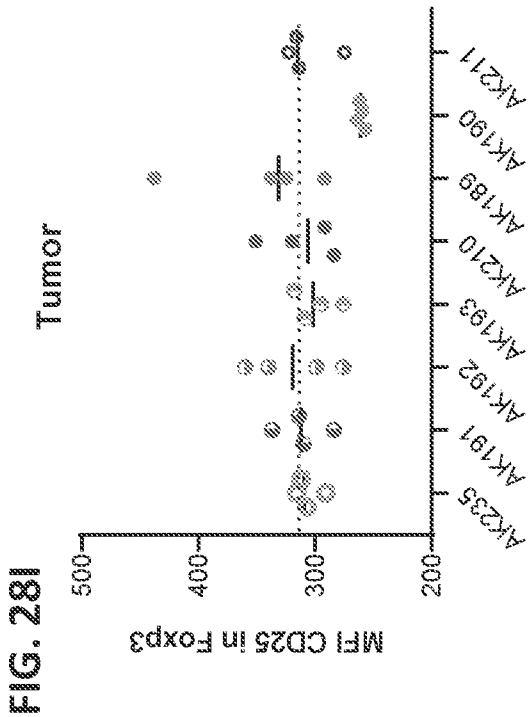
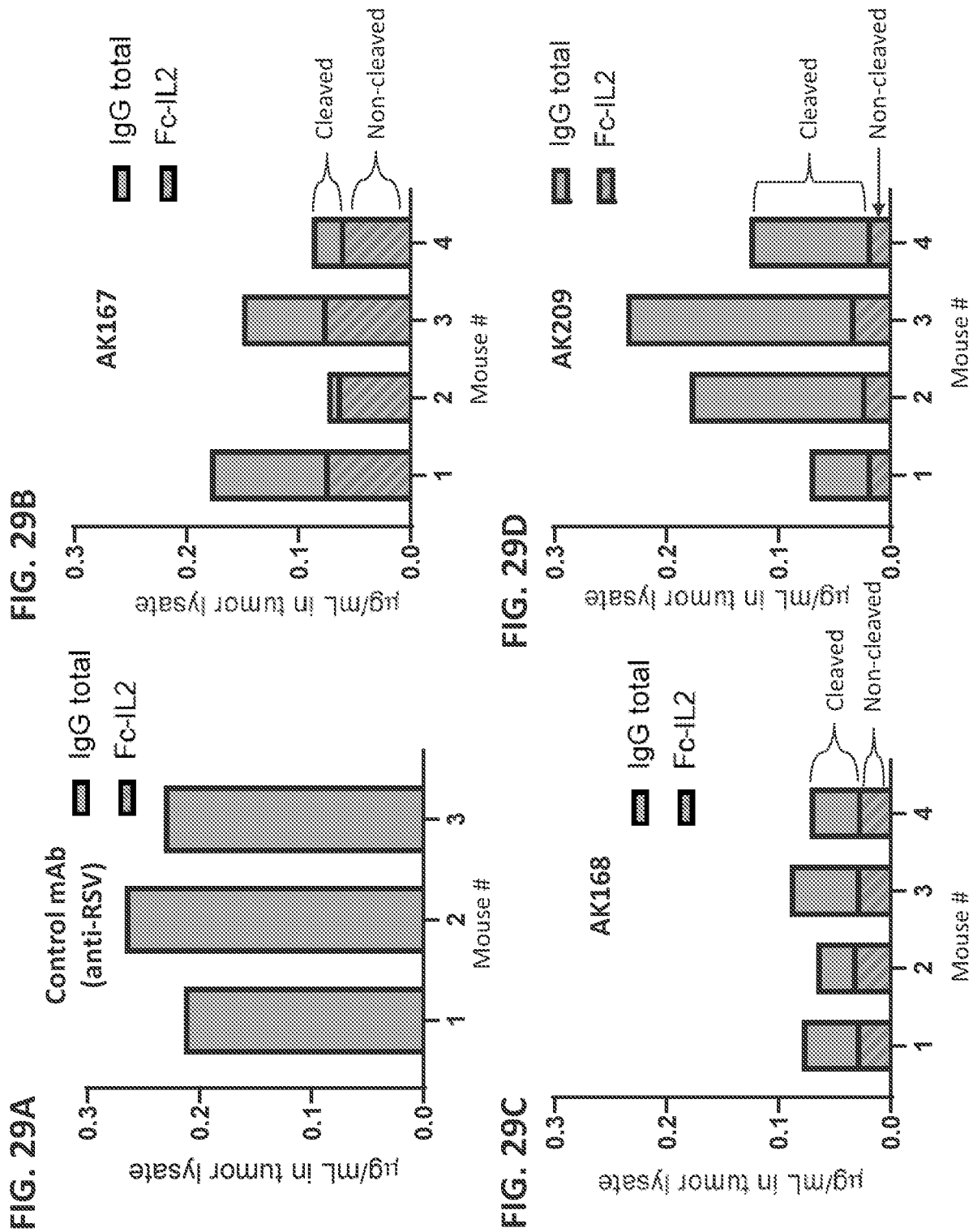


FIG. 28I




FIG. 29A
Control mAb (anti-RSV)
IgG total
Fc-IL2
μg/mL in tumor lysate
0.0
0.1
0.2
0.3
1
2
3
Mouse #
FIG. 29B
AK167
IgG total
Fc-IL2
Cleaved
Non-cleaved
μg/mL in tumor lysate
0.0
0.1
0.2
0.3
1
2
3
4
Mouse #
FIG. 29C
AK168
IgG total
Fc-IL2
Cleaved
Non-cleaved
μg/mL in tumor lysate
0.0
0.1
0.2
0.3
1
2
3
4
Mouse #
FIG. 29D
AK209
IgG total
Fc-IL2
Cleaved
Non-cleaved
μg/mL in tumor lysate
0.0
0.1
0.2
0.3
1
2
3
4
Mouse #

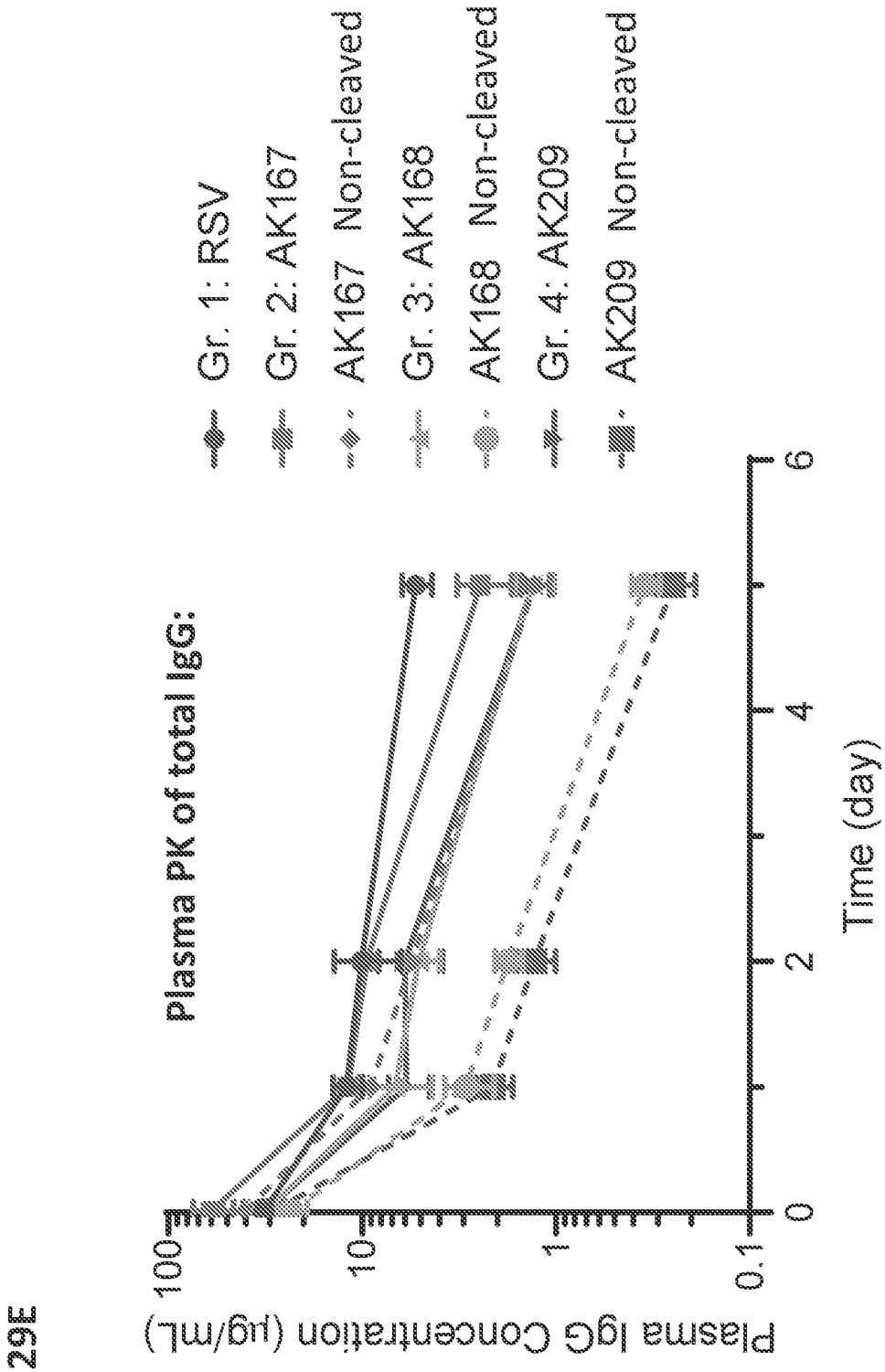

Plasma PK of total IgG:
Gr. 1: RSV
Gr. 2: AK167
AK167 Non-cleaved
Gr. 3: AK168
AK168 Non-cleaved
Gr. 4: AK209
AK209 Non-cleaved
Plasma IgG Concentration (μg/mL)
100
10
1
0.1
0
2
4
6
Time (day)

FIG. 29E

FIG. 30A Body weight loss

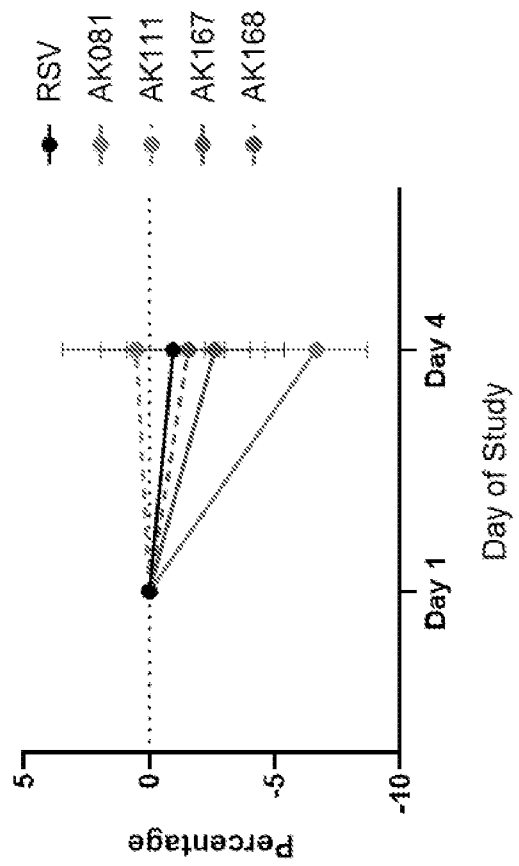


FIG. 30B Liver

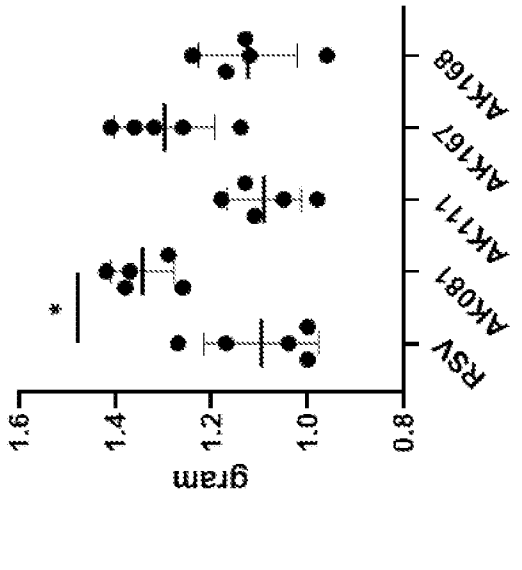


FIG. 30C Lung

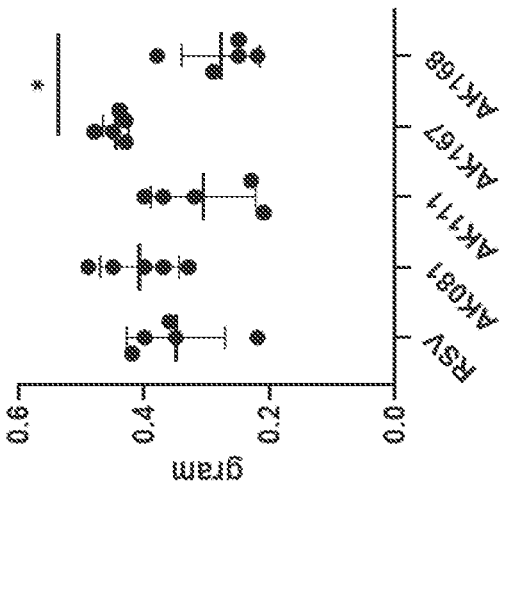


FIG. 30D Spleen

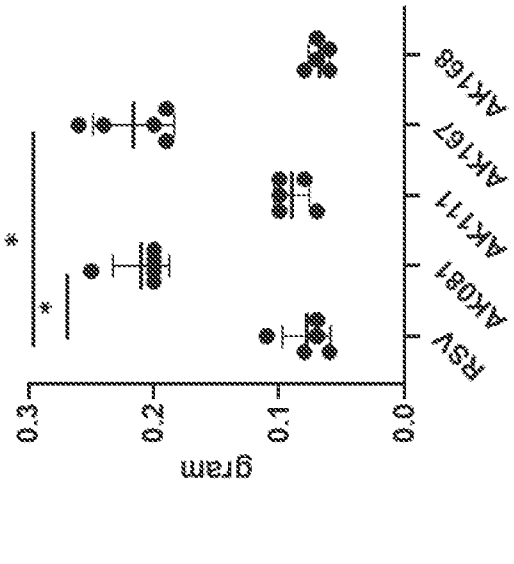


FIG. 31B

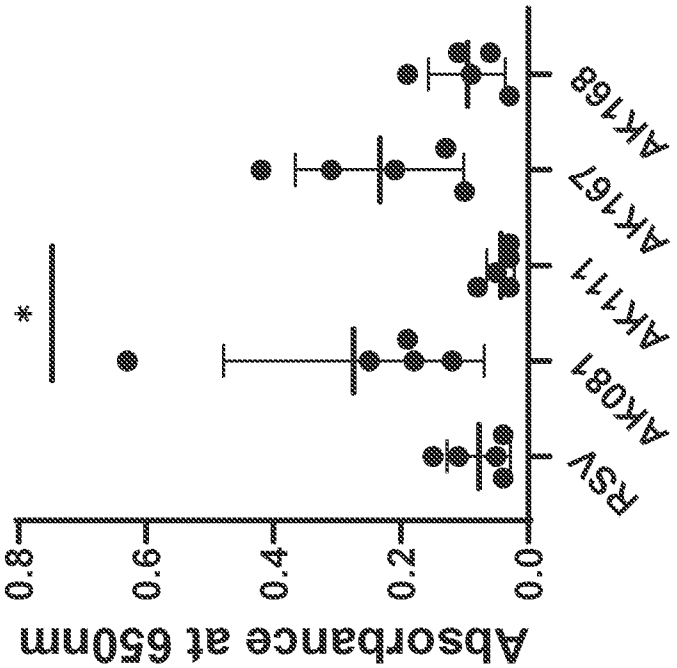


FIG. 31A

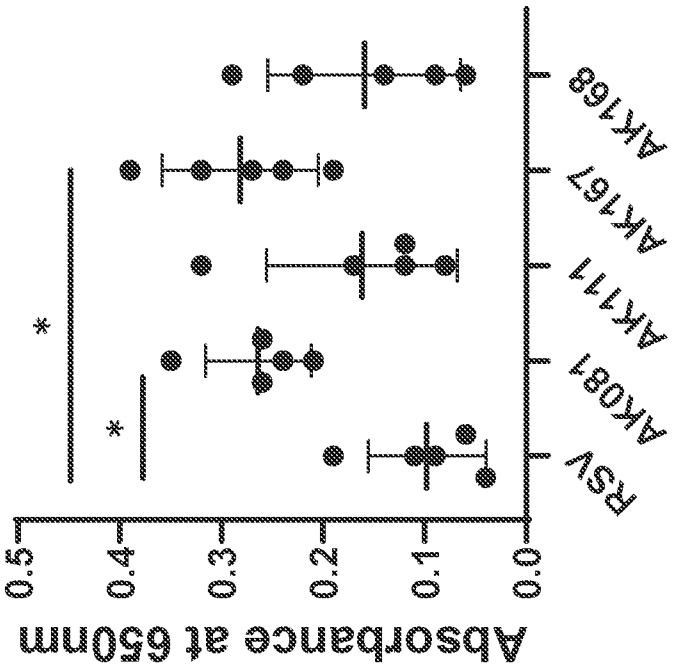


FIG. 32A

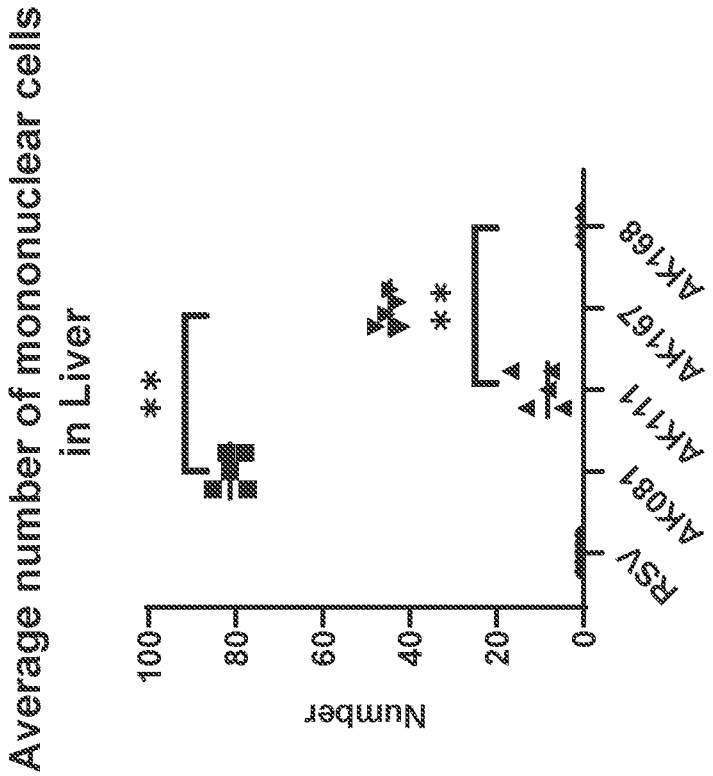


FIG. 32B

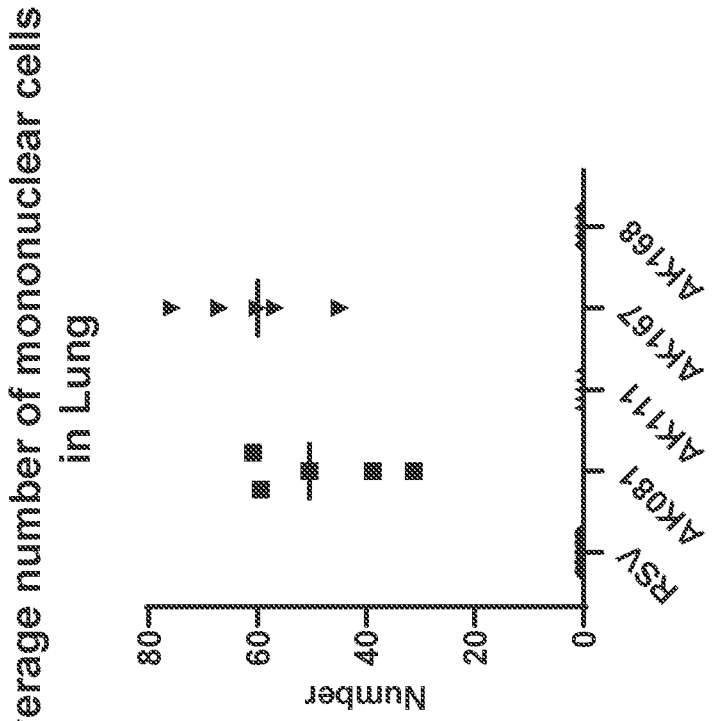
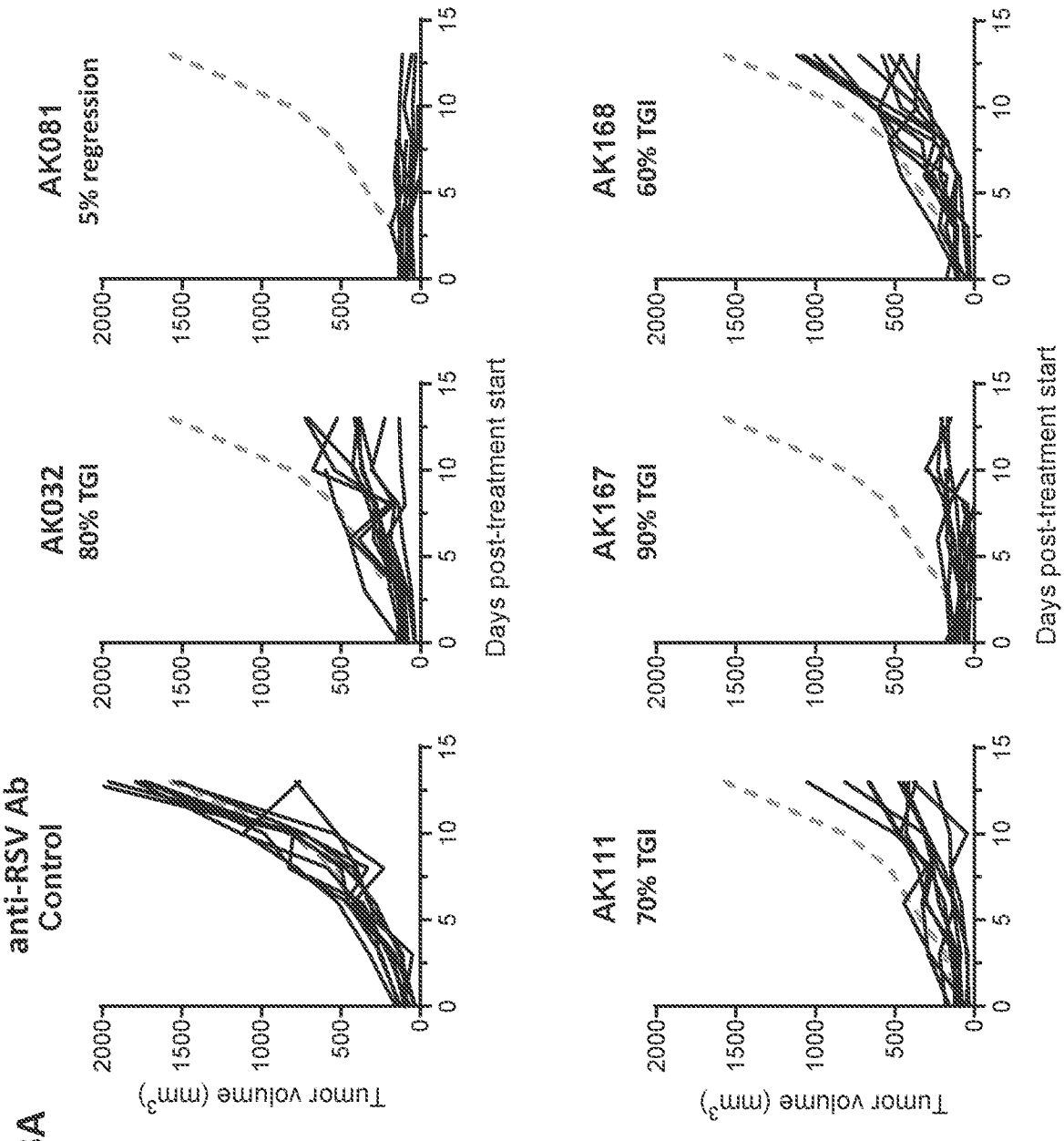


FIG. 33A


anti-RSV Ab
Control
AK032
80% TGI
AK081
5% regression
AK111
70% TGI
AK167
90% TGI
AK168
60% TGI
Tumor volume (mm3)
Days post-treatment start
0
500
1000
1500
2000
0
5
10
15

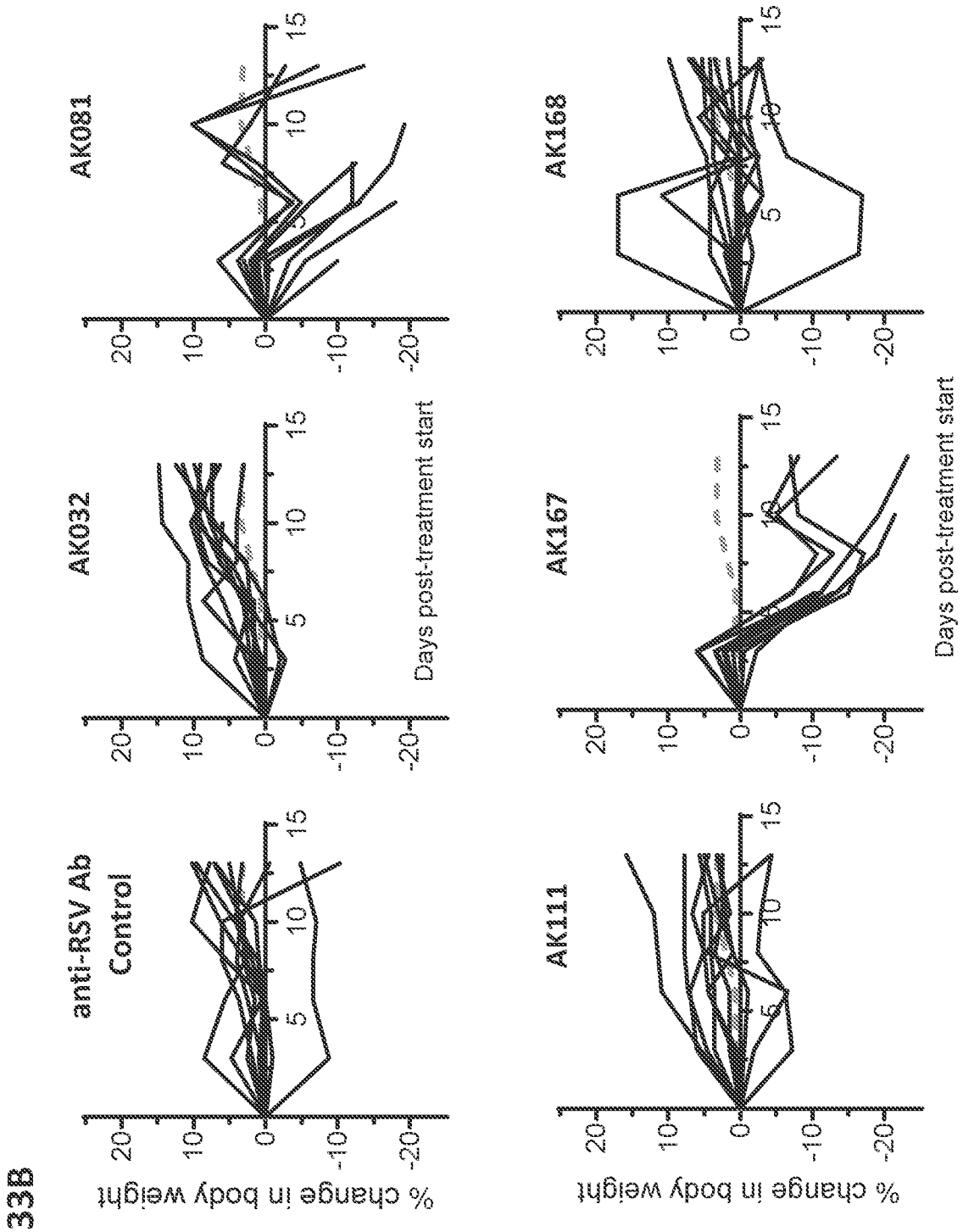

anti-RSV Ab Control
AK032
AK081
AK111
AK167
AK168
% change in body weight
Days post-treatment start
20
10
0
-10
-20
5
10
15

FIG. 33B

SEQUENCE LISTING

<110> Akrevia Therapeutics Inc.
Karow, Margaret
Lai, Deborah M.
Tomar, Dheeraj
Johnson, Parker
Rozenfeld, Raphael
O'Hagan, Ronan

<120> Masked Cytokine Polypeptides

<130> 73776-20009.40

<140> Not Yet Assigned
<141> Concurrently Herewith

<150> US 62/891,199
<151> 2019-08-23

<150> US 62/888,276
<151> 2019-08-16

<150> US 62/737,803
<151> 2018-09-27

<160> 830

<170> FastSEQ for Windows Version 4.0

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

<220>
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Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His
1 5 10 15
Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys
20 25 30
Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys
35 40 45
Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys
50 55 60
Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu
65 70 75 80
Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu
85 90 95
Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala

```
            100                 105                 110
Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser Ile
        115                 120                 125
Ile Ser Thr Leu Thr
    130
```

<210> 2
<211> 133
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 2

```
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 1               5                  10                  15
Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys
            20                  25                  30
Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys
        35                  40                  45
Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys
    50                  55                  60
Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His Phe
65                  70                  75                  80
Asp Pro Arg Asp Val Val Ser Asn Ile Asn Val Phe Val Leu Glu Leu
                85                  90                  95
Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala
            100                 105                 110
Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser Ile
        115                 120                 125
Ile Ser Thr Leu Thr
    130
```

<210> 3
<211> 133
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 3

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Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His
 1               5                  10                  15
Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys
            20                  25                  30
Asn Pro Lys Leu Thr Ala Met Leu Thr Ala Lys Phe Ala Met Pro Lys
        35                  40                  45
Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Ala Leu Lys
    50                  55                  60
Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu
```

65 70 75 80
Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu
85 90 95
Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala
100 105 110
Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser Ile
115 120 125
Ile Ser Thr Leu Thr
130

<210> 4
<211> 133
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 4
Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His
1 5 10 15
Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys
20 25 30
Asn Pro Lys Leu Thr Arg Met Leu Thr Lys Lys Phe Tyr Met Pro Lys
35 40 45
Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys
50 55 60
Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu
65 70 75 80
Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu
85 90 95
Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala
100 105 110
Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser Ile
115 120 125
Ile Ser Thr Leu Thr
130

<210> 5
<211> 133
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 5
Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His
1 5 10 15
Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys
20 25 30
Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Ala Phe Ala Met Pro Lys

```
        35                  40                  45
Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys
    50                  55                  60
Pro Leu Glu Glu Val Leu Asn Gly Ala Gln Ser Lys Asn Phe His Leu
65                  70                  75                  80
Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu
                85                  90                  95
Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala
            100                 105                 110
Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser Ile
        115                 120                 125
Ile Ser Thr Leu Thr
    130
```

<210> 6
<211> 133
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 6

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Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His
 1               5                  10                  15
Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys
            20                  25                  30
Asn Pro Lys Leu Thr Ala Met Leu Thr Ala Lys Phe Ala Met Pro Lys
        35                  40                  45
Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Ala Leu Lys
    50                  55                  60
Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His Phe
65                  70                  75                  80
Asp Pro Arg Asp Val Val Ser Asn Ile Asn Val Phe Val Leu Glu Leu
                85                  90                  95
Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala
            100                 105                 110
Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser Ile
        115                 120                 125
Ile Ser Thr Leu Thr
    130
```

<210> 7
<211> 133
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 7

```
Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His
```

```
 1               5                  10                  15
Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys
            20                  25                  30
Asn Pro Lys Leu Thr Arg Met Leu Thr Lys Lys Phe Tyr Met Pro Lys
        35                  40                  45
Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys
    50                  55                  60
Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His Phe
65                  70                  75                  80
Asp Pro Arg Asp Val Val Ser Asn Ile Asn Val Phe Val Leu Glu Leu
                85                  90                  95
Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala
            100                 105                 110
Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser Ile
        115                 120                 125
Ile Ser Thr Leu Thr
    130
```

<210> 8
<211> 133
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 8

```
Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His
 1               5                  10                  15
Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys
            20                  25                  30
Asn Pro Lys Leu Thr Arg Met Leu Thr Ala Lys Phe Ala Met Pro Lys
        35                  40                  45
Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys
    50                  55                  60
Pro Leu Glu Glu Val Leu Asn Gly Ala Gln Ser Lys Asn Phe His Phe
65                  70                  75                  80
Asp Pro Arg Asp Val Val Ser Asn Ile Asn Val Phe Val Leu Glu Leu
                85                  90                  95
Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala
            100                 105                 110
Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser Ile
        115                 120                 125
Ile Ser Thr Leu Thr
    130
```

<210> 9
<211> 164
<212> PRT
<213> Homo sapiens

<400> 9

```
Glu Leu Cys Asp Asp Asp Pro Pro Glu Ile Pro His Ala Thr Phe Lys
 1               5                  10                  15
Ala Met Ala Tyr Lys Glu Gly Thr Met Leu Asn Cys Glu Cys Lys Arg
            20                  25                  30
Gly Phe Arg Arg Ile Lys Ser Gly Ser Leu Tyr Met Leu Cys Thr Gly
        35                  40                  45
Asn Ser Ser His Ser Ser Trp Asp Asn Gln Cys Gln Cys Thr Ser Ser
    50                  55                  60
Ala Thr Arg Asn Thr Thr Lys Gln Val Thr Pro Gln Pro Glu Glu Gln
65                  70                  75                  80
Lys Glu Arg Lys Thr Thr Glu Met Gln Ser Pro Met Gln Pro Val Asp
                85                  90                  95
Gln Ala Ser Leu Pro Gly His Cys Arg Glu Pro Pro Pro Trp Glu Asn
            100                 105                 110
Glu Ala Thr Glu Arg Ile Tyr His Phe Val Val Gly Gln Met Val Tyr
        115                 120                 125
Tyr Gln Cys Val Gln Gly Tyr Arg Ala Leu His Arg Gly Pro Ala Glu
    130                 135                 140
Ser Val Cys Lys Met Thr His Gly Lys Thr Arg Trp Thr Gln Pro Gln
145                 150                 155                 160
Leu Ile Cys Thr
```

<210> 10
<211> 188
<212> PRT
<213> Homo sapiens

<400> 10

```
Ala Val Asn Gly Thr Ser Gln Phe Thr Cys Phe Tyr Asn Ser Arg Ala
 1               5                  10                  15
Asn Ile Ser Cys Val Trp Ser Gln Asp Gly Ala Leu Gln Asp Thr Ser
            20                  25                  30
Cys Gln Val His Ala Trp Pro Asp Arg Arg Arg Trp Asn Gln Thr Cys
        35                  40                  45
Glu Leu Leu Pro Val Ser Gln Ala Ser Trp Ala Cys Asn Leu Ile Leu
    50                  55                  60
Gly Ala Pro Asp Ser Gln Lys Leu Thr Thr Val Asp Ile Val Thr Leu
65                  70                  75                  80
Arg Val Leu Cys Arg Glu Gly Val Arg Trp Arg Val Met Ala Ile Gln
                85                  90                  95
Asp Phe Lys Pro Phe Glu Asn Leu Arg Leu Met Ala Pro Ile Ser Leu
            100                 105                 110
Gln Val Val His Val Glu Thr His Arg Cys Asn Ile Ser Trp Glu Ile
        115                 120                 125
Ser Gln Ala Ser His Tyr Phe Glu Arg His Leu Glu Phe Glu Ala Arg
    130                 135                 140
Thr Leu Ser Pro Gly His Thr Trp Glu Glu Ala Pro Leu Leu Thr Leu
145                 150                 155                 160
Lys Gln Lys Gln Glu Trp Ile Cys Leu Glu Thr Leu Thr Pro Asp Thr
                165                 170                 175
Gln Tyr Glu Phe Gln Val Arg Val Lys Pro Leu Gln
            180                 185
```

<210> 11
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 11
Gly Gly Ser Ser Pro Pro Met Pro Tyr Asp Leu Tyr His Pro Ser Gly
 1   5   10   15
Pro

<210> 12
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 12
Gly Ser Pro Met Pro Tyr Asp Leu Tyr His Pro
 1   5   10

<210> 13
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 13
Gly Ser Pro Pro Met Pro Tyr Asp Leu Tyr His Pro Ser Gly Pro
 1   5   10   15

<210> 14
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 14
Gly Ser Pro Ser Met Pro Tyr Asp Leu Tyr His Pro Ser Gly Pro
 1   5   10   15

<210> 15
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 15
Gly Pro Pro Ser Gly Ser Ser Pro Met Pro Tyr Asp Leu Tyr His Pro
 1   5   10   15
Ser Gly Gly Gly
            20

<210> 16
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 16
Gly Ser Ser Gly Gly Pro Pro Gly Gly Met Pro Tyr Asp Leu Tyr His
 1   5   10   15
Pro Ser Gly Gly Gly
            20

<210> 17
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 17
Ser Gly Ser Pro Ser Gly Ser Gly Gly Gly Met Pro Tyr Asp Leu Tyr
 1   5   10   15
His Pro Ser Gly Gly Gly
            20

<210> 18
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 18
Gly Pro Pro Gly Pro Pro Gly Ser Ser Gly Met Pro Tyr Asp Leu Tyr
 1   5   10   15
His Pro Ser Gly Gly Gly
            20

<210> 19
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 19
Gly Ser Ser Ser Gly Pro Pro Gly Pro Pro Ser Met Pro Tyr Asp Leu
 1   5   10   15
Tyr His Pro Ser Gly Gly Gly
            20

<210> 20
<211> 2
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 20
Pro Ala
 1

<210> 21
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 21
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 1   5   10   15

<210> 22
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 22
Pro Ser Gly Pro Ser Ala Gly Gly Ala Ala
 1   5   10

<210> 23
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 23
Gly Gly Pro Pro Ala Ser Ala Gly Ser
 1   5

<210> 24
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 24
Gly Ser Pro Pro Ala Gly Gly Ala Pro
 1   5

<210> 25
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 25
Gly Pro Gly Ser Gly Ser Gly Gly Ala Ala
 1   5   10

<210> 26
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 26
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 1   5   10

<210> 27
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 27
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 1   5   10   15
Gly Gly Gly Ser
            20

<210> 28
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 28
Pro Gly Ser Gly Ser
 1   5

<210> 29
<211> 35
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 29
Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
 1   5   10   15
Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
            20   25   30
Gly Gly Gly
        35

<210> 30
<211> 25
<212> PRT

<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 30
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> 31
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 31
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 Gly Gly Gly Gly Ser
            20   25   30

<210> 32
<211> 35
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 32
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 Gly Gly Gly Gly Ser Gly Gly
            20   25   30
Gly Gly Ser
        35

<210> 33
<211> 40
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 33
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 Gly Gly Gly Gly Ser Gly Gly
            20                  25                  30
Gly Gly Ser Gly Gly Gly Gly Ser
        35                  40
```

<210> 34
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 34
```
Gly Gly Ser Ser Pro Pro
 1               5
```

<210> 35
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 35
```
Ser Gly Pro
 1
```

<210> 36
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 36
```
Gly Ser Pro
 1
```

<210> 37
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 37
Gly Ser Pro Pro
 1

<210> 38
<211> 4
<212> PRT
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Gly Pro Pro Gly Pro Pro Gly Ser Ser Gly
1 5 10

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Ser Gly Gly Gly
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1 5 10

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Ser Gly Gly
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Ser Ser Gly
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Ser His Gly Gly
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His Gly Gly Gly
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<400> 66

Ser Gly Pro Ala
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Gly Gly Ser Gly Gly Ser
 1   5

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Gly Gly Ser Gly Gly Pro
 1   5

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Gly Gly Ser Gly Gly Gly
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Gly Ser Gly Gly Pro Gly Pro Ser
 1   5

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Ser Gly Pro Pro Gly Ser Ser
 1   5

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Ser Ser Gly Gly Ser Gly Pro
 1   5

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Ser Ser Pro Ser Pro Ser Gly Gly
 1   5

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Ser Pro Gly Gly Ser Ser
 1   5

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Gly Gly Pro Gly Ser Ser Pro
 1   5

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Ser Gly Pro Pro Gly Gly Pro Ser Ser
 1   5

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Gly Pro Gly Pro Gly Ser Pro Pro Gly Gly Ser Ser
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Ser Gly Pro Pro
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Pro Gly Ser Pro Ser Ser Ser
 1   5

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Pro Ser Pro Gly Gly Pro Ser
 1   5

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Gly Gly Pro Pro Ser
 1   5

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Pro Ser Pro Pro Ser Ser
 1   5

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Ser Gly Gly Pro Gly Pro
 1   5

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Gly Pro Ser Pro Gly Ser
 1   5

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Gly Ser Pro Gly Pro Ser Pro
 1   5

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Ser Gly Ser Ser Gly Pro
 1   5

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Gly Gly Ser Ser Ser Pro Pro
 1   5

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Gly Ser Pro Gly Ser Pro
 1   5

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Pro Pro Pro Ser
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<400> 91
Ala Pro Pro Pro Ser
 1   5

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Ala Ala Pro Pro Pro Ser
 1   5

<210> 93
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Ser Ala Pro Pro Pro Ser
 1   5

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Ser Ser Gly Pro
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<400> 95
Ser Ser Pro Gly Pro

1 5

<210> 96
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<400> 96
Met Pro Tyr Asp Leu Tyr His Pro
1 5

<210> 97
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<400> 97
Gly Gly Ile Gly Gln Leu Thr Ala
1 5

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<400> 98
Asp Leu Gly Arg Phe Gln Thr Phe
1 5

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<400> 99
Asp Ser Gly Gly Phe Met Leu Thr
1 5

<210> 100
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<400> 100
Thr Ser Val Leu Met Ala Ala Pro
 1   5

<210> 101
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<400> 101
Thr Ser Glu Phe Val Phe Ala Pro Asp Gln
 1   5   10

<210> 102
<211> 8
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<400> 102
Lys Leu Val Leu Pro Val Leu Pro
 1   5

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<400> 103
Lys Pro Ile Leu Phe Phe Arg Leu
 1   5

<210> 104

<211> 6
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<400> 104
Ala Asn Gln Leu Lys Gly
 1   5

<210> 105
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<400> 105
Gln Ser Gln Leu Lys Glu
 1   5

<210> 106
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<400> 106
His Glu Gln Leu Thr Val
 1   5

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<400> 107
Pro Ala Asn Leu Val Ala Pro Asp Pro
 1   5

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Pro Ala Pro Gly Val Tyr Pro Gly Pro
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Ala Pro Ala Gly Leu Ile Val Pro Tyr Asn
 1   5   10

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Pro Gln Ala Leu Val Ala
 1   5

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Val Gly Asn Leu Asn Phe
 1   5

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Val Ala Asn Leu Leu Tyr Glu
 1   5

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Val Tyr Asn Leu Met Asp
 1   5

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<400> 114
Thr Phe Asn Ile Lys Gln
 1   5

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Asp Leu Trp Lys Leu Leu Pro
 1   5

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Pro Gly Ser Thr Lys Arg Ala
 1   5

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Gln Gln Tyr Arg Ala Leu Lys Ser
 1   5

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Tyr Val Pro Arg Ala Val Leu
 1   5

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Gly Val Asn Lys Trp Pro Thr
 1   5

<210> 120
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<400> 120

Leu Ala Gln Ala Val Arg Ser Ser
 1   5

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Arg Ala Ala Ala Val Lys Ser Pro
 1   5

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<400> 122
Asp Leu Leu Ala Val Val Ala Ala Ser
 1   5

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Val Gln Thr Val Thr Trp Pro Asp
 1   5

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Ala Ile Pro Met Ser Ile Pro Pro
 1   5

<210> 125
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<400> 125
Gly Tyr Glu Val His His Gln Lys
 1   5

<210> 126
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<400> 126
Val His His Gln Lys Leu Val Phe
 1   5

<210> 127
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<400> 127
Ile Arg Arg Val Ser Tyr Ser Phe
 1   5

<210> 128
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<220>
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<400> 128
Met Pro Tyr Asp Leu Tyr His Pro Ile Leu Phe Phe Arg Leu
 1   5   10

<210> 129
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<400> 129
Gly Gly Ile Gly Gln Leu Thr Ser Val Leu Met Ala Ala Pro
 1   5   10

<210> 130
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<400> 130
Asp Ser Gly Gly Phe Met Leu Thr Leu Val Leu Pro Val Leu Pro
 1   5   10   15

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<400> 131
Thr Ser Glu Phe Val Phe Ala Pro Asp Leu Gly Arg Phe Gln Thr Phe
 1   5   10   15

<210> 132
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<400> 132
Thr Ser Thr Ser Gly Arg Ser Ala Asn Pro Arg
 1   5   10

<210> 133
<211> 11

<212> PRT
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<220>
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<400> 133
Thr Ser Thr Ser Gly Arg Ser Ala Asn Pro Gly
 1   5   10

<210> 134
<211> 11
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<220>
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<400> 134
Thr Ser Thr Ser Gly Arg Ser Ala Asn Pro His
 1   5   10

<210> 135
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<220>
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<400> 135
Val Pro Leu Ser Leu Tyr
 1   5

<210> 136
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<400> 136
Thr Ser Ala Ser Gly Ala Ser Ala Ser Ala Ala
 1   5   10

<210> 137
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<400> 137
Pro Ser Ser Pro Gly Gly Gly Ser Ser Pro
 1   5   10

<210> 138
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<400> 138
Ile Ser Ser Gly Leu Leu Ser Gly Arg Ser Asp Asn His
 1   5   10

<210> 139
<211> 13
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<400> 139
Ile Ser Ser Gly Leu Leu Ser Gly Arg Ser Asp Asp His
 1   5   10

<210> 140
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<400> 140
Ile Ser Ser Gly Leu Leu Ser Gly Arg Ser Asp Ile His
 1   5   10

<210> 141
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<220>

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<400> 141
Ile Ser Ser Gly Leu Leu Ser Gly Arg Ser Asp Gln His
 1   5   10

<210> 142
<211> 13
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<400> 142
Ile Ser Ser Gly Leu Leu Ser Gly Arg Ser Asp Thr His
 1   5   10

<210> 143
<211> 13
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<400> 143
Ile Ser Ser Gly Leu Leu Ser Gly Arg Ser Ala Asn Pro
 1   5   10

<210> 144
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<220>
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<400> 144
Ile Ser Ser Gly Leu Leu Ser Gly Arg Ser Asp Asn Pro
 1   5   10

<210> 145
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
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<400> 145
Ile Ser Ser Gly Leu Leu Ser Gly Arg Ser Ala Asn Pro Arg Gly
 1   5   10   15

<210> 146
<211> 18
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<220>
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<400> 146
Ala Val Gly Leu Leu Ala Pro Pro Gly Gly Leu Ser Gly Arg Ser Asp
 1   5   10   15
Asn His

<210> 147
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
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<400> 147
Ala Val Gly Leu Leu Ala Pro Pro Gly Gly Leu Ser Gly Arg Ser Asp
 1   5   10   15
Asp His

<210> 148
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
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<400> 148
Ala Val Gly Leu Leu Ala Pro Pro Gly Gly Leu Ser Gly Arg Ser Asp
 1   5   10   15
Ile His

<210> 149
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
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<400> 149
Ala Val Gly Leu Leu Ala Pro Pro Gly Gly Leu Ser Gly Arg Ser Asp
 1   5   10   15
Gln His

<210> 150
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<220>
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<400> 150
Ala Val Gly Leu Leu Ala Pro Pro Gly Gly Leu Ser Gly Arg Ser Asp
 1   5   10   15
Thr His

<210> 151
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<213> Artificial Sequence

<220>
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<400> 151
Ala Val Gly Leu Leu Ala Pro Pro Gly Gly Leu Ser Gly Arg Ser Ala
 1   5   10   15
Asn Pro

<210> 152
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
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<400> 152
Ala Val Gly Leu Leu Ala Pro Pro Gly Gly Leu Ser Gly Arg Ser Asp
 1   5   10   15
Asn Pro

<210> 153
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
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<400> 153
Ala Val Gly Leu Leu Ala Pro Pro Ser Gly Arg Ser Ala Asn Pro Arg
 1   5   10   15
Gly

<210> 154
<211> 226
<212> PRT
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<220>
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<400> 154
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1   5   10   15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20   25   30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35   40   45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50   55   60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65   70   75   80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85   90   95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100   105   110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115   120   125
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130   135   140
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145   150   155   160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165   170   175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180   185   190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195   200   205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210   215   220

Pro Gly
225

<210> 155
<211> 226
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<213> Artificial Sequence

<220>
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<400> 155
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1   5   10   15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20   25   30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35   40   45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50   55   60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65   70   75   80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85   90   95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100   105   110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115   120   125
Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130   135   140
Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145   150   155   160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165   170   175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val
            180   185   190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195   200   205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210   215   220
Pro Gly
225

<210> 156
<211> 226
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 156

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1   5   10   15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20   25   30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35   40   45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50   55   60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65   70   75   80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85   90   95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100   105   110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115   120   125
Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130   135   140
Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145   150   155   160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165   170   175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180   185   190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195   200   205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210   215   220
Pro Gly
225

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

<220>
<223> Synthetic Construct

<400> 157
Glu Ile Val Leu Thr Gln Ser Pro Asp Phe Gln Ser Val Thr Pro Lys
 1   5   10   15
Glu Lys Val Thr Ile Thr Cys Ser Ala Asn Ser Ala Leu Ser Tyr Met
            20   25   30
Tyr Trp Tyr Gln Gln Lys Pro Asp Gln Ser Pro Lys Leu Trp Val His
        35   40   45
Gly Thr Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
    50   55   60
Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Ser Leu Glu Ala Glu
65   70   75   80
Asp Ala Ala Thr Tyr Tyr Cys His His Trp Ser Asn Thr Gln Trp Thr
                85   90   95
Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro

```
            100                 105                 110
Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
        115                 120                 125
Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
    130                 135                 140
Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
145                 150                 155                 160
Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
                165                 170                 175
Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
            180                 185                 190
Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
        195                 200                 205
Asn Arg Gly Glu Cys
    210


<210> 158
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 158
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
 1               5                  10                  15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
            20                  25                  30
Phe Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45
Gly Arg Val Asp Pro Glu Gln Gly Arg Ala Asp Tyr Ala Glu Lys Phe
    50                  55                  60
Lys Lys Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65                  70                  75                  80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
Ala Arg Arg Ala Met Asp Asn Tyr Gly Phe Ala Tyr Trp Gly Gln Gly
            100                 105                 110
Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
        115                 120                 125
Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
    130                 135                 140
Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145                 150                 155                 160
Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
                165                 170                 175
Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
            180                 185                 190
Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
        195                 200                 205
Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
    210                 215                 220
```

```
Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
225                 230                 235                 240
Asp Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
                245                 250                 255
Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
            260                 265                 270
Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
        275                 280                 285
Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
    290                 295                 300
Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
305                 310                 315                 320
Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Glu Glu Lys
                325                 330                 335
Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
            340                 345                 350
Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
        355                 360                 365
Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
    370                 375                 380
Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
385                 390                 395                 400
Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
                405                 410                 415
Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
            420                 425                 430
Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
        435                 440                 445
Lys
```

<210> 159
<211> 153
<212> PRT
<213> Homo sapiens

<400> 159

```
Met Tyr Arg Met Gln Leu Leu Ser Cys Ile Ala Leu Ser Leu Ala Leu
 1               5                  10                  15
Val Thr Asn Ser Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu
            20                  25                  30
Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile
        35                  40                  45
Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe
    50                  55                  60
Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu
65                  70                  75                  80
Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys
                85                  90                  95
Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile
            100                 105                 110
Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala
        115                 120                 125
```

Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe
    130   135   140
Cys Gln Ser Ile Ile Ser Thr Leu Thr
145   150

<210> 160
<211> 133
<212> PRT
<213> Homo sapiens

<400> 160
Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His
 1   5   10   15
Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys
            20   25   30
Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys
        35   40   45
Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys
    50   55   60
Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu
65   70   75   80
Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu
                85   90   95
Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala
            100   105   110
Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Cys Gln Ser Ile
        115   120   125
Ile Ser Thr Leu Thr
    130

<210> 161
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 161
Cys Gly Gly His Gln Tyr Glu Arg Arg Gly Gly Cys
 1   5   10

<210> 162
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 162

Cys Ser Gly His Gln Tyr Glu Arg Arg Glu Gly Cys
 1   5   10

<210> 163
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 163
Cys Gly Gly His Tyr Phe Glu Arg His Gly Gly Cys
 1   5   10

<210> 164
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 164
Cys Ser Gly His Tyr Phe Glu Arg His Glu Gly Cys
 1   5   10

<210> 165
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 165
Cys Ser Phe His Gln Tyr Glu Arg His Glu Gly Cys
 1   5   10

<210> 166
<211> 162
<212> PRT
<213> Homo sapiens

<400> 166
Met Arg Ile Ser Lys Pro His Leu Arg Ser Ile Ser Ile Gln Cys Tyr
 1   5   10   15
Leu Cys Leu Leu Leu Asn Ser His Phe Leu Thr Glu Ala Gly Ile His
            20   25   30
Val Phe Ile Leu Gly Cys Phe Ser Ala Gly Leu Pro Lys Thr Glu Ala

```
        35                  40                  45
Asn Trp Val Asn Val Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile
    50                  55                  60
Gln Ser Met His Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His
65                  70                  75                  80
Pro Ser Cys Lys Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln
                85                  90                  95
Val Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu
            100                 105                 110
Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val
        115                 120                 125
Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile
    130                 135                 140
Lys Glu Phe Leu Gln Ser Phe Val His Ile Val Gln Met Phe Ile Asn
145                 150                 155                 160
Thr Ser
```

<210> 167
<211> 114
<212> PRT
<213> Homo sapiens

<400> 167

```
Asn Trp Val Asn Val Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile
 1               5                  10                  15
Gln Ser Met His Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His
            20                  25                  30
Pro Ser Cys Lys Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln
        35                  40                  45
Val Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu
    50                  55                  60
Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val
65                  70                  75                  80
Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile
                85                  90                  95
Lys Glu Phe Leu Gln Ser Phe Val His Ile Val Gln Met Phe Ile Asn
            100                 105                 110
Thr Ser
```

<210> 168
<211> 330
<212> PRT
<213> Homo sapiens

<400> 168

```
Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
 1               5                  10                  15
Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
            20                  25                  30
Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
```

```
        35                  40                  45
Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
    50                  55                  60
Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65                  70                  75                  80
Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
                85                  90                  95
Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
            100                 105                 110
Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
        115                 120                 125
Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
    130                 135                 140
Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
145                 150                 155                 160
Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
                165                 170                 175
Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
            180                 185                 190
His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
        195                 200                 205
Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
    210                 215                 220
Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu
225                 230                 235                 240
Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
                245                 250                 255
Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
            260                 265                 270
Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
        275                 280                 285
Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
    290                 295                 300
Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
305                 310                 315                 320
Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
                325                 330
```

<210> 169
<211> 227
<212> PRT
<213> Homo sapiens

<400> 169

```
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
```

65 70 75 80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
85 90 95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
100 105 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
115 120 125
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
130 135 140
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145 150 155 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
165 170 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
180 185 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
195 200 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
210 215 220
Pro Gly Lys
225

<210> 170
<211> 106
<212> PRT
<213> Homo sapiens

<400> 170
Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
1 5 10 15
Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
20 25 30
Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
35 40 45
Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
50 55 60
Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
65 70 75 80
His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
85 90 95
Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
100 105

<210> 171
<211> 585
<212> PRT
<213> Homo sapiens

<400> 171
Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
1 5 10 15
Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln

```
            20                  25                  30
Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
        35                  40                  45
Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
    50                  55                  60
Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
65                  70                  75                  80
Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
                85                  90                  95
Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
            100                 105                 110
Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
        115                 120                 125
Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
    130                 135                 140
Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
145                 150                 155                 160
Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
                165                 170                 175
Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
            180                 185                 190
Ser Ala Lys Gln Gly Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
        195                 200                 205
Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro
    210                 215                 220
Lys Ala Glu Phe Ala Glu Val Ser Lys Leu Val Thr Asp Leu Thr Lys
225                 230                 235                 240
Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
                245                 250                 255
Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
            260                 265                 270
Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
        275                 280                 285
Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser
    290                 295                 300
Leu Ala Ala Asp Phe Val Gly Ser Lys Asp Val Cys Lys Asn Tyr Ala
305                 310                 315                 320
Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
                325                 330                 335
Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
            340                 345                 350
Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu
        355                 360                 365
Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
    370                 375                 380
Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
385                 390                 395                 400
Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
                405                 410                 415
Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
            420                 425                 430
Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
        435                 440                 445
Ala Glu Asp Cys Leu Ser Val Phe Leu Asn Gln Leu Cys Val Leu His
```

```
    450                 455                 460
Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
465                 470                 475                 480
Leu Val Asn Gly Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
                485                 490                 495
Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
            500                 505                 510
Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
        515                 520                 525
Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
    530                 535                 540
Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
545                 550                 555                 560
Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
                565                 570                 575
Ala Ala Ser Gln Ala Ala Leu Gly Leu
            580                 585
```

<210> 172
<211> 46
<212> PRT
<213> Streptococcus

<220>
<223> Synthetic Construct

<400> 172
```
Leu Ala Glu Ala Lys Val Leu Ala Asn Arg Glu Leu Asp Lys Tyr Gly
 1               5                  10                  15
Val Ser Asp Tyr Tyr Lys Asn Leu Ile Asn Asn Ala Lys Thr Val Glu
            20                  25                  30
Gly Val Lys Ala Leu Ile Asp Glu Ile Leu Ala Ala Leu Pro
        35                  40                  45
```

<210> 173
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 173
```
Asp Ile Cys Leu Pro Arg Trp Gly Cys Leu Trp
 1               5                  10
```

<210> 174
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 174
Arg Leu Ile Glu Asp Ile Cys Leu Pro Arg Trp Gly Cys Leu Trp Glu
 1   5   10   15
Asp Asp

<210> 175
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 175
Asp Cys Ala Trp His Leu Gly Glu Leu Val Trp Cys Thr
 1   5   10

<210> 176
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 176
Asn Lys Phe Arg Gly Lys Tyr Lys
 1   5

<210> 177
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 177
Asn Ala Arg Lys Phe Tyr Lys Gly
 1   5

<210> 178
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 178
Phe Tyr Trp His Cys Leu Asp Glu
 1   5

<210> 179
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 179
Phe Tyr Cys His Trp Ala Leu Glu
 1   5

<210> 180
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 180
Phe Tyr Cys His Thr Ile Asp Glu
 1   5

<210> 181
<211> 51
<212> PRT
<213> Staphylococcus aureus

<400> 181
Ala Gln Gln Asn Ala Phe Tyr Gln Val Leu Asn Met Pro Asn Leu Asn
 1   5   10   15
Ala Asp Gln Arg Asn Gly Phe Ile Gln Ser Leu Lys Asp Asp Pro Ser
            20   25   30
Gln Ser Ala Asn Val Leu Gly Glu Ala Gln Lys Leu Asn Asp Ser Gln
        35   40   45
Ala Pro Lys
    50

<210> 182
<211> 61
<212> PRT
<213> Staphylococcus aureus

<400> 182
Ala Asp Ala Gln Gln Asn Lys Phe Asn Lys Asp Gln Gln Ser Ala Phe
 1   5   10   15
Tyr Glu Ile Leu Asn Met Pro Asn Leu Asn Glu Glu Gln Arg Asn Gly
            20   25   30
Phe Ile Gln Ser Leu Lys Asp Asp Pro Ser Gln Ser Thr Asn Val Leu
        35   40   45
Gly Glu Ala Lys Lys Leu Asn Glu Ser Gln Ala Pro Lys
    50   55   60

<210> 183
<211> 58
<212> PRT
<213> Staphylococcus aureus

<400> 183
Ala Asp Asn Asn Phe Asn Lys Glu Gln Gln Asn Ala Phe Tyr Glu Ile
 1   5   10   15
Leu Asn Met Pro Asn Leu Asn Glu Glu Gln Arg Asn Gly Phe Ile Gln
            20   25   30
Ser Leu Lys Asp Asp Pro Ser Gln Ser Ala Asn Leu Leu Ala Glu Ala
        35   40   45
Lys Lys Leu Asn Glu Ser Gln Ala Pro Lys
    50   55

<210> 184
<211> 58
<212> PRT
<213> Staphylococcus aureus

<400> 184
Ala Asp Asn Lys Phe Asn Lys Glu Gln Gln Asn Ala Phe Tyr Glu Ile
 1   5   10   15
Leu His Leu Pro Asn Leu Asn Glu Glu Gln Arg Asn Gly Phe Ile Gln
            20   25   30
Ser Leu Lys Asp Asp Pro Ser Gln Ser Ala Asn Leu Leu Ala Glu Ala
        35   40   45
Lys Lys Leu Asn Asp Ala Gln Ala Pro Lys
    50   55

<210> 185
<211> 58
<212> PRT
<213> Staphylococcus aureus

<400> 185
Ala Asp Asn Lys Phe Asn Lys Glu Gln Gln Asn Ala Phe Tyr Glu Ile
 1   5   10   15
Leu His Leu Pro Asn Leu Thr Glu Glu Gln Arg Asn Gly Phe Ile Gln
            20   25   30

```
Ser Leu Lys Asp Asp Pro Ser Val Ser Lys Glu Ile Leu Ala Glu Ala
        35                  40                  45
Lys Lys Leu Asn Asp Ala Gln Ala Pro Lys
    50                  55
```

<210> 186
<211> 58
<212> PRT
<213> Staphylococcus aureus

<400> 186

```
Val Asp Asn Lys Phe Asn Lys Glu Gln Gln Asn Ala Phe Tyr Glu Ile
 1               5                  10                  15
Leu His Leu Pro Asn Leu Asn Glu Glu Gln Arg Asn Ala Phe Ile Gln
            20                  25                  30
Ser Leu Lys Asp Asp Pro Ser Gln Ser Ala Asn Leu Leu Ala Glu Ala
        35                  40                  45
Lys Lys Leu Asn Asp Ala Gln Ala Pro Lys
    50                  55
```

<210> 187
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 187

```
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1               5                  10                  15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ile Tyr
            20                  25                  30
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
Thr Val Ile Trp Tyr Asp Gly Ser Asn Glu Tyr Tyr Ala Asp Ser Val
    50                  55                  60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
Ala Arg Glu Asp Trp Leu Gly Glu Ala Asp Tyr Gly Met Asp Val Trp
            100                 105                 110
Gly Gln Gly Thr Thr Val Thr Val Ser Ser
        115                 120
```

<210> 188
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 188
Asp Ile Val Met Thr Gln Thr Pro Leu Ser Ser Pro Val Thr Leu Gly
 1   5   10   15
Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
            20   25   30
Asp Gly Asn Thr Tyr Leu Ser Trp Leu Gln Gln Arg Pro Gly Gln Pro
        35   40   45
Pro Arg Leu Leu Ile Tyr Lys Ile Ser Asn Arg Phe Ser Gly Val Pro
    50   55   60
Asp Arg Phe Ser Gly Ser Gly Ala Gly Thr Asp Phe Thr Leu Lys Ile
65   70   75   80
Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ala
                85   90   95
Thr Gln Phe Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100   105   110

<210> 189
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 189
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ile Tyr
            20   25   30
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45
Thr Val Ile Trp Tyr Asp Gly Ser Asn Glu Tyr Tyr Ala Asp Ser Val
    50   55   60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65   70   75   80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95
Ala Arg Asp Gly Glu Gln Trp Arg Gly Phe Asp Tyr Trp Gly Gln Gly
            100   105   110
Thr Thr Val Thr Val Ser Ser
        115

<210> 190
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 190
Asp Ile Val Met Thr Gln Thr Pro Leu Ser Ser Pro Val Thr Leu Gly
 1   5   10   15
Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
            20   25   30
Asp Gly Asn Thr Tyr Leu Ser Trp Leu Gln Gln Arg Pro Gly Gln Pro
        35   40   45
Pro Arg Leu Leu Ile Tyr Lys Ile Ser Asn Arg Phe Ser Gly Val Pro
    50   55   60
Asp Arg Phe Ser Gly Ser Gly Ala Gly Thr Asp Phe Thr Leu Lys Ile
65   70   75   80
Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ala
                85   90   95
Thr Gln Phe Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100   105   110

<210> 191
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 191
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ile Tyr
            20   25   30
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45
Thr Val Ile Trp Tyr Asp Gly Ser Asn Glu Tyr Tyr Ala Asp Ser Val
    50   55   60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65   70   75   80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95
Ala Arg Asp Gln Glu Gln Trp Arg Leu Ala Phe Asp Tyr Trp Gly Gln
            100   105   110
Gly Thr Thr Val Thr Val Ser Ser
        115   120

<210> 192
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 192

```
Asp Ile Val Met Thr Gln Thr Pro Leu Ser Ser Pro Val Thr Leu Gly
 1               5                  10                  15
Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
            20                  25                  30
Asp Gly Asn Thr Tyr Leu Ser Trp Leu Gln Gln Arg Pro Gly Gln Pro
        35                  40                  45
Pro Arg Leu Leu Ile Tyr Lys Ile Ser Asn Arg Phe Ser Gly Val Pro
    50                  55                  60
Asp Arg Phe Ser Gly Ser Gly Ala Gly Thr Asp Phe Thr Leu Lys Ile
65                  70                  75                  80
Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ala
                85                  90                  95
Thr Gln Phe Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105                 110
```

<210> 193
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 193

```
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1               5                  10                  15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ile Tyr
            20                  25                  30
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
Thr Val Ile Trp Tyr Asp Gly Ser Asn Glu Tyr Tyr Ala Asp Ser Val
    50                  55                  60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
Ala Arg Gly Ala Val Ala Gly Thr Gly Arg Asp Tyr Tyr Tyr Tyr Gly
            100                 105                 110
Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
        115                 120                 125
```

<210> 194
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 194

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

```
Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser
            20                  25                  30
Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser
        35                  40                  45
Pro Gln Leu Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro
    50                  55                  60
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Leu
65                  70                  75                  80
Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln
                85                  90                  95
Ala Leu Gln Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile
            100                 105                 110
Lys Arg
```

<210> 195
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 195

```
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1               5                  10                  15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ile Tyr
            20                  25                  30
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
Thr Val Ile Trp Tyr Asp Gly Ser Asn Glu Tyr Tyr Ala Asp Ser Val
    50                  55                  60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
Ala Arg Gly Ser Tyr Tyr Asp Ser Ser Gly Tyr Tyr Tyr Gly Glu Asp
            100                 105                 110
Phe Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
        115                 120                 125
```

<210> 196
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 196

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

```
Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
            20                  25                  30
Asp Gly Asn Thr Tyr Leu Ser Trp Leu Gln Gln Arg Pro Gly Gln Pro
        35                  40                  45
Pro Arg Leu Leu Ile Tyr Lys Ile Ser Asn Arg Phe Ser Gly Val Pro
    50                  55                  60
Asp Arg Phe Ser Gly Ser Gly Ala Gly Thr Asp Phe Thr Leu Lys Ile
65                  70                  75                  80
Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Thr
                85                  90                  95
Ser Gln Phe Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105                 110
```

<210> 197
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 197

```
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1               5                  10                  15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ile Tyr
            20                  25                  30
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
Thr Val Ile Trp Tyr Asp Gly Ser Asn Glu Tyr Tyr Ala Asp Ser Val
    50                  55                  60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
Ala Arg Glu Glu Trp Glu Leu Glu Asp Tyr Gly Met Asp Val Trp Gly
            100                 105                 110
Gln Gly Thr Thr Val Thr Val Ser Ser
        115                 120
```

<210> 198
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 198

```
Asp Ile Val Met Thr Gln Thr Pro Leu Ser Ser Pro Val Thr Leu Gly
 1               5                  10                  15
Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
            20                  25                  30
```

```
Asp Gly Asn Thr Tyr Leu Ser Trp Leu Gln Gln Arg Pro Gly Gln Pro
        35                  40                  45
Pro Arg Leu Leu Ile Tyr Lys Ile Ser Asn Arg Phe Ser Gly Val Pro
    50                  55                  60
Asp Arg Phe Ser Gly Ser Gly Ala Gly Thr Asp Phe Thr Leu Lys Ile
65                  70                  75                  80
Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Thr
                85                  90                  95
Thr Gln Phe Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105                 110
```

<210> 199
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 199

```
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1               5                  10                  15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
Ala Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
    50                  55                  60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
Ala Arg Glu Asp Phe Asp Ser His Tyr Gly Met Asp Val Trp Gly Gln
            100                 105                 110
Gly Thr Thr Val Thr Val Ser Ser
        115                 120
```

<210> 200
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 200

```
Asp Ile Val Met Thr Gln Thr Pro Leu Ser Ser Pro Val Thr Leu Gly
 1               5                  10                  15
Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
            20                  25                  30
Asp Gly Asn Thr Tyr Leu Ser Trp Leu Gln Gln Arg Pro Gly Gln Pro
        35                  40                  45
```

```
Pro Arg Leu Leu Ile Tyr Lys Ile Ser Asn Arg Phe Ser Gly Val Pro
    50                  55                  60
Asp Arg Phe Ser Gly Ser Gly Ala Gly Thr Asp Phe Thr Leu Lys Ile
65                  70                  75                  80
Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Thr
                85                  90                  95
Thr Gln Phe Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105                 110


<210> 201
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 201
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1               5                  10                  15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ile Tyr
            20                  25                  30
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
Thr Val Ile Trp Tyr Asp Gly Ser Asn Glu Tyr Tyr Ala Asp Ser Val
    50                  55                  60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
Ala Arg Asp Asn Trp Gly Ser Asp Ala Phe Asp Ile Trp Gly Gln Gly
            100                 105                 110
Thr Thr Val Thr Val Ser Ser
        115


<210> 202
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 202
Asp Ile Val Met Thr Gln Thr Pro Leu Ser Ser Pro Val Thr Leu Gly
 1               5                  10                  15
Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
            20                  25                  30
Asp Gly Asn Thr Tyr Leu Ser Trp Leu Gln Gln Arg Pro Gly Gln Pro
        35                  40                  45
Pro Arg Leu Leu Ile Tyr Lys Ile Ser Asn Arg Phe Ser Gly Val Pro
    50                  55                  60
```

```
Asp Arg Phe Ser Gly Ser Gly Ala Gly Thr Asp Phe Thr Leu Lys Ile
65                  70                  75                  80
Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Val
                85                  90                  95
Thr Gln Phe Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105                 110
```

<210> 203
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 203

```
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1               5                  10                  15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ile Tyr
            20                  25                  30
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
Thr Val Ile Trp Tyr Asp Gly Ser Asn Glu Tyr Tyr Ala Asp Ser Val
    50                  55                  60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
Ala Arg Asp Asp Trp Phe Gly Glu Ala Asp Tyr Gly Met Asp Val Trp
            100                 105                 110
Gly Gln Gly Thr Thr Val Thr Val Ser Ser
        115                 120
```

<210> 204
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 204

```
Asp Ile Val Met Thr Gln Thr Pro Leu Ser Ser Pro Val Thr Leu Gly
 1               5                  10                  15
Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
            20                  25                  30
Asp Gly Asn Thr Tyr Leu Ser Trp Leu Gln Gln Arg Pro Gly Gln Pro
        35                  40                  45
Pro Arg Leu Leu Ile Tyr Lys Ile Ser Asn Arg Phe Ser Gly Val Pro
    50                  55                  60
Asp Arg Phe Ser Gly Ser Gly Ala Gly Thr Asp Phe Thr Leu Lys Ile
65                  70                  75                  80
```

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Thr
                85   90   95
Thr Gln Phe Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100   105   110

<210> 205
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 205
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ile Tyr
            20   25   30
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45
Thr Val Ile Trp Tyr Asp Gly Ser Asn Glu Tyr Tyr Ala Asp Ser Val
    50   55   60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65   70   75   80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95
Ala Arg Arg Ile Ser Ile Thr Pro Phe Asp Tyr Trp Gly Gln Gly Thr
            100   105   110
Thr Val Thr Val Ser Ser
        115

<210> 206
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 206
Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
 1   5   10   15
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
            20   25   30
Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
        35   40   45
Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
    50   55   60
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65   70   75   80
Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
                85   90   95

Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 207
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 207
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1 5 10 15
Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Ser Tyr
20 25 30
Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
35 40 45
Gly Ile Ile Tyr Pro Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe
50 55 60
Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
65 70 75 80
Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
85 90 95
Ala Arg Gln Gln Val Ala Gly Met Leu Asp Tyr Trp Gly Gln Gly Thr
100 105 110
Thr Val Thr Val Ser Ser
115

<210> 208
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 208
Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1 5 10 15
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
20 25 30
Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45
Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
50 55 60
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65 70 75 80
Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
85 90 95
Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 209
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 209
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ile Tyr
            20   25   30
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45
Thr Val Ile Trp Tyr Asp Gly Ser Asn Glu Tyr Tyr Ala Asp Ser Val
    50   55   60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65   70   75   80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95
Ala Arg Asp Asp Phe Trp Ser Asp Tyr Pro Phe Asp Tyr Trp Gly Gln
            100   105   110
Gly Thr Thr Val Thr Val Ser Ser
        115   120

<210> 210
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 210
Asp Ile Val Met Thr Gln Thr Pro Leu Ser Ser Pro Val Thr Leu Gly
 1   5   10   15
Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
            20   25   30
Asp Gly Asn Thr Tyr Leu Ser Trp Leu Gln Gln Arg Pro Gly Gln Pro
        35   40   45
Pro Arg Leu Leu Ile Tyr Lys Ile Ser Asn Arg Phe Ser Gly Val Pro
    50   55   60
Asp Arg Phe Ser Gly Ser Gly Ala Gly Thr Asp Phe Thr Leu Lys Ile
65   70   75   80
Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Thr
                85   90   95
Thr Gln Phe Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100   105   110

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

<220>
<223> Synthetic Construct

<400> 211
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ile Tyr
            20   25   30
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45
Thr Val Ile Trp Tyr Asp Gly Ser Asn Glu Tyr Tyr Ala Asp Ser Val
    50   55   60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65   70   75   80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95
Ala Arg Glu Glu Trp Phe Gly Glu Ala Asp Tyr Gly Met Asp Val Trp
            100   105   110
Gly Gln Gly Thr Thr Val Thr Val Ser Ser
        115   120

<210> 212
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 212
Asp Ile Val Met Thr Gln Thr Pro Leu Ser Ser Pro Val Thr Leu Gly
 1   5   10   15
Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
            20   25   30
Asp Gly Asn Thr Tyr Leu Ser Trp Leu Gln Gln Arg Pro Gly Gln Pro
        35   40   45
Pro Arg Leu Leu Ile Tyr Lys Ile Ser Asn Arg Phe Ser Gly Val Pro
    50   55   60
Asp Arg Phe Ser Gly Ser Gly Ala Gly Thr Asp Phe Thr Leu Lys Ile
65   70   75   80
Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Thr
                85   90   95
Thr Gln Phe Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100   105   110

<210> 213
<211> 126

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 213
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ile Tyr
            20   25   30
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45
Thr Val Ile Trp Tyr Asp Gly Ser Asn Glu Tyr Tyr Ala Asp Ser Val
    50   55   60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65   70   75   80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95
Ala Arg Gly Ala Val Ala Gly Thr Gly Arg Asp Tyr Tyr Tyr Tyr Gly
            100   105   110
Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
        115   120   125

<210> 214
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 214
Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly
 1   5   10   15
Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser
            20   25   30
Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser
        35   40   45
Pro Gln Leu Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro
    50   55   60
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Leu
65   70   75   80
Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln
                85   90   95
Ala Leu Gln Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile
            100   105   110
Lys Arg

<210> 215
<211> 126

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 215
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ile Tyr
            20   25   30
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45
Thr Val Ile Trp Tyr Asp Gly Ser Asn Glu Tyr Tyr Ala Asp Ser Val
    50   55   60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65   70   75   80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95
Ala Arg Gly Ser Tyr Tyr Asp Ser Ser Gly Tyr Tyr Phe Gly Glu Asp
            100   105   110
Phe Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
        115   120   125

<210> 216
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 216
Asp Ile Val Met Thr Gln Thr Pro Leu Ser Ser Pro Val Thr Leu Gly
 1   5   10   15
Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
            20   25   30
Asp Gly Asn Thr Tyr Leu Ser Trp Leu Gln Gln Arg Pro Gly Gln Pro
        35   40   45
Pro Arg Leu Leu Ile Tyr Lys Ile Ser Asn Arg Phe Ser Gly Val Pro
    50   55   60
Asp Arg Phe Ser Gly Ser Gly Ala Gly Thr Asp Phe Thr Leu Lys Ile
65   70   75   80
Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Val
                85   90   95
Thr Gln Phe Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100   105   110

<210> 217
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 217
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ile Tyr
            20   25   30
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45
Thr Val Ile Trp Tyr Asp Gly Ser Asn Glu Tyr Tyr Ala Asp Ser Val
    50   55   60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65   70   75   80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95
Ala Arg Gly Thr Val Ala Gly Thr Gly Arg Asp Tyr Tyr Tyr Tyr Gly
            100   105   110
Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
        115   120   125

<210> 218
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 218
Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly
 1   5   10   15
Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser
            20   25   30
Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser
        35   40   45
Pro Gln Leu Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro
    50   55   60
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Leu
65   70   75   80
Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln
                85   90   95
Ala Leu Gln Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile
            100   105   110
Lys Arg

<210> 219
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 219
Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
 1   5   10   15
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
            20   25   30
Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
        35   40   45
Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
    50   55   60
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65   70   75   80
Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser His
                85   90   95
Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Ser Arg
            100   105

<210> 220
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 220
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
 1   5   10   15
Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Ser Tyr
            20   25   30
Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
        35   40   45
Gly Ile Ile Tyr Pro Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe
    50   55   60
Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
65   70   75   80
Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
                85   90   95
Ala Arg Gly Gly Asn Trp Asn Cys Phe Asp Tyr Trp Gly Gln Gly Thr
            100   105   110
Leu Val Thr Val Ser Ser
        115

<210> 221
<211> 201
<212> PRT
<213> Homo sapiens

<400> 221

```
Gly Met Leu Ser Leu Ala Val Asn Gly Thr Ser Gln Phe Thr Cys Phe
 1               5                  10                  15
Tyr Asn Ser Arg Ala Asn Ile Ser Cys Val Trp Ser Gln Asp Gly Ala
            20                  25                  30
Leu Gln Asp Thr Ser Cys Gln Val His Ala Trp Pro Asp Arg Arg Arg
        35                  40                  45
Trp Asn Gln Thr Cys Glu Leu Leu Pro Val Ser Gln Ala Ser Trp Ala
    50                  55                  60
Cys Asn Leu Ile Leu Gly Ala Pro Asp Ser Gln Lys Leu Thr Thr Val
65                  70                  75                  80
Asp Ile Val Thr Leu Arg Val Leu Cys Arg Glu Gly Val Arg Trp Arg
                85                  90                  95
Val Met Ala Ile Gln Asp Phe Lys Pro Phe Glu Asn Leu Arg Leu Met
            100                 105                 110
Ala Pro Ile Ser Leu Gln Val Val His Val Glu Thr His Arg Cys Asn
        115                 120                 125
Ile Ser Trp Glu Ile Ser Gln Ala Ser His Tyr Phe Glu Arg His Leu
    130                 135                 140
Glu Phe Glu Ala Arg Thr Leu Ser Pro Gly His Thr Trp Glu Glu Ala
145                 150                 155                 160
Pro Leu Leu Thr Leu Lys Gln Lys Gln Glu Trp Ile Cys Leu Glu Thr
                165                 170                 175
Leu Thr Pro Asp Thr Gln Tyr Glu Phe Gln Val Arg Val Lys Pro Leu
            180                 185                 190
Gln Ala Phe Arg Thr Leu Thr Gly His
        195                 200
```

<210> 222
<211> 8
<212> PRT
<213> Homo sapiens

<400> 222
```
Gln Lys Leu Thr Thr Val Asp Ile
 1               5
```

<210> 223
<211> 10
<212> PRT
<213> Homo sapiens

<400> 223
```
Cys Gln Lys Leu Thr Thr Val Asp Ile Cys
 1               5                  10
```

<210> 224
<211> 6
<212> PRT
<213> Homo sapiens

<400> 224

Ser His Tyr Phe Glu Arg
 1   5

<210> 225
<211> 8
<212> PRT
<213> Homo sapiens

<400> 225
Cys Ser His Tyr Phe Glu Arg Cys
 1   5

<210> 226
<211> 98
<212> PRT
<213> Homo sapiens

<400> 226
Ala Val Asn Gly Thr Ser Gln Phe Thr Cys Phe Tyr Asn Ser Arg Ala
 1   5   10   15
Asn Ile Ser Cys Val Trp Ser Gln Asp Gly Ala Leu Gln Asp Thr Ser
            20   25   30
Cys Gln Val His Ala Trp Pro Asp Arg Arg Arg Trp Asn Gln Thr Cys
        35   40   45
Glu Leu Leu Pro Val Ser Gln Ala Ser Trp Ala Cys Asn Leu Ile Leu
    50   55   60
Gly Ala Pro Asp Ser Gln Lys Leu Thr Thr Val Asp Ile Val Thr Leu
65   70   75   80
Arg Val Leu Cys Arg Glu Gly Val Arg Trp Arg Val Met Ala Ile Gln
                85   90   95
Asp Phe

<210> 227
<211> 241
<212> PRT
<213> Homo sapiens

<400> 227
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
```

<210> 228
<211> 197
<212> PRT
<213> Homo sapiens

<400> 228

```
Thr Leu Pro Leu Pro Glu Val Gln Cys Phe Val Phe Asn Val Glu Tyr
 1               5                  10                  15
Met Asn Cys Thr Trp Asn Ser Ser Ser Glu Pro Gln Pro Thr Asn Leu
            20                  25                  30
Thr Leu His Tyr Trp Tyr Lys Asn Ser Asp Asn Asp Lys Val Gln Lys
        35                  40                  45
Cys Ser His Tyr Leu Phe Ser Glu Glu Ile Thr Ser Gly Cys Gln Leu
    50                  55                  60
Gln Lys Lys Glu Ile His Leu Tyr Gln Thr Phe Val Val Gln Leu Gln
65                  70                  75                  80
Asp Pro Arg Glu Pro Arg Arg Gln Ala Thr Gln Met Leu Lys Leu Gln
                85                  90                  95
Asn Leu Val Ile Pro Trp Ala Pro Glu Asn Leu Thr Leu His Lys Leu
            100                 105                 110
Ser Glu Ser Gln Leu Glu Leu Asn Trp Asn Asn Arg Phe Leu Asn His
        115                 120                 125
Cys Leu Glu His Leu Val Gln Tyr Arg Thr Asp Trp Asp His Ser Trp
    130                 135                 140
Thr Glu Gln Ser Val Asp Tyr Arg His Lys Phe Ser Leu Pro Ser Val
145                 150                 155                 160
Asp Gly Gln Lys Arg Tyr Thr Phe Arg Val Arg Ser Arg Phe Asn Pro
                165                 170                 175
Leu Cys Gly Ser Ala Gln His Trp Ser Glu Trp Ser His Pro Ile His
            180                 185                 190
Trp Gly Ser Asn Thr
        195
```

<210> 229
<211> 100
<212> PRT
<213> Homo sapiens

<400> 229
Thr Leu Pro Leu Pro Glu Val Gln Cys Phe Val Phe Asn Val Glu Tyr
 1   5   10   15
Met Asn Cys Thr Trp Asn Ser Ser Ser Glu Pro Gln Pro Thr Asn Leu
            20   25   30
Thr Leu His Tyr Trp Tyr Lys Asn Ser Asp Asn Asp Lys Val Gln Lys
        35   40   45
Cys Ser His Tyr Leu Phe Ser Glu Glu Ile Thr Ser Gly Cys Gln Leu
    50   55   60
Gln Lys Lys Glu Ile His Leu Tyr Gln Thr Phe Val Val Gln Leu Gln
65   70   75   80
Asp Pro Arg Glu Pro Arg Arg Gln Ala Thr Gln Met Leu Lys Leu Gln
                85   90   95
Asn Leu Val Ile
            100

<210> 230
<211> 130
<212> PRT
<213> Homo sapiens

<400> 230
Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His Leu Leu Leu
 1   5   10   15
Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys Asn Pro Lys
            20   25   30
Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys Lys Ala Thr
        35   40   45
Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys Pro Leu Glu
    50   55   60
Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu Arg Pro Arg
65   70   75   80
Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu Lys Gly Ser
                85   90   95
Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala Thr Ile Val
            100   105   110
Glu Phe Leu Asn Arg Trp Ile Thr Phe Cys Gln Ser Ile Ile Ser Thr
        115   120   125
Leu Thr
    130

<210> 231
<211> 212
<212> PRT
<213> Homo sapiens

<400> 231
Glu Leu Cys Asp Asp Asp Pro Pro Glu Ile Pro His Ala Thr Phe Lys
 1   5   10   15
Ala Met Ala Tyr Lys Glu Gly Thr Met Leu Asn Cys Glu Cys Lys Arg
            20   25   30
Gly Phe Arg Arg Ile Lys Ser Gly Ser Leu Tyr Met Leu Cys Thr Gly
        35   40   45
Asn Ser Ser His Ser Ser Trp Asp Asn Gln Cys Gln Cys Thr Ser Ser
    50   55   60
Ala Thr Arg Asn Thr Thr Lys Gln Val Thr Pro Gln Pro Glu Glu Gln
65   70   75   80
Lys Glu Arg Lys Thr Thr Glu Met Gln Ser Pro Met Gln Pro Val Asp
                85   90   95
Gln Ala Ser Leu Pro Gly His Cys Arg Glu Pro Pro Pro Trp Glu Asn
            100   105   110
Glu Ala Thr Glu Arg Ile Tyr His Phe Val Val Gly Gln Met Val Tyr
        115   120   125
Tyr Gln Cys Val Gln Gly Tyr Arg Ala Leu His Arg Gly Pro Ala Glu
    130   135   140
Ser Val Cys Lys Met Thr His Gly Lys Thr Arg Trp Thr Gln Pro Gln
145   150   155   160
Leu Ile Cys Thr Gly Glu Met Glu Thr Ser Gln Phe Pro Gly Glu Glu
                165   170   175
Lys Pro Gln Ala Ser Pro Glu Gly Arg Pro Glu Ser Glu Thr Ser Cys
            180   185   190
Leu Val Thr Thr Thr Asp Phe Gln Ile Gln Thr Glu Met Ala Ala Thr
        195   200   205
Met Glu Thr Ser
    210

<210> 232
<211> 77
<212> PRT
<213> Homo sapiens

<400> 232
Ile Thr Cys Pro Pro Pro Met Ser Val Glu His Ala Asp Ile Trp Val
 1   5   10   15
Lys Ser Tyr Ser Leu Tyr Ser Arg Glu Arg Tyr Ile Cys Asn Ser Gly
            20   25   30
Phe Lys Arg Lys Ala Gly Thr Ser Ser Leu Thr Glu Cys Val Leu Asn
        35   40   45
Lys Ala Thr Asn Val Ala His Trp Thr Thr Pro Ser Leu Lys Cys Ile
    50   55   60
Arg Asp Pro Ala Leu Val His Gln Arg Pro Ala Pro Pro
65   70   75

<210> 233
<211> 67
<212> PRT
<213> Homo sapiens

<400> 233
Ile Thr Cys Pro Pro Pro Met Ser Val Glu His Ala Asp Ile Trp Val
 1   5   10   15
Lys Ser Tyr Ser Leu Tyr Ser Arg Glu Arg Tyr Ile Cys Asn Ser Gly
            20   25   30
Phe Lys Arg Lys Ala Gly Thr Ser Ser Leu Thr Glu Cys Val Leu Asn
        35   40   45
Lys Ala Thr Asn Val Ala His Trp Thr Thr Pro Ser Leu Lys Cys Ile
    50   55   60
Arg Asp Pro
65

<210> 234
<211> 65
<212> PRT
<213> Homo sapiens

<400> 234
Ile Thr Cys Pro Pro Pro Met Ser Val Glu His Ala Asp Ile Trp Val
 1   5   10   15
Lys Ser Tyr Ser Leu Tyr Ser Arg Glu Arg Tyr Ile Cys Asn Ser Gly
            20   25   30
Phe Lys Arg Lys Ala Gly Thr Ser Ser Leu Thr Glu Cys Val Leu Asn
        35   40   45
Lys Ala Thr Asn Val Ala His Trp Thr Thr Pro Ser Leu Lys Cys Ile
    50   55   60
Arg
65

<210> 235
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 235
Ser Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly
 1   5   10   15
Gly Ser Leu Gln
            20

<210> 236
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 236
Ser Gly Arg Ser Ala
 1   5

<210> 237
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 237
Ser Gly Arg Ser Ala Asn Ala
 1   5

<210> 238
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 238
Ser Gly Arg Asn Ala Gln
 1   5

<210> 239
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 239
Ser Gly Arg Asn Ala Gln Val Arg
 1   5

<210> 240
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 240

Ser Gly Arg Ser Asp Asn
 1   5

<210> 241
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 241
Ser Gly Arg Ser Asp Asn Pro Asn
 1   5

<210> 242
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 242
Gly Ser Gly Lys Ser Ala
 1   5

<210> 243
<211> 133
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 243
Ala Pro Ala Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His
 1   5   10   15
Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys
            20   25   30
Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys
        35   40   45
Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys
    50   55   60
Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu
65   70   75   80
Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu
                85   90   95
Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala
            100   105   110
Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser Ile

```
        115                 120                 125
Ile Ser Thr Leu Thr
    130
```

<210> 244
<211> 133
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 244

```
Ala Pro Ala Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His
 1               5                  10                  15
Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys
            20                  25                  30
Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys
        35                  40                  45
Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys
    50                  55                  60
Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His Phe
65                  70                  75                  80
Asp Pro Arg Asp Val Val Ser Asn Ile Asn Val Phe Val Leu Glu Leu
                85                  90                  95
Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala
            100                 105                 110
Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser Ile
        115                 120                 125
Ile Ser Thr Leu Thr
    130
```

<210> 245
<211> 133
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 245

```
Ala Pro Ala Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His
 1               5                  10                  15
Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys
            20                  25                  30
Asn Pro Lys Leu Thr Ala Met Leu Thr Ala Lys Phe Ala Met Pro Lys
        35                  40                  45
Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Ala Leu Lys
    50                  55                  60
Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu
65                  70                  75                  80
Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu
```

```
                85                  90                  95
Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala
            100                 105                 110
Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser Ile
        115                 120                 125
Ile Ser Thr Leu Thr
    130
```

<210> 246
<211> 133
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 246

```
Ala Pro Ala Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His
 1               5                  10                  15
Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys
            20                  25                  30
Asn Pro Lys Leu Thr Arg Met Leu Thr Lys Lys Phe Tyr Met Pro Lys
        35                  40                  45
Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys
    50                  55                  60
Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu
65                  70                  75                  80
Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu
                85                  90                  95
Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala
            100                 105                 110
Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser Ile
        115                 120                 125
Ile Ser Thr Leu Thr
    130
```

<210> 247
<211> 133
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 247

```
Ala Pro Ala Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His
 1               5                  10                  15
Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys
            20                  25                  30
Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Ala Phe Ala Met Pro Lys
        35                  40                  45
Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys
```

```
    50                  55                  60
Pro Leu Glu Glu Val Leu Asn Gly Ala Gln Ser Lys Asn Phe His Leu
65                  70                  75                  80
Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu
                85                  90                  95
Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala
            100                 105                 110
Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser Ile
        115                 120                 125
Ile Ser Thr Leu Thr
    130
```

<210> 248
<211> 133
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 248

```
Ala Pro Ala Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His
 1               5                  10                  15
Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys
            20                  25                  30
Asn Pro Lys Leu Thr Ala Met Leu Thr Ala Lys Phe Ala Met Pro Lys
        35                  40                  45
Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Ala Leu Lys
    50                  55                  60
Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His Phe
65                  70                  75                  80
Asp Pro Arg Asp Val Val Ser Asn Ile Asn Val Phe Val Leu Glu Leu
                85                  90                  95
Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala
            100                 105                 110
Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser Ile
        115                 120                 125
Ile Ser Thr Leu Thr
    130
```

<210> 249
<211> 133
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 249

```
Ala Pro Ala Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His
 1               5                  10                  15
Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys
```

```
            20                  25                  30
Asn Pro Lys Leu Thr Arg Met Leu Thr Lys Lys Phe Tyr Met Pro Lys
        35                  40                  45
Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys
    50                  55                  60
Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His Phe
65                  70                  75                  80
Asp Pro Arg Asp Val Val Ser Asn Ile Asn Val Phe Val Leu Glu Leu
                85                  90                  95
Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala
            100                 105                 110
Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser Ile
        115                 120                 125
Ile Ser Thr Leu Thr
    130


<210> 250
<211> 133
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 250
Ala Pro Ala Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His
 1               5                  10                  15
Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys
            20                  25                  30
Asn Pro Lys Leu Thr Arg Met Leu Thr Ala Lys Phe Ala Met Pro Lys
        35                  40                  45
Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys
    50                  55                  60
Pro Leu Glu Glu Val Leu Asn Gly Ala Gln Ser Lys Asn Phe His Phe
65                  70                  75                  80
Asp Pro Arg Asp Val Val Ser Asn Ile Asn Val Phe Val Leu Glu Leu
                85                  90                  95
Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala
            100                 105                 110
Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser Ile
        115                 120                 125
Ile Ser Thr Leu Thr
    130


<210> 251
<211> 133
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct
```

<400> 251
Ala Pro Ala Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His
 1   5   10   15
Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys
            20   25   30
Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys
        35   40   45
Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys
    50   55   60
Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu
65   70   75   80
Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu
                85   90   95
Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala
            100   105   110
Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Cys Gln Ser Ile
        115   120   125
Ile Ser Thr Leu Thr
    130

<210> 252
<211> 115
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 252
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Ser Phe
            20   25   30
Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Glu Pro Glu Trp Val
        35   40   45
Ser Ser Ile Ser Gly Ser Gly Ser Asp Thr Leu Tyr Ala Asp Ser Val
    50   55   60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Thr Thr Leu Tyr
65   70   75   80
Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95
Thr Ile Gly Gly Ser Leu Ser Arg Ser Ser Gln Gly Thr Gln Val Thr
            100   105   110
Val Ser Ser
        115

<210> 253
<211> 115
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 253
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Phe
            20   25   30
Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Glu Pro Glu Trp Val
        35   40   45
Ser Ser Ile Ser Gly Ser Gly Ser Asp Thr Leu Tyr Ala Asp Ser Val
    50   55   60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Thr Thr Leu Tyr
65   70   75   80
Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95
Thr Ile Gly Gly Ser Leu Ser Arg Ser Ser Gln Gly Thr Gln Val Thr
            100   105   110
Val Ser Ser
        115

<210> 254
<211> 115
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 254
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Ser Phe
            20   25   30
Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45
Ser Ser Ile Ser Gly Ser Gly Ser Asp Thr Leu Tyr Ala Asp Ser Val
    50   55   60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Thr Thr Leu Tyr
65   70   75   80
Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95
Thr Ile Gly Gly Ser Leu Ser Arg Ser Ser Gln Gly Thr Gln Val Thr
            100   105   110
Val Ser Ser
        115

<210> 255
<211> 115
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 255
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Asn
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Ser Phe
            20   25   30
Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45
Ser Ser Ile Ser Gly Ser Gly Ser Asp Thr Leu Tyr Ala Asp Ser Val
    50   55   60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Thr Thr Leu Tyr
65   70   75   80
Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95
Thr Ile Gly Gly Ser Leu Ser Arg Ser Ser Gln Gly Thr Leu Val Thr
            100   105   110
Val Ser Ser
        115

<210> 256
<211> 115
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 256
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Asn
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Ser Phe
            20   25   30
Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45
Ser Ser Ile Ser Gly Ser Gly Ser Asp Thr Leu Tyr Ala Asp Ser Val
    50   55   60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Thr Thr Leu Tyr
65   70   75   80
Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95
Thr Ile Gly Gly Ser Leu Ser Arg Ser Ser Gln Gly Thr Leu Val Thr
            100   105   110
Val Ser Ser
        115

<210> 257
<211> 115
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 257
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Asn
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Phe
            20   25   30
Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45
Ser Ser Ile Ser Gly Ser Gly Ser Asp Thr Leu Tyr Ala Asp Ser Val
    50   55   60
Lys Gly Arg Glu Thr Ile Ser Arg Asp Asn Ala Lys Thr Thr Leu Tyr
65   70   75   80
Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95
Thr Ile Gly Gly Ser Leu Ser Arg Ser Ser Gln Gly Thr Leu Val Thr
            100   105   110
Val Ser Ser
        115

<210> 258
<211> 115
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 258
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Asn
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Phe
            20   25   30
Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45
Ser Ser Ile Ser Gly Ser Gly Ser Asp Thr Leu Tyr Ala Asp Ser Val
    50   55   60
Lys Gly Arg Glu Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
65   70   75   80
Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95
Thr Ile Gly Gly Ser Leu Ser Arg Ser Ser Gln Gly Thr Leu Val Thr
            100   105   110
Val Ser Ser
        115

<210> 259
<211> 115
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 259
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Asn
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Phe
            20   25   30
Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45
Ser Ser Ile Ser Gly Ser Gly Ser Asp Thr Leu Tyr Ala Asp Ser Val
    50   55   60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
65   70   75   80
Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95
Thr Ile Gly Gly Ser Leu Ser Arg Ser Gly Gln Gly Thr Leu Val Thr
            100   105   110
Val Ser Ser
        115

<210> 260
<211> 131
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 260
Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His Leu Leu
 1   5   10   15
Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys Asn Pro
            20   25   30
Lys Leu Thr Ala Met Leu Thr Ala Lys Phe Ala Met Pro Lys Lys Ala
        35   40   45
Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Ala Leu Lys Pro Leu
    50   55   60
Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu Arg Pro
65   70   75   80
Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu Lys Gly
                85   90   95
Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala Thr Ile
            100   105   110
Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser Ile Ile Ser
        115   120   125
Thr Leu Thr
    130

<210> 261
<211> 213
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 261
Ala Val Asn Gly Thr Ser Gln Phe Thr Cys Phe Tyr Asn Ser Arg Ala
 1   5   10   15
Asn Ile Ser Cys Val Trp Ser Gln Asp Gly Ala Leu Gln Asp Thr Ser
            20   25   30
Cys Gln Val His Ala Trp Pro Asp Arg Arg Arg Trp Asn Gln Thr Cys
        35   40   45
Glu Leu Leu Pro Val Ser Gln Ala Ser Trp Ala Cys Asn Leu Ile Leu
    50   55   60
Gly Ala Pro Asp Ser Gln Lys Leu Thr Thr Val Asp Ile Val Thr Leu
65   70   75   80
Arg Val Leu Cys Arg Glu Gly Val Arg Trp Arg Val Met Ala Ile Gln
                85   90   95
Asp Phe Lys Pro Phe Glu Asn Leu Arg Leu Met Ala Pro Ile Ser Leu
            100   105   110
Gln Val Val His Val Glu Thr His Arg Cys Asn Ile Ser Trp Glu Ile
        115   120   125
Ser Gln Ala Ser His Tyr Phe Glu Arg His Leu Glu Phe Glu Ala Arg
    130   135   140
Thr Leu Ser Pro Gly His Thr Trp Glu Glu Ala Pro Leu Leu Thr Leu
145   150   155   160
Lys Gln Lys Gln Glu Trp Ile Cys Leu Glu Thr Leu Thr Pro Asp Thr
                165   170   175
Gln Tyr Glu Phe Gln Val Arg Val Lys Pro Leu Gln Gly Glu Phe Thr
            180   185   190
Thr Trp Ser Pro Trp Ser Gln Pro Leu Ala Phe Arg Thr Lys Pro Ala
        195   200   205
Ala Leu Gly Lys Asp
    210

<210> 262
<211> 17
<212> PRT
<213> Homo sapiens

<400> 262
Gly Ser Gly Pro Asp Ser Gly Gly Phe Met Leu Thr Ser Gly Pro Ala
 1   5   10   15
Pro

<210> 263
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 263
Gly Ser Ser Pro Pro Gly Asp Ser Gly Gly Phe Met Leu Thr Ser Gly
 1   5   10   15
Pro

<210> 264
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 264
Asp Ser Gly Gly Phe Met Leu Thr Ser
 1   5

<210> 265
<211> 227
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 265
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1   5   10   15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20   25   30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35   40   45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50   55   60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65   70   75   80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85   90   95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100   105   110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115   120   125
Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130   135   140
Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145   150   155   160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165   170   175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val
            180   185   190

```
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Lys
225
```

<210> 266
<211> 374
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 266

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Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Gly Ser Gly Pro Asp Ser Gly Gly Phe Met Leu Thr Ser Gly
225                 230                 235                 240
Pro Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu
                245                 250                 255
His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr
            260                 265                 270
Lys Asn Pro Lys Leu Thr Ala Met Leu Thr Ala Lys Phe Ala Met Pro
        275                 280                 285
Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Ala Leu
```

```
    290                 295                 300
Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His
305                 310                 315                 320
Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu
                325                 330                 335
Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr
            340                 345                 350
Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser
        355                 360                 365
Ile Ile Ser Thr Leu Thr
    370


<210> 267
<211> 444
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 267
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Pro Gly Ser Gly Ser Ala Val Asn Gly Thr Ser Gln Phe Thr
225                 230                 235                 240
Cys Phe Tyr Asn Ser Arg Ala Asn Ile Ser Cys Val Trp Ser Gln Asp
                245                 250                 255
```

```
Gly Ala Leu Gln Asp Thr Ser Cys Gln Val His Ala Trp Pro Asp Arg
            260                 265                 270
Arg Arg Trp Asn Gln Thr Cys Glu Leu Leu Pro Val Ser Gln Ala Ser
        275                 280                 285
Trp Ala Cys Asn Leu Ile Leu Gly Ala Pro Asp Ser Gln Lys Leu Thr
    290                 295                 300
Thr Val Asp Ile Val Thr Leu Arg Val Leu Cys Arg Glu Gly Val Arg
305                 310                 315                 320
Trp Arg Val Met Ala Ile Gln Asp Phe Lys Pro Phe Glu Asn Leu Arg
                325                 330                 335
Leu Met Ala Pro Ile Ser Leu Gln Val Val His Val Glu Thr His Arg
            340                 345                 350
Cys Asn Ile Ser Trp Glu Ile Ser Gln Ala Ser His Tyr Phe Glu Arg
        355                 360                 365
His Leu Glu Phe Glu Ala Arg Thr Leu Ser Pro Gly His Thr Trp Glu
    370                 375                 380
Glu Ala Pro Leu Leu Thr Leu Lys Gln Lys Gln Glu Trp Ile Cys Leu
385                 390                 395                 400
Glu Thr Leu Thr Pro Asp Thr Gln Tyr Glu Phe Gln Val Arg Val Lys
                405                 410                 415
Pro Leu Gln Gly Glu Phe Thr Thr Trp Ser Pro Trp Ser Gln Pro Leu
            420                 425                 430
Ala Phe Arg Thr Lys Pro Ala Ala Leu Gly Lys Asp
        435                 440
```

<210> 268
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 268
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Gly Ser Gly Pro
 1
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<210> 269
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 269
```
Gly Pro Ala Pro
 1
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<210> 270
<211> 16

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 270
Ile Ser Ser Gly Leu Leu Gly Gly Leu Ser Gly Arg Ser Asp Gln Pro
 1   5   10   15

<210> 271
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 271
Ile Ser Ser Gly Leu Leu Ser Gly Arg Ser Asp Gln Gly
 1   5   10

<210> 272
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 272
Ile Ser Ser Gly Leu Leu Ser Gly Arg Ser Asp Gln Ala
 1   5   10

<210> 273
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 273
Ile Ser Ser Gly Leu Leu Ser Gly Arg Ser Asp Ser Pro
 1   5   10

<210> 274
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 274
Ile Ser Ser Gly Leu Leu Ser Gly Arg Ser Asp Thr Pro
 1   5   10

<210> 275
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 275
Ile Ser Ser Gly Leu Leu Ser Gly Arg Ser Asp Met Pro
 1   5   10

<210> 276
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 276
Ile Ser Ser Gly Leu Leu Ser Gly Arg Ser Asp
 1   5   10

<210> 277
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Sequence

<400> 277
Ile Ser Ser Gly Leu Leu Ser Gly Arg Ser Asp Gln Pro
 1   5   10

<210> 278
<211> 16
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 278
Ile Ser Ser Gly Leu Leu Gly Gly Leu Ser Gly Arg Ser Asp Asn Pro
 1   5   10   15

<210> 279
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 279
Ile Ser Ser Gly Leu Leu Ser Ser Gly Gly Leu Ser Gly Arg Ser Asp
 1   5   10   15
Gln Pro

<210> 280
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 280
Ile Ser Ser Gly Leu Leu Ser Ser Gly Gly Leu Ser Gly Arg Ser Asp
 1   5   10   15
Asn Pro

<210> 281
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 281
Ile Ser Ser Gly Leu Leu Ser Gly Arg Ser
 1   5   10

<210> 282
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 282
Ile Ser Ser Gly Leu Leu Ser Gly Arg Ser Glu Ser Pro
 1   5   10

<210> 283
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 283
Ile Ser Ser Gly Leu Leu Ser Gly Arg Ser Glu Gln Pro
 1   5   10

<210> 284
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 284
Ile Ser Ser Gly Leu Leu Ser Gly Arg Ser Glu Gln His
 1   5   10

<210> 285
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 285
Leu Ser Ser Gly Leu Leu Ser Gly Arg Ser Asp Gln Pro
 1   5   10

<210> 286
<211> 16
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 286
Leu Ser Ser Gly Leu Leu Gly Gly Leu Ser Gly Arg Ser Asp Gln Pro
 1   5   10   15

<210> 287
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 287
Leu Ser Ser Gly Leu Leu Ser Gly Arg Ser Asp Gln Gly
 1   5   10

<210> 288
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 288
Leu Ser Ser Gly Leu Leu Ser Gly Arg Ser Asp Gln Ala
 1   5   10

<210> 289
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 289
Leu Ser Ser Gly Leu Leu Ser Gly Arg Ser Asp Ser Pro
 1   5   10

<210> 290
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 290
Leu Ser Ser Gly Leu Leu Ser Gly Arg Ser Asp Thr Pro
 1   5   10

<210> 291
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 291
Leu Ser Ser Gly Leu Leu Ser Gly Arg Ser Asp Met Pro
 1   5   10

<210> 292
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 292
Leu Ser Ser Gly Leu Leu Ser Gly Arg Ser Asp
 1   5   10

<210> 293
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 293
Gly Lys Gln Leu Arg Val Val Asn Glu Tyr Ser Ser Met Asp Asn Met
 1   5   10   15
Leu Leu Gly

<210> 294
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 294
Leu Ser Ser Gly Leu Leu Gly Gly Leu Ser Gly Arg Ser Asp Asn Pro
 1   5   10   15

<210> 295
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 295
Leu Ser Ser Gly Leu Leu Ser Ser Gly Gly Leu Ser Gly Arg Ser Asp
 1   5   10   15
Gln Pro

<210> 296
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 296
Leu Ser Ser Gly Leu Leu Ser Ser Gly Gly Leu Ser Gly Arg Ser Asp
 1   5   10   15
Asn Pro

<210> 297
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 297
Gly Lys Gln Leu Arg Val Val Asn Glu Tyr Ser Ser Glu Asp Asn Met
 1   5   10   15
Leu Leu Gly

<210> 298
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 298
Leu Ser Ser Gly Leu Leu Ser Gly Arg Ser Glu Ser Pro
 1   5   10

<210> 299
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 299
Leu Ser Ser Gly Leu Leu Ser Gly Arg Ser Glu Gln Pro
 1   5   10

<210> 300
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 300
Leu Ser Ser Gly Leu Leu Ser Gly Arg Ser Glu Gln His
 1   5   10

<210> 301
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 301
Met Pro Tyr Asp Leu Tyr His
 1   5

<210> 302
<211> 8
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 302
Leu Ser Gly Arg Ser Asp Asn His
 1   5

<210> 303
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 303
Gly Gly Gly Ser Ser Pro
 1   5

<210> 304
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 304
Ser Gly Gly Pro
 1

<210> 305
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 305
Ser Gly Pro Ser Gly Ser Pro Gly
 1   5

<210> 306
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 306
Gly Ser Ile Pro Val Ser Leu Arg Ser Gly
 1   5   10

<210> 307
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 307
Gly Pro Ser Gly Pro Ala Gly Leu Lys Gly Ala Pro Gly
 1   5   10

<210> 308
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 308
Gly Pro Pro Gly Pro Ala Gly Met Lys Gly Leu Pro Gly
 1   5   10

<210> 309
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 309
Gly Tyr Val Ala Asp Ala Pro Lys
 1   5

<210> 310
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 310
Lys Lys Leu Ala Asp Glu Pro Glu

1 5

<210> 311
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 311
Gly Gly Ser Arg Pro Ala His Leu Arg Asp Ser Gly Lys
1 5 10

<210> 312
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 312
Ser Phe Thr Gln Ala Arg Val Val Gly Gly
1 5 10

<210> 313
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 313
Val His Met Pro Leu Gly Phe Leu Gly Pro Arg Gln Ala Arg Val Val
1 5 10 15
Asn

<210> 314
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 314
Leu Ser Gly Arg Ser Asp Asn His Ser Pro Leu Gly Leu Ala Gly Ser

1 5 10 15

<210> 315
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 315
Val Pro Leu Ser Leu Tyr Ser Gly
1 5

<210> 316
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 316
Ile Pro Glu Ser Leu Arg Ala Gly
1 5

<210> 317
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 317
Ile Pro Val Ser Leu Arg Ser Gly
1 5

<210> 318
<211> 17
<212> PRT
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<220>
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<400> 318
Ser Gly Ser Gly Gly Ser Pro Val Pro Leu Ser Leu Tyr Ser Gly Gly
1 5 10 15
Pro

<210> 319
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 319
Gly Gly Gly Ser Ser Pro Val Pro Leu Ser Leu Tyr Ser Gly Gly Pro
 1   5   10   15

<210> 320
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 320
Gly Gly Ser Ser Pro Pro Val Pro Leu Ser Leu Tyr Ser Gly Pro Ser
 1   5   10   15
Gly Ser Pro Gly
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<210> 321
<211> 20
<212> PRT
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<220>
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<400> 321
Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
 1   5   10   15
Gly Gly Ser Gly
            20

<210> 322
<211> 24
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<220>
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<400> 322
Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
 1   5   10   15
Gly Gly Ser Gly Gly Gly Ser Gly
            20

<210> 323
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 323
Pro Gly Pro Gly Pro
 1   5

<210> 324
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
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<400> 324
Ser Gly Gly Cys Gly Gly His Gln Tyr Glu Arg Arg Gly Gly Cys
 1   5   10   15

<210> 325
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
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<400> 325
Ser Gly Gly Cys Ser Gly His Gln Tyr Glu Arg Arg Glu Gly Cys
 1   5   10   15

<210> 326
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
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<400> 326
Ser Gly Gly Cys Gly Gly His Tyr Phe Glu Arg His Gly Gly Cys
 1   5   10   15

<210> 327
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
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<400> 327
Ser Gly Gly Cys Ser Gly His Tyr Phe Glu Arg His Glu Gly Cys
 1   5   10   15

<210> 328
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
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<400> 328
Ser Gly Gly Cys Ser Phe His Gln Tyr Glu Arg His Glu Gly Cys
 1   5   10   15

<210> 329
<211> 5
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<213> Artificial Sequence

<220>
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<400> 329
Pro Ser Gly Ser Ser
 1   5

<210> 330
<211> 4
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<213> Artificial Sequence

<220>
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<400> 330
Gly Ser Pro Gly

1

<210> 331
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 331
Gly Gly Ser Pro Gly Gly
1 5

<210> 332
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
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<400> 332
Gly Gly Pro Gly Gly Pro
1 5

<210> 333
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
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<400> 333
Gly Gly Ser Gly
1

<210> 334
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
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<400> 334
Gly Ser Pro Pro Gly Gly
1 5

<210> 335
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
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<400> 335
Gly Pro Gly Ser Pro Gly
 1   5

<210> 336
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
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<400> 336
Gly Ser Ser Pro Pro Gly
 1   5

<210> 337
<211> 3
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<213> Artificial Sequence

<220>
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<400> 337
Gly Gly Pro
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<210> 338
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 338
Ser Gly Pro Gly Ser Gly Ser
 1   5

<210> 339

<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 339
Gly Gly Ser Ser Pro Pro Gly Gly Gly Ser Ser Gly Gly Gly Ser Gly
 1   5   10   15
Pro

<210> 340
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
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<400> 340
Ser Gly Pro Gly Ser Gly Ser
 1   5

<210> 341
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
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<400> 341
Ser Gly Ser Gly Gly Ser Pro
 1   5

<210> 342
<211> 6
<212> PRT
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<220>
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<400> 342
Ile Tyr Asp Gln Lys Thr
 1   5

<210> 343

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

<220>
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<400> 343
Ala His Asn Tyr Lys Thr
 1   5

<210> 344
<211> 6
<212> PRT
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<220>
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<400> 344
Met Met Asp Gln Ala Asn
 1   5

<210> 345
<211> 8
<212> PRT
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<220>
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<400> 345
Met Leu Gly Glu Phe Val Ser Glu
 1   5

<210> 346
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
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<400> 346
Gly Leu Val Ala Leu Arg Gly Ala
 1   5

<210> 347
<211> 8
<212> PRT

<213> Artificial Sequence

<220>
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<400> 347
Lys Glu His Lys Tyr Lys Ala Glu
 1   5

<210> 348
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
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<400> 348
Gly Gly Ser Ser Pro Pro Gly Gly Gly Ser Ser Gly Gly Gly Ser Gly
 1   5   10   15
Pro Gly Ser Gly Ser
            20

<210> 349
<211> 19
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<213> Artificial Sequence

<220>
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<400> 349
Gly Gly Ser Ser Pro Pro Val Pro Leu Ser Leu Tyr Ser Gly Pro Gly
 1   5   10   15
Ser Gly Ser

<210> 350
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 350
Gly Asn Pro Met Gly Ser Glu Pro Val Asn Phe Lys Gln Leu Arg Val
 1   5   10   15
Val Asn Gly Gly Pro
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<210> 351
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
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<400> 351
Gly Asn Pro Met Gly Ser Glu Pro Val Asn Phe Lys Leu Leu Arg Val
 1   5   10   15
Val Asn Gly Gly Pro
            20

<210> 352
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
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<400> 352
Gly Asn Pro Met Gly Ser Asp Pro Val Asn Phe Lys Gln Leu Arg Val
 1   5   10   15
Val Asn Gly Gly Pro
            20

<210> 353
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<212> PRT
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<220>
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<400> 353
Gly Asn Pro Met Gly Ser Asp Pro Val Asn Phe Lys Leu Leu Arg Val
 1   5   10   15
Val Asn Gly Gly Pro
            20

<210> 354
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<220>
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<400> 354
Gly Gly Ser Ser Pro Pro Met Pro Tyr Asp Leu Tyr His Pro Ser Gly
 1   5   10   15
Pro Ser Gly Ser Pro Gly
            20

<210> 355
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
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<400> 355
Gly Gly Ser Ser Pro Pro Gly Gly Gly Ser Ser Gly Gly Gly Ser Gly
 1   5   10   15
Pro Ser Gly Ser Pro Gly
            20

<210> 356
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<212> PRT
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<220>
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<400> 356
Arg Gln Ala Arg Val Val Gly
 1   5

<210> 357
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
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<400> 357
Leu Gly Gly Ser Gly Arg Ser Asn Ala Gln Val Arg Leu Glu
 1   5   10

<210> 358
<211> 13
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<220>

<223> Synthetic Construct

<400> 358
Leu Gly Gly Ser Gly Arg Lys Ala Ser Leu Ser Leu Glu
 1   5   10

<210> 359
<211> 10
<212> PRT
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<400> 359
Ser Gly Arg Ile Gly Phe Leu Arg Thr Ala
 1   5   10

<210> 360
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<212> PRT
<213> Artificial Sequence

<220>
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<400> 360
Ser Gly Ala Ile Gly Phe Leu Arg Thr Ala
 1   5   10

<210> 361
<211> 14
<212> PRT
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<220>
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<400> 361
Arg Pro Ala Arg Ser Gly Arg Ser Ala Gly Gly Ser Val Ala
 1   5   10

<210> 362
<211> 11
<212> PRT
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<220>
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<400> 362
Val Thr Gly Arg Gly Asp Ser Pro Ala Ser Ser
 1   5   10

<210> 363
<211> 8
<212> PRT
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<220>
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<400> 363
Pro Arg Phe Lys Ile Ile Gly Gly
 1   5

<210> 364
<211> 11
<212> PRT
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<220>
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<400> 364
Leu Ser Gly Arg Ile Gly Phe Leu Arg Thr Ala
 1   5   10

<210> 365
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<213> Artificial Sequence

<220>
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<400> 365
Leu Ser Gly Arg Ser Asn Ala Met Pro Tyr Asp Leu Tyr His Pro
 1   5   10   15

<210> 366
<211> 15
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<213> Artificial Sequence

<220>
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<400> 366
Leu Ser Gly Arg Ser Asn Ala Gly Gly Ile Gly Gln Leu Thr Ala

1 5 10 15

<210> 367
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
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<400> 367
Leu Ser Gly Arg Ser Asn Ala Val Pro Leu Ser Leu Tyr
1 5 10

<210> 368
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
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<400> 368
Leu Ser Gly Arg Ser Asn Ala Asp Ser Gly Gly Phe Met Leu Thr
1 5 10 15

<210> 369
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
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<400> 369
Leu Ser Gly Arg Ser Asn Ala His Glu Gln Leu Thr Ala
1 5 10

<210> 370
<211> 15
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<220>
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<400> 370
Leu Ser Gly Arg Ser Asn Ala Arg Ala Ala Ala Val Lys Ser Pro
1 5 10 15

<210> 371
<211> 15
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<220>
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<400> 371
Leu Ser Gly Arg Ser Asn Ala Thr Ser Val Leu Met Ala Ala Pro
 1   5   10   15

<210> 372
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<220>
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<400> 372
Val Pro Leu Ser Leu Tyr Leu Ser Gly Arg Ser Asn Ala
 1   5   10

<210> 373
<211> 15
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<213> Artificial Sequence

<220>
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<400> 373
Asp Ser Gly Gly Phe Met Leu Thr Leu Ser Gly Arg Ser Asn Ala
 1   5   10   15

<210> 374
<211> 15
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<220>
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<400> 374
Gly Gly Ile Gly Gln Leu Thr Ala Leu Ser Gly Arg Ser Asn Ala
 1   5   10   15

<210> 375

<211> 15
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<220>
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<400> 375
Met Pro Tyr Asp Leu Tyr His Pro Leu Ser Gly Arg Ser Asn Ala
 1   5   10   15

<210> 376
<211> 13
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<400> 376
His Glu Gln Leu Thr Val Leu Ser Gly Arg Ser Asn Ala
 1   5   10

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<220>
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<400> 377
Arg Ala Ala Ala Val Lys Ser Pro Leu Ser Gly Arg Ser Asn Ala
 1   5   10   15

<210> 378
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<213> Artificial Sequence

<220>
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<400> 378
Thr Ser Val Leu Met Ala Ala Pro Leu Ser Gly Arg Ser Asn Ala
 1   5   10   15

<210> 379
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<220>
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<400> 379
Ile Pro Val Ser Leu Arg Ser Gly Arg Ser Asn Ala Gln Arg Leu Glu
 1   5   10   15

<210> 380
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<213> Artificial Sequence

<220>
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<400> 380
Val Pro Leu Ser Leu Tyr Arg Gln Ala Arg Val Val Gly
 1   5   10

<210> 381
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<220>
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<400> 381
Asp Ser Gly Gly Phe Met Leu Thr Arg Gln Ala Arg Val Val Gly
 1   5   10   15

<210> 382
<211> 15
<212> PRT
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<220>
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<400> 382
Gly Gly Ile Gly Gln Leu Thr Ala Arg Gln Ala Arg Val Val Gly
 1   5   10   15

<210> 383
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<220>
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<400> 383
Met Pro Tyr Asp Leu Tyr His Pro Arg Gln Ala Arg Val Val Gly
 1   5   10   15

<210> 384
<211> 13
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<213> Artificial Sequence

<220>
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<400> 384
His Glu Gln Leu Thr Val Arg Gln Ala Arg Val Val Gly
 1   5   10

<210> 385
<211> 15
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<220>
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<400> 385
Arg Ala Ala Ala Val Lys Ser Pro Arg Gln Ala Arg Val Val Gly
 1   5   10   15

<210> 386
<211> 15
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<213> Artificial Sequence

<220>
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<400> 386
Thr Ser Val Leu Met Ala Ala Pro Arg Gln Ala Arg Val Val Gly
 1   5   10   15

<210> 387
<211> 18
<212> PRT
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<220>
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<400> 387
Lys Gln Leu Arg Val Val Asn Glu Tyr Ser Ser Met Asp Asn Met Leu
 1   5   10   15
Leu Gly

<210> 388
<211> 18
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<220>
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<400> 388
Lys Gln Leu Arg Val Val Asn Glu Tyr Ser Ser Glu Asp Asn Met Leu
 1   5   10   15
Leu Gly

<210> 389
<211> 18
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<220>
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<400> 389
Lys Gln Leu Arg Val Val Asn Gly Tyr Ser Ser Glu Asp Asn Met Leu
 1   5   10   15
Leu Gly

<210> 390
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<220>
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<400> 390
Lys Gln Leu Arg Val Val Gly Gly Leu Val His Leu Lys Asn Thr Met
 1   5   10   15
Glu Thr

<210> 391

<211> 18
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<220>
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<400> 391
Thr Arg Asp Arg Leu Asp Glu Val Asn Phe Lys Gln Leu Arg Val Val
 1   5   10   15
Asn Gly

<210> 392
<211> 18
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<220>
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<400> 392
Thr Arg Asp Arg Leu Asp Glu Val Asn Phe Lys Leu Leu Arg Val Val
 1   5   10   15
Asn Gly

<210> 393
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<220>
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<400> 393
Thr Arg Asp Arg Leu Asp Pro Val Asn Phe Lys Gln Leu Arg Val Val
 1   5   10   15
Asn Gly

<210> 394
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<220>
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<400> 394
Thr Arg Asp Arg Leu Asp Pro Val Asn Phe Lys Leu Leu Arg Val Val

 1   5   10   15
Asn Gly

<210> 395
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<220>
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<400> 395
Asn Pro Met Gly Ser Glu Pro Val Asn Phe Lys Gln Leu Arg Val Val
 1   5   10   15
Asn Gly

<210> 396
<211> 18
<212> PRT
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<220>
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<400> 396
Asn Pro Met Gly Ser Glu Pro Val Asn Phe Lys Leu Leu Arg Val Val
 1   5   10   15
Asn Gly

<210> 397
<211> 18
<212> PRT
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<220>
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<400> 397
Asn Pro Met Gly Ser Asp Pro Val Asn Phe Lys Gln Leu Arg Val Val
 1   5   10   15
Asn Gly

<210> 398
<211> 18
<212> PRT
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<220>
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<400> 398
Asn Pro Met Gly Ser Asp Pro Val Asn Phe Lys Leu Leu Arg Val Val
 1   5   10   15
Asn Gly

<210> 399
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
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<400> 399
Thr Tyr Ser Arg Ser Lys Tyr Leu Ala Thr Ala
 1   5   10

<210> 400
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
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<400> 400
Thr Tyr Ser Arg Ser Arg Tyr Leu Ala Thr Ala
 1   5   10

<210> 401
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
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<400> 401
Lys Gln Leu Arg Val Val Asn Glu Tyr Ser Ser Glu
 1   5   10

<210> 402
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
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<400> 402
Lys Gln Leu Arg Val Val Asn Gly Tyr Ser Ser Glu
 1   5   10

<210> 403
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
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<400> 403
Lys Gln Leu Arg Val Val Gly Gly Leu Val Ala Leu
 1   5   10

<210> 404
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
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<400> 404
Lys Gln Leu Arg Val Val Asn Gly Leu Val Ala Leu
 1   5   10

<210> 405
<211> 12
<212> PRT
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<220>
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<400> 405
Ser Pro Gly Arg Val Val Gly Gly Leu Val Ala Leu
 1   5   10

<210> 406
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<400> 406
Pro Gln Pro Arg Thr Tyr Ser Arg Ser Arg Tyr Leu
 1   5   10

<210> 407
<211> 12
<212> PRT
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<400> 407
Pro Gln Pro Arg Thr Thr Ser Arg Ser Arg Tyr Leu
 1   5   10

<210> 408
<211> 13
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<400> 408
Val Val Asn Glu Tyr Ser Ser Ser Arg Gly Pro Tyr His
 1   5   10

<210> 409
<211> 13
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<220>
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<400> 409
Val Val Asn Glu Tyr Ser Ser Glu Arg Gly Pro Tyr His
 1   5   10

<210> 410
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
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<400> 410
Asn Lys Val Ser Met Ser Ser Ser Arg Gly Pro Tyr His
 1   5   10

<210> 411
<211> 13
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<213> Artificial Sequence

<220>
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<400> 411
Asn Lys Val Ser Met Ser Ser Thr Arg Gly Pro Tyr His
 1   5   10

<210> 412
<211> 13
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<220>
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<400> 412
Ala Pro Ala Met Met Arg Gly Ser Val Ile Leu Thr Val
 1   5   10

<210> 413
<211> 13
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<400> 413
Ala Pro Ala Met Met Glu Gly Ser Val Ile Leu Thr Val
 1   5   10

<210> 414
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
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<400> 414
Arg Gly Ser Val Ile Ile Thr Val Gln Thr Val Thr Trp

1 5 10

<210> 415
<211> 13
<212> PRT
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<220>
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<400> 415
Arg Gly Ser Val Ile Leu Thr Val Gln Thr Val Thr Trp
1 5 10

<210> 416
<211> 21
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<220>
<223> Synthetic Construct

<400> 416
Gly Thr Arg Asp Arg Leu Asp Glu Val Asn Phe Lys Gln Leu Arg Val
1 5 10 15
Val Asn Gly Gly Pro
20

<210> 417
<211> 21
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<220>
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<400> 417
Gly Thr Arg Asp Arg Leu Asp Glu Val Asn Phe Lys Leu Leu Arg Val
1 5 10 15
Val Asn Gly Gly Pro
20

<210> 418
<211> 21
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<220>
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<400> 418
Gly Thr Arg Asp Arg Leu Asp Pro Val Asn Phe Lys Gln Leu Arg Val
 1   5   10   15
Val Asn Gly Gly Pro
            20

<210> 419
<211> 21
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<220>
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<400> 419
Gly Thr Arg Asp Arg Leu Asp Pro Val Asn Phe Lys Leu Leu Arg Val
 1   5   10   15
Val Asn Gly Gly Pro
            20

<210> 420
<211> 12
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<400> 420
Arg Lys Gly Lys Ala Leu Ala Ala Tyr Arg Leu Glu
 1   5   10

<210> 421
<211> 12
<212> PRT
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<220>
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<400> 421
Arg Lys Gly Lys Ala Gly Ala Ala Tyr Arg Leu Glu
 1   5   10

<210> 422
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<400> 422
Arg Gln Ala Arg Val Val Gly Gly Leu Val Ala Leu
 1   5   10

<210> 423
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<400> 423
Gly Gly Val Arg Gly Pro Arg Phe Lys Ile Ile Gly Gly
 1   5   10

<210> 424
<211> 13
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<400> 424
Gly Gly Val Arg Gly Pro Arg Val Lys Ile Ile Gly Gly
 1   5   10

<210> 425
<211> 13
<212> PRT
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<400> 425
Val Thr Gly Arg Gly Asp Ser His Ser Leu Thr Thr Asn
 1   5   10

<210> 426
<211> 13
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<400> 426
Val Thr Gly Arg Gly Asp Ser Pro Ser Leu Thr Thr Asn
 1   5   10

<210> 427
<211> 13
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<400> 427
Thr Gly His Gly Gln Ala Ser Gln Gly Leu Leu Asp Arg
 1   5   10

<210> 428
<211> 13
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<213> Artificial Sequence

<220>
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<400> 428
Thr Gly His Gly Gln Ala Ser Ser Gly Leu Leu Asp Arg
 1   5   10

<210> 429
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
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<400> 429
Lys Gln Leu Arg Val Val Asn Glu Asn Leu Glu Asn Tyr
 1   5   10

<210> 430
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<400> 430
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1 5 10

<210> 431
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<400> 431
Ser Asn Val Asn Asp Val Ala Asn Tyr Asn Phe Phe
1 5 10

<210> 432
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<400> 432
Ser Asn Val Asn Asp Val Ser Asn Tyr Asn Phe Phe
1 5 10

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<400> 433
Ile Asp Phe Asn Ala Ala Gln Asn Leu Tyr Glu Lys
1 5 10

<210> 434
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<400> 434
Ile Asp Phe Asn Ala Ala Tyr Asn Leu Tyr Glu Lys
1 5 10

<210> 435
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<400> 435
Ile Gln Trp Asn Ala Gly Gln Pro Leu Gln Glu Arg
 1   5   10

<210> 436
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<400> 436
Ile Gln Trp Asn Ala Pro Gln Pro Leu Gln Glu Arg
 1   5   10

<210> 437
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<400> 437
Ser Met Asp Asn Arg Leu Leu Gly Leu Phe Gly Glu
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<400> 438
Ser Met Asp Asn Met Leu Leu Gly Leu Phe Gly Glu
 1   5   10

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<400> 439
Val Pro Ile Asp Asp Pro Gln Asp Leu Leu Glu Gly
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<400> 440
Val Pro Ile Asp Asp Pro Glu Asp Leu Leu Glu Gly
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<400> 441
Ile Pro Glu Asn Leu Pro Pro Gly Leu Pro Leu Thr
 1   5   10

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<400> 442
Ile Pro Glu Asn Leu Pro Pro Leu Leu Pro Leu Thr
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<400> 443
Gln Pro Pro Ser Leu Thr Lys Asn Gln Val Ser Leu
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<210> 444
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<400> 444
Gln Pro Pro Ser Leu Thr Arg Asn Gln Val Ser Leu
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<400> 445
Asp Ser His Ser Leu Thr Lys Asn Gln Val Ser Leu
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<400> 446
Asp Ser His Ser Leu Thr Thr Asn Gln Val Ser Leu
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<400> 447
Lys Ala Ile Gln Leu Thr Lys Asn Gln Val Ser Leu
 1   5   10

<210> 448
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<220>
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<400> 448
Lys Ala Ile Gln Leu Thr Tyr Asn Gln Val Ser Leu
 1   5   10

<210> 449
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<400> 449
Ala Glu Pro Trp Thr Asn Arg Asn Thr Asp Gly Ser
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<220>
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<400> 450
Ala Glu Pro Trp Thr Val Arg Asn Thr Asp Gly Ser
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<400> 451
Lys Gln Leu Arg Val Val Asn Gly
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<210> 452
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<400> 452
Lys Gln Leu Arg Val Val Thr Gly Arg Gly Asp Ser Pro
 1   5   10

<210> 453
<211> 13
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<220>
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<400> 453
Lys Gln Leu Arg Val Val Asn Gly Arg Gly Asp Ser Pro
 1   5   10

<210> 454
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<220>
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<400> 454
Pro Ser Ser Arg Arg Arg Val Val Arg Lys Gly Val Ser
 1   5   10

<210> 455
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<220>
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<400> 455

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

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<220>
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<400> 456
Ser Pro Gly Arg Val Val Thr Gly Arg Gly Asp Ser Pro
 1   5   10

<210> 457
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<220>
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<400> 457
Ser Pro Gly Arg Val Val Gly Gly Arg Gly Asp Ser Pro
 1   5   10

<210> 458
<211> 13
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<213> Artificial Sequence

<220>
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<400> 458
Asn Ser Gly Arg Ala Val Thr Gly Arg Gly Asp Ser Pro
 1   5   10

<210> 459
<211> 13
<212> PRT
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<220>
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<400> 459
Asn Ser Gly Arg Ala Val Thr Tyr Arg Gly Asp Ser Pro
 1   5   10

<210> 460
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<220>
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<400> 460
Thr Gly His Gly Gln Pro Ser Ser Arg Arg Arg Val Asn
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<220>
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<400> 461
Thr Gly His Gly Gln Ala Ser Ser Arg Arg Arg Val Asn
 1   5   10

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<400> 462
Thr Gly His Gly Gln Ser Ser Ser Arg Gly Pro Tyr His
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<400> 463
Thr Gly His Gly Gln Ala Ser Ser Arg Gly Pro Tyr His
 1   5   10

<210> 464
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<400> 464
Arg Gly Ser Val Ile Leu Thr Lys Asn Gln Val Ser Leu
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<400> 465
Arg Gly Ser Val Ile Leu Thr Val Asn Gln Val Ser Leu
 1   5   10

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<400> 466
Ser Pro Gly Arg Val Val Gly Ile Asn Tyr Trp Leu Ala
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<210> 467
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<400> 467
Ser Pro Gly Arg Val Val Gly Gly Asn Tyr Trp Leu Ala
 1   5   10

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<400> 468
Ser Pro Gly Arg Val Val Gly Ser Asn Lys Gly Ala Ile
 1   5   10

<210> 469
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<400> 469
Ser Pro Gly Arg Val Val Gly Gly Asn Lys Gly Ala Ile
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<400> 470
Pro Gly Ala Arg Gly Arg Ala Pro Asn His Ala Val Val
 1   5   10

<210> 471
<211> 13
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<213> Artificial Sequence

<220>
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<400> 471
Pro Gly Ala Arg Gly Arg Ala Phe Asn His Ala Val Val
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<210> 472
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<400> 472
Pro Gly Ala Arg Gly Asn Ala Phe Asn Asn Leu Asp Arg
 1   5   10

<210> 473
<211> 13
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<213> Artificial Sequence

<220>
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<400> 473
Pro Gly Ala Arg Gly Arg Ala Phe Asn Asn Leu Asp Arg
 1   5   10

<210> 474
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<213> Artificial Sequence

<220>
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<400> 474
Val Ser Asn Lys Tyr Ile Ser Asn Asn Glu Gln Leu Pro
 1   5   10

<210> 475
<211> 13
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<220>
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<400> 475
Val Ser Asn Lys Tyr Phe Ser Asn Asn Glu Gln Leu Pro
 1   5   10

<210> 476
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<223> Synthetic Construct

<400> 476
Lys Val Ser Asn Lys Ala Leu His Val Thr Asn Ile
 1   5   10

<210> 477
<211> 12
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<220>
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<400> 477
Lys Val Ser Asn Lys Ala Leu Pro Val Thr Asn Ile
 1   5   10

<210> 478
<211> 13
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<213> Artificial Sequence

<220>
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<400> 478
Val Thr Gly Arg Gly Pro Ser Pro Asp Val Pro Leu Thr
 1   5   10

<210> 479
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
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<400> 479
Val Thr Gly Arg Gly Asp Ser Pro Asp Val Pro Leu Thr
 1   5   10

<210> 480
<211> 13
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<400> 480
Thr Gly His Gly Gln Arg Ser Ser Asn Ile Arg Thr Ser
 1   5   10

<210> 481
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<400> 481
Thr Gly His Gly Gln Ala Ser Ser Asn Ile Arg Thr Ser
 1   5   10

<210> 482
<211> 13
<212> PRT
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<220>
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<400> 482
Thr Gly His Gly Gln His Ser Ser Asn Ile Ala Asn Ile
 1   5   10

<210> 483
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<220>
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<400> 483
Thr Gly His Gly Gln Ala Ser Ser Asn Ile Ala Asn Ile
 1   5   10

<210> 484
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<220>
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<400> 484
Thr Gly His Gly Gln Ala Ser Arg Asn Asp Tyr Ser Tyr

1 5 10

<210> 485
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
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<400> 485
Thr Gly His Gly Gln Ala Ser Ser Asn Asp Tyr Ser Tyr
1 5 10

<210> 486
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<213> Artificial Sequence

<220>
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<400> 486
Lys Ala Leu His Val Thr Asn Arg Asn Thr Asp Gly Ser
1 5 10

<210> 487
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<220>
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<400> 487
Lys Ala Leu His Val Thr Asn Ile Asn Thr Asp Gly Ser
1 5 10

<210> 488
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<220>
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<400> 488
Arg Val Val Arg Lys Lys Val Ser Asn Lys Ala Leu Pro
1 5 10

<210> 489
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<212> PRT
<213> Artificial Sequence

<220>
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<400> 489
Arg Val Val Arg Lys Gly Val Ser Asn Lys Ala Leu Pro
 1   5   10

<210> 490
<211> 13
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<213> Artificial Sequence

<220>
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<400> 490
Arg Gln Ala Arg Val Val Gly Ile Asn Tyr Trp Leu Ala
 1   5   10

<210> 491
<211> 13
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<213> Artificial Sequence

<220>
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<400> 491
Arg Gln Ala Arg Val Val Gly Gly Asn Tyr Trp Leu Ala
 1   5   10

<210> 492
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<220>
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<400> 492
Gly Lys Gln Leu Arg Val Val Asn Gly Tyr Ser Ser Glu Asp Asn Met
 1   5   10   15
Leu Leu Gly Gly Pro
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<210> 493
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
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<400> 493
Gly Lys Gln Leu Arg Val Val Gly Gly Leu Val His Leu Lys Asn Thr
 1   5   10   15
Met Glu Thr Gly Pro
            20

<210> 494
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<220>
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<400> 494
Ala Gly Gln Pro Lys Gln Leu Arg Val Val Asn Gly
 1   5   10

<210> 495
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<220>
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<400> 495
Ala Gly Gln Pro Leu Gln Leu Arg Val Val Asn Gly
 1   5   10

<210> 496
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<220>
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<400> 496
Ala Gly Gln Pro Leu Gln Glu Arg Val Val Asn Gly
 1   5   10

<210> 497
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<220>
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<400> 497
Ala Gly Gln Pro Lys Gln Glu Arg Val Val Asn Gly
 1   5   10

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<220>
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<400> 498
Gly Thr Ala Asn Lys Gln Leu Arg Val Val Asn Gly
 1   5   10

<210> 499
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<212> PRT
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<220>
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<400> 499
Gly Thr Ala Asn Lys Gln Leu His Val Val Asn Gly
 1   5   10

<210> 500
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<220>
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<400> 500
Gly Thr Ala Asn Ile Gln Leu Arg Val Val Asn Gly
 1   5   10

<210> 501

<211> 12
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<213> Artificial Sequence

<220>
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<400> 501
Gly Thr Ala Asn Ile Gln Leu His Val Val Asn Gly
 1   5   10

<210> 502
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
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<400> 502
Gly Lys Gln Leu Arg Val Val Asn Glu Tyr Ser Ser Met Asp Asn Met
 1   5   10   15
Leu Leu Gly Gly Pro
            20

<210> 503
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<213> Artificial Sequence

<220>
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<400> 503
Gly Lys Gln Leu Arg Val Val Asn Glu Tyr Ser Ser Glu Asp Asn Met
 1   5   10   15
Leu Leu Gly Gly Pro
            20

<210> 504
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<220>
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<400> 504
Lys Gln Leu Arg Thr Val Ala Gly Leu Ala Gly Lys
 1   5   10

<210> 505
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
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<400> 505
Lys Gln Leu Arg Thr Val Asn Gly Leu Ala Gly Lys
 1   5   10

<210> 506
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
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<400> 506
Lys Gln Leu Arg Val Val Ala Gly Leu Ala Gly Lys
 1   5   10

<210> 507
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
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<400> 507
Lys Gln Leu Arg Val Val Asn Gly Leu Ala Gly Lys
 1   5   10

<210> 508
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<213> Artificial Sequence

<220>
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<400> 508
Gly Ile Lys Tyr Lys Gln Leu Arg Val Val Asn Gly
 1   5   10

<210> 509

<211> 12
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<220>
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<400> 509
Gly Ile Lys Tyr Lys Tyr Leu Arg Val Val Asn Gly
 1   5   10

<210> 510
<211> 12
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<220>
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<400> 510
Gly Ile Lys Tyr Leu Gln Leu Arg Val Val Asn Gly
 1   5   10

<210> 511
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
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<400> 511
Gly Ile Lys Tyr Leu Tyr Leu Arg Val Val Asn Gly
 1   5   10

<210> 512
<211> 16
<212> PRT
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<220>
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<400> 512
Thr His Leu Asp Leu Thr Tyr Ser Arg Ser Lys Tyr Leu Ala Thr Ala
 1   5   10   15

<210> 513
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<212> PRT

<213> Artificial Sequence

<220>
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<400> 513
Thr His Leu Asp Leu Thr Pro Ser Arg Ser Lys Tyr Leu Ala Thr Ala
 1   5   10   15

<210> 514
<211> 16
<212> PRT
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<220>
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<400> 514
Thr His Leu Asp Leu Thr Tyr Ser Arg Ser Arg Tyr Leu Ala Thr Ala
 1   5   10   15

<210> 515
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<212> PRT
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<220>
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<400> 515
Thr His Leu Asp Leu Thr Pro Ser Arg Ser Arg Tyr Leu Ala Thr Ala
 1   5   10   15

<210> 516
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<212> PRT
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<220>
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<400> 516
Thr Tyr Ser Arg Ser Lys Tyr Leu Ala Pro Ala Asn Gly Asn Ala Glu
 1   5   10   15

<210> 517
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<220>
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<400> 517
Thr Tyr Ser Arg Ser Lys Tyr Leu Ala Thr Ala Asn Gly Asn Ala Glu
 1   5   10   15

<210> 518
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<220>
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<400> 518
Thr Tyr Ser Arg Ser Arg Tyr Leu Ala Pro Ala Asn Gly Asn Ala Glu
 1   5   10   15

<210> 519
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<400> 519
Thr Tyr Ser Arg Ser Arg Tyr Leu Ala Thr Ala Asn Gly Asn Ala Glu
 1   5   10   15

<210> 520
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<220>
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<400> 520
Asp Pro Val Asn Phe Lys Gln Leu Arg Val Val Asn Glu Tyr Ser Ser
 1   5   10   15
Glu

<210> 521
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<220>
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<400> 521
Asp Pro Val Asn Phe Lys Gln Leu Arg Val Val Asn Gly Tyr Ser Ser
 1   5   10   15
Glu

<210> 522
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<400> 522
Asp Pro Val Asn Phe Lys Lys Leu Arg Val Val Asn Glu Tyr Ser Ser
 1   5   10   15
Glu

<210> 523
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<220>
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<400> 523
Asp Pro Val Asn Phe Lys Lys Leu Arg Val Val Asn Gly Tyr Ser Ser
 1   5   10   15
Glu

<210> 524
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<400> 524
Arg Lys Gly Lys Ala Gly Ala Ala Lys Asn Leu Asn Glu Lys Asp Tyr
 1   5   10   15

<210> 525

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<400> 525
Arg Lys Gly Lys Ala Gly Ala Ala Lys Asn Leu Tyr Glu Lys Asp Tyr
 1   5   10   15

<210> 526
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<220>
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<400> 526
Arg Lys Gly Lys Ala Gly Ala Ala Gln Asn Leu Asn Glu Lys Asp Tyr
 1   5   10   15

<210> 527
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<400> 527
Arg Lys Gly Lys Ala Gly Ala Ala Gln Asn Leu Tyr Glu Lys Asp Tyr
 1   5   10   15

<210> 528
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<400> 528
Val Thr Gly Arg Gly Asp Ser His Ser Leu Thr Lys Asn Gln Val Ser
 1   5   10   15
Leu

<210> 529

<211> 17
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<220>
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<400> 529
Val Thr Gly Arg Gly Asp Ser His Ser Leu Thr Thr Asn Gln Val Ser
 1   5   10   15
Leu

<210> 530
<211> 17
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<213> Artificial Sequence

<220>
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<400> 530
Val Thr Gly Arg Gly Asp Ser Pro Ser Leu Thr Lys Asn Gln Val Ser
 1   5   10   15
Leu

<210> 531
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<220>
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<400> 531
Val Thr Gly Arg Gly Asp Ser Pro Ser Leu Thr Thr Asn Gln Val Ser
 1   5   10   15
Leu

<210> 532
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<220>
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<400> 532
Thr Gly His Gly Gln Ala Ser Ser Glu Arg Ser Ser Asn Ile Arg Thr

 1   5   10   15
Ser

<210> 533
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
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<400> 533
Thr Gly His Gly Gln Ala Ser Ser Glu Arg Ser Ser Asn Ser Arg Thr
 1   5   10   15
Ser

<210> 534
<211> 17
<212> PRT
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<220>
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<400> 534
Thr Gly His Gly Gln Ala Ser Ser Glu Arg Ser Ser Thr Ile Arg Thr
 1   5   10   15
Ser

<210> 535
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
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<400> 535
Thr Gly His Gly Gln Ala Ser Ser Glu Arg Ser Ser Thr Ser Arg Thr
 1   5   10   15
Ser

<210> 536
<211> 17
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<213> Artificial Sequence

<220>
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<400> 536
Gly Ile Ser Ser Gly Leu Leu Ser Gly Arg Ser Asp Gln Pro Ser Gly
 1   5   10   15
Pro

<210> 537
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
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<400> 537
Gly Gly Ser Gly Ile Ser Ser Gly Leu Leu Ser Gly Arg Ser Asp Gln
 1   5   10   15
Pro Ser Gly Pro
            20

<210> 538
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
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<400> 538
Asp Pro Val Asn Phe Lys Leu Leu Arg Val Val Asn Glu Tyr Ser Ser
 1   5   10   15
Glu

<210> 539
<211> 17
<212> PRT
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<220>
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<400> 539
Asp Pro Val Asn Phe Lys Leu Leu Arg Val Val Asn Gly Tyr Ser Ser
 1   5   10   15
Glu

<210> 540
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<220>
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<400> 540
Asp Pro Val Asn Phe Lys Gln Leu Arg Val Val Gly Gly Leu Val Ala
 1   5   10   15
Leu

<210> 541
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 541
Asp Pro Val Asn Phe Lys Gln Leu Arg Val Val Asn Gly Leu Val Ala
 1   5   10   15
Leu

<210> 542
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 542
Asp Pro Val Asn Phe Lys Leu Leu Arg Val Val Gly Gly Leu Val Ala
 1   5   10   15
Leu

<210> 543
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 543
Asp Pro Val Asn Phe Lys Leu Leu Arg Val Val Asn Gly Leu Val Ala
 1   5   10   15
Leu

<210> 544
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 544
Lys Gln Leu Arg Val Gln Asn Gly Asp Ser Thr Glu
 1   5   10

<210> 545
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 545
Lys Gln Leu Arg Val Val Asn Asn Asp Ala Thr Glu
 1   5   10

<210> 546
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 546
Lys Gln Leu Arg Val Val Asn Gly Asp Ser Thr Glu
 1   5   10

<210> 547
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 547
Ile Ser Asn Asn Lys Gln Leu Arg Val Val Asn Gly
 1   5   10

<210> 548
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 548
Ile Ser Asn Asn Lys Gln Leu Pro Val Val Asn Gly
 1   5   10

<210> 549
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 549
Ile Ser Asn Asn Glu Gln Leu Arg Val Val Asn Gly
 1   5   10

<210> 550
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 550
Ile Ser Asn Asn Glu Gln Leu Pro Val Val Asn Gly
 1   5   10

<210> 551
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 551

Lys Val Ser Asn Lys Gln Leu Arg Val Val Asn Gly
 1   5   10

<210> 552
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 552
Lys Val Ser Asn Lys Gln Leu Pro Val Val Asn Gly
 1   5   10

<210> 553
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 553
Lys Val Ser Asn Lys Ala Leu Arg Val Val Asn Gly
 1   5   10

<210> 554
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 554
Lys Val Ser Asn Lys Ala Leu Pro Val Val Asn Gly
 1   5   10

<210> 555
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 555
Lys Gln Leu Arg Val Gln Asn Asn Asp Ala Thr Glu
 1   5   10

<210> 556
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 556
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1   5   10   15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20   25   30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35   40   45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50   55   60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65   70   75   80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85   90   95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100   105   110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115   120   125
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130   135   140
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145   150   155   160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165   170   175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180   185   190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195   200   205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210   215   220
Pro Gly Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu
225   230   235   240
Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn
                245   250   255
Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met
            260   265   270
Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu
        275   280   285
Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe
    290   295   300
His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu
305   310   315   320
Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu
                325   330   335
Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln

```
            340                 345                 350
Ser Ile Ile Ser Thr Leu Thr
        355
```

<210> 557
<211> 560
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 557

```
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Pro Ala Glu Leu Cys Asp Asp Asp Pro Pro Glu Ile Pro His
225                 230                 235                 240
Ala Thr Phe Lys Ala Met Ala Tyr Lys Glu Gly Thr Met Leu Asn Cys
                245                 250                 255
Glu Cys Lys Arg Gly Phe Arg Arg Ile Lys Ser Gly Ser Leu Tyr Met
            260                 265                 270
Leu Cys Thr Gly Asn Ser Ser His Ser Ser Trp Asp Asn Gln Cys Gln
        275                 280                 285
Cys Thr Ser Ser Ala Thr Arg Asn Thr Thr Lys Gln Val Thr Pro Gln
    290                 295                 300
Pro Glu Glu Gln Lys Glu Arg Lys Thr Thr Glu Met Gln Ser Pro Met
305                 310                 315                 320
```

```
Gln Pro Val Asp Gln Ala Ser Leu Pro Gly His Cys Arg Glu Pro Pro
                325                 330                 335
Pro Trp Glu Asn Glu Ala Thr Glu Arg Ile Tyr His Phe Val Val Gly
            340                 345                 350
Gln Met Val Tyr Tyr Gln Cys Val Gln Gly Tyr Arg Ala Leu His Arg
        355                 360                 365
Gly Pro Ala Glu Ser Val Cys Lys Met Thr His Gly Lys Thr Arg Trp
    370                 375                 380
Thr Gln Pro Gln Leu Ile Cys Thr Gly Gly Gly Gly Gly Gly Gly Gly
385                 390                 395                 400
Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
                405                 410                 415
Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Ala Pro Thr Ser Ser
            420                 425                 430
Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His Leu Leu Leu Asp Leu
        435                 440                 445
Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr
    450                 455                 460
Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu
465                 470                 475                 480
Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu Val
                485                 490                 495
Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu Arg Pro Arg Asp Leu
            500                 505                 510
Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr
        515                 520                 525
Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu Phe
    530                 535                 540
Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser Ile Ile Ser Thr Leu Thr
545                 550                 555                 560


<210> 558
<211> 538
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Sequence

<400> 558
Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His
 1               5                  10                  15
Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys
            20                  25                  30
Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys
        35                  40                  45
Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys
    50                  55                  60
Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu
65                  70                  75                  80
Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu
                85                  90                  95
Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala
```

```
            100                 105                 110
Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser Ile
        115                 120                 125
Ile Ser Thr Leu Thr Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
    130                 135                 140
Gly Gly Gly Ser Glu Leu Cys Asp Asp Asp Pro Pro Glu Ile Pro His
145                 150                 155                 160
Ala Thr Phe Lys Ala Met Ala Tyr Lys Glu Gly Thr Met Leu Asn Cys
                165                 170                 175
Glu Cys Lys Arg Gly Phe Arg Arg Ile Lys Ser Gly Ser Leu Tyr Met
            180                 185                 190
Leu Cys Thr Gly Asn Ser Ser His Ser Ser Trp Asp Asn Gln Cys Gln
        195                 200                 205
Cys Thr Ser Ser Ala Thr Arg Asn Thr Thr Lys Gln Val Thr Pro Gln
    210                 215                 220
Pro Glu Glu Gln Lys Glu Arg Lys Thr Thr Glu Met Gln Ser Pro Met
225                 230                 235                 240
Gln Pro Val Asp Gln Ala Ser Leu Pro Gly His Cys Arg Glu Pro Pro
                245                 250                 255
Pro Trp Glu Asn Glu Ala Thr Glu Arg Ile Tyr His Phe Val Val Gly
            260                 265                 270
Gln Met Val Tyr Tyr Gln Cys Val Gln Gly Tyr Arg Ala Leu His Arg
        275                 280                 285
Gly Pro Ala Glu Ser Val Cys Lys Met Thr His Gly Lys Thr Arg Trp
    290                 295                 300
Thr Gln Pro Gln Leu Ile Cys Thr Asp Lys Thr His Thr Cys Pro Pro
305                 310                 315                 320
Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro
                325                 330                 335
Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
            340                 345                 350
Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
        355                 360                 365
Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
    370                 375                 380
Glu Glu Gln Tyr Ala Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
385                 390                 395                 400
Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
                405                 410                 415
Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
            420                 425                 430
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
        435                 440                 445
Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
    450                 455                 460
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
465                 470                 475                 480
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
                485                 490                 495
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
            500                 505                 510
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
        515                 520                 525
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
```

530 535

<210> 559
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 559
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
1 5 10 15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
20 25 30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
35 40 45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
50 55 60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65 70 75 80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
85 90 95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
100 105 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
115 120 125
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
130 135 140
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145 150 155 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
165 170 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
180 185 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
195 200 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
210 215 220
Pro Gly Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu
225 230 235 240
Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn
245 250 255
Tyr Lys Asn Pro Lys Leu Thr Ala Met Leu Thr Ala Lys Phe Ala Met
260 265 270
Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Ala
275 280 285
Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe
290 295 300
His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu
305 310 315 320
Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu
325 330 335

Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln
            340   345   350
Ser Ile Ile Ser Thr Leu Thr
        355

<210> 560
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 560
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1   5   10   15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20   25   30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35   40   45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50   55   60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65   70   75   80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85   90   95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100   105   110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115   120   125
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130   135   140
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145   150   155   160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165   170   175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180   185   190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195   200   205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210   215   220
Pro Gly Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu
225   230   235   240
Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn
                245   250   255
Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Lys Lys Phe Tyr Met
            260   265   270
Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu
        275   280   285
Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe
    290   295   300
His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu

305 310 315 320
Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu
325 330 335
Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln
340 345 350
Ser Ile Ile Ser Thr Leu Thr
355

<210> 561
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 561
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
1 5 10 15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
20 25 30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
35 40 45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
50 55 60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65 70 75 80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
85 90 95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
100 105 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
115 120 125
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
130 135 140
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145 150 155 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
165 170 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
180 185 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
195 200 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
210 215 220
Pro Gly Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu
225 230 235 240
Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn
245 250 255
Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Ala Phe Ala Met
260 265 270
Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu
275 280 285

```
Leu Lys Pro Leu Glu Glu Val Leu Asn Gly Ala Gln Ser Lys Asn Phe
    290                 295                 300
His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu
305                 310                 315                 320
Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu
                325                 330                 335
Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln
            340                 345                 350
Ser Ile Ile Ser Thr Leu Thr
        355
```

<210> 562
<211> 356
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 562

```
Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His
 1               5                  10                  15
Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys
            20                  25                  30
Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys
        35                  40                  45
Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys
    50                  55                  60
Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu
65                  70                  75                  80
Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu
                85                  90                  95
Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala
            100                 105                 110
Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser Ile
        115                 120                 125
Ile Ser Thr Leu Thr Pro Ser Gly Pro Ser Ala Gly Gly Ala Ala Glu
    130                 135                 140
Ile Val Leu Thr Gln Ser Pro Asp Phe Gln Ser Val Thr Pro Lys Glu
145                 150                 155                 160
Lys Val Thr Ile Thr Cys Ser Ala Asn Ser Ala Leu Ser Tyr Met Tyr
                165                 170                 175
Trp Tyr Gln Gln Lys Pro Asp Gln Ser Pro Lys Leu Trp Val His Gly
            180                 185                 190
Thr Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
        195                 200                 205
Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp
    210                 215                 220
Ala Ala Thr Tyr Tyr Cys His His Trp Ser Asn Thr Gln Trp Thr Phe
225                 230                 235                 240
Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser
                245                 250                 255
Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala
```

```
            260                 265                 270
Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val
        275                 280                 285
Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser
    290                 295                 300
Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr
305                 310                 315                 320
Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys
                325                 330                 335
Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn
            340                 345                 350
Arg Gly Glu Cys
        355


<210> 563
<211> 622
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 563
Glu Leu Cys Asp Asp Asp Pro Pro Glu Ile Pro His Ala Thr Phe Lys
 1               5                  10                  15
Ala Met Ala Tyr Lys Glu Gly Thr Met Leu Asn Cys Glu Cys Lys Arg
            20                  25                  30
Gly Phe Arg Arg Ile Lys Ser Gly Ser Leu Tyr Met Leu Cys Thr Gly
        35                  40                  45
Asn Ser Ser His Ser Ser Trp Asp Asn Gln Cys Gln Cys Thr Ser Ser
    50                  55                  60
Ala Thr Arg Asn Thr Thr Lys Gln Val Thr Pro Gln Pro Glu Glu Gln
65                  70                  75                  80
Lys Glu Arg Lys Thr Thr Glu Met Gln Ser Pro Met Gln Pro Val Asp
                85                  90                  95
Gln Ala Ser Leu Pro Gly His Cys Arg Glu Pro Pro Pro Trp Glu Asn
            100                 105                 110
Glu Ala Thr Glu Arg Ile Tyr His Phe Val Val Gly Gln Met Val Tyr
        115                 120                 125
Tyr Gln Cys Val Gln Gly Tyr Arg Ala Leu His Arg Gly Pro Ala Glu
    130                 135                 140
Ser Val Cys Lys Met Thr His Gly Lys Thr Arg Trp Thr Gln Pro Gln
145                 150                 155                 160
Leu Ile Cys Thr Gly Gly Pro Pro Ala Ser Ala Gly Ser Gln Val Gln
                165                 170                 175
Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser Ser Val Lys
            180                 185                 190
Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr Phe Met Asn
        195                 200                 205
Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Arg Val
    210                 215                 220
Asp Pro Glu Gln Gly Arg Ala Asp Tyr Ala Glu Lys Phe Lys Lys Arg
225                 230                 235                 240
```

```
Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu
                245                 250                 255
Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Arg
            260                 265                 270
Ala Met Asp Asn Tyr Gly Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val
        275                 280                 285
Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
    290                 295                 300
Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
305                 310                 315                 320
Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
                325                 330                 335
Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser
            340                 345                 350
Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
        355                 360                 365
Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
    370                 375                 380
Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr
385                 390                 395                 400
Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Asp Val Phe
                405                 410                 415
Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
            420                 425                 430
Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
        435                 440                 445
Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
    450                 455                 460
Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
465                 470                 475                 480
Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
                485                 490                 495
Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Glu Glu Lys Thr Ile Ser
            500                 505                 510
Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
        515                 520                 525
Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
    530                 535                 540
Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
545                 550                 555                 560
Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
                565                 570                 575
Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
            580                 585                 590
Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
        595                 600                 605
Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
    610                 615                 620
```

<210> 564
<211> 622
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 564
Glu Leu Cys Asp Asp Asp Pro Pro Glu Ile Pro His Ala Thr Phe Lys
 1   5   10   15
Ala Met Ala Tyr Lys Glu Gly Thr Met Leu Asn Cys Glu Cys Lys Arg
            20   25   30
Gly Phe Arg Arg Ile Lys Ser Gly Ser Leu Tyr Met Leu Cys Thr Gly
        35   40   45
Asn Ser Ser His Ser Ser Trp Asp Asn Gln Cys Gln Cys Thr Ser Ser
    50   55   60
Ala Thr Arg Asn Thr Thr Lys Gln Val Thr Pro Gln Pro Glu Glu Gln
65   70   75   80
Lys Glu Arg Lys Thr Thr Glu Met Gln Ser Pro Met Gln Pro Val Asp
                85   90   95
Gln Ala Ser Leu Pro Gly His Cys Arg Glu Pro Pro Pro Trp Glu Asn
            100   105   110
Glu Ala Thr Glu Arg Ile Tyr His Phe Val Val Gly Gln Met Val Tyr
        115   120   125
Tyr Gln Cys Val Gln Gly Tyr Arg Ala Leu His Arg Gly Pro Ala Glu
    130   135   140
Ser Val Cys Lys Met Thr His Gly Lys Thr Arg Trp Thr Gln Pro Gln
145   150   155   160
Leu Ile Cys Thr Gly Ser Pro Pro Ala Gly Gly Ala Pro Gln Val Gln
                165   170   175
Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser Ser Val Lys
            180   185   190
Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr Phe Met Asn
        195   200   205
Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Arg Val
    210   215   220
Asp Pro Glu Gln Gly Arg Ala Asp Tyr Ala Glu Lys Phe Lys Lys Arg
225   230   235   240
Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu
                245   250   255
Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Arg
            260   265   270
Ala Met Asp Asn Tyr Gly Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val
        275   280   285
Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
    290   295   300
Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
305   310   315   320
Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
                325   330   335
Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser
            340   345   350
Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
        355   360   365
Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
    370   375   380
Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr

385 390 395 400
Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Asp Val Phe
405 410 415
Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
420 425 430
Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
435 440 445
Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
450 455 460
Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
465 470 475 480
Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
485 490 495
Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Glu Glu Lys Thr Ile Ser
500 505 510
Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
515 520 525
Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
530 535 540
Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
545 550 555 560
Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
565 570 575
Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
580 585 590
Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
595 600 605
Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
610 615 620

<210> 565
<211> 356
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 565
Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His
1 5 10 15
Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys
20 25 30
Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys
35 40 45
Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys
50 55 60
Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu
65 70 75 80
Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu
85 90 95
Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala
100 105 110

```
Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser Ile
        115                 120                 125
Ile Ser Thr Leu Thr Gly Pro Gly Ser Gly Ser Gly Gly Ala Ala Glu
    130                 135                 140
Ile Val Leu Thr Gln Ser Pro Asp Phe Gln Ser Val Thr Pro Lys Glu
145                 150                 155                 160
Lys Val Thr Ile Thr Cys Ser Ala Asn Ser Ala Leu Ser Tyr Met Tyr
                165                 170                 175
Trp Tyr Gln Gln Lys Pro Asp Gln Ser Pro Lys Leu Trp Val His Gly
            180                 185                 190
Thr Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
        195                 200                 205
Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp
    210                 215                 220
Ala Ala Thr Tyr Tyr Cys His His Trp Ser Asn Thr Gln Trp Thr Phe
225                 230                 235                 240
Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser
                245                 250                 255
Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala
            260                 265                 270
Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val
        275                 280                 285
Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser
    290                 295                 300
Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr
305                 310                 315                 320
Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys
                325                 330                 335
Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn
            340                 345                 350
Arg Gly Glu Cys
        355
```

<210> 566
<211> 567
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 566

```
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
```

```
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu
225                 230                 235                 240
Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn
                245                 250                 255
Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met
            260                 265                 270
Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu
        275                 280                 285
Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe
    290                 295                 300
His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu
305                 310                 315                 320
Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu
                325                 330                 335
Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln
            340                 345                 350
Ser Ile Ile Ser Thr Leu Thr Gly Pro Pro Ser Gly Ser Ser Pro Met
        355                 360                 365
Pro Tyr Asp Leu Tyr His Pro Ser Gly Gly Gly Ala Val Asn Gly Thr
    370                 375                 380
Ser Gln Phe Thr Cys Phe Tyr Asn Ser Arg Ala Asn Ile Ser Cys Val
385                 390                 395                 400
Trp Ser Gln Asp Gly Ala Leu Gln Asp Thr Ser Cys Gln Val His Ala
                405                 410                 415
Trp Pro Asp Arg Arg Arg Trp Asn Gln Thr Cys Glu Leu Leu Pro Val
            420                 425                 430
Ser Gln Ala Ser Trp Ala Cys Asn Leu Ile Leu Gly Ala Pro Asp Ser
        435                 440                 445
Gln Lys Leu Thr Thr Val Asp Ile Val Thr Leu Arg Val Leu Cys Arg
    450                 455                 460
Glu Gly Val Arg Trp Arg Val Met Ala Ile Gln Asp Phe Lys Pro Phe
465                 470                 475                 480
Glu Asn Leu Arg Leu Met Ala Pro Ile Ser Leu Gln Val Val His Val
                485                 490                 495
Glu Thr His Arg Cys Asn Ile Ser Trp Glu Ile Ser Gln Ala Ser His
            500                 505                 510
Tyr Phe Glu Arg His Leu Glu Phe Glu Ala Arg Thr Leu Ser Pro Gly
```

```
        515                 520                 525
His Thr Trp Glu Glu Ala Pro Leu Leu Thr Leu Lys Gln Lys Gln Glu
    530                 535                 540
Trp Ile Cys Leu Glu Thr Leu Thr Pro Asp Thr Gln Tyr Glu Phe Gln
545                 550                 555                 560
Val Arg Val Lys Pro Leu Gln
                565
```

<210> 567
<211> 768
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 567

```
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Pro Ala Glu Leu Cys Asp Asp Asp Pro Pro Glu Ile Pro His
225                 230                 235                 240
Ala Thr Phe Lys Ala Met Ala Tyr Lys Glu Gly Thr Met Leu Asn Cys
                245                 250                 255
Glu Cys Lys Arg Gly Phe Arg Arg Ile Lys Ser Gly Ser Leu Tyr Met
            260                 265                 270
Leu Cys Thr Gly Asn Ser Ser His Ser Ser Trp Asp Asn Gln Cys Gln
        275                 280                 285
```

```
Cys Thr Ser Ser Ala Thr Arg Asn Thr Thr Lys Gln Val Thr Pro Gln
    290                 295                 300
Pro Glu Glu Gln Lys Glu Arg Lys Thr Thr Glu Met Gln Ser Pro Met
305                 310                 315                 320
Gln Pro Val Asp Gln Ala Ser Leu Pro Gly His Cys Arg Glu Pro Pro
                325                 330                 335
Pro Trp Glu Asn Glu Ala Thr Glu Arg Ile Tyr His Phe Val Val Gly
            340                 345                 350
Gln Met Val Tyr Tyr Gln Cys Val Gln Gly Tyr Arg Ala Leu His Arg
        355                 360                 365
Gly Pro Ala Glu Ser Val Cys Lys Met Thr His Gly Lys Thr Arg Trp
    370                 375                 380
Thr Gln Pro Gln Leu Ile Cys Thr Gly Gly Gly Gly Gly Gly Gly Gly
385                 390                 395                 400
Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
                405                 410                 415
Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Ala Pro Thr Ser Ser
            420                 425                 430
Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His Leu Leu Leu Asp Leu
        435                 440                 445
Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr
    450                 455                 460
Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu
465                 470                 475                 480
Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu Val
                485                 490                 495
Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu Arg Pro Arg Asp Leu
            500                 505                 510
Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr
        515                 520                 525
Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu Phe
    530                 535                 540
Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser Ile Ile Ser Thr Leu Thr
545                 550                 555                 560
Gly Pro Pro Ser Gly Ser Ser Pro Met Pro Tyr Asp Leu Tyr His Pro
                565                 570                 575
Ser Gly Gly Gly Ala Val Asn Gly Thr Ser Gln Phe Thr Cys Phe Tyr
            580                 585                 590
Asn Ser Arg Ala Asn Ile Ser Cys Val Trp Ser Gln Asp Gly Ala Leu
        595                 600                 605
Gln Asp Thr Ser Cys Gln Val His Ala Trp Pro Asp Arg Arg Arg Trp
    610                 615                 620
Asn Gln Thr Cys Glu Leu Leu Pro Val Ser Gln Ala Ser Trp Ala Cys
625                 630                 635                 640
Asn Leu Ile Leu Gly Ala Pro Asp Ser Gln Lys Leu Thr Thr Val Asp
                645                 650                 655
Ile Val Thr Leu Arg Val Leu Cys Arg Glu Gly Val Arg Trp Arg Val
            660                 665                 670
Met Ala Ile Gln Asp Phe Lys Pro Phe Glu Asn Leu Arg Leu Met Ala
        675                 680                 685
Pro Ile Ser Leu Gln Val Val His Val Glu Thr His Arg Cys Asn Ile
    690                 695                 700
Ser Trp Glu Ile Ser Gln Ala Ser His Tyr Phe Glu Arg His Leu Glu
705                 710                 715                 720
```

```
Phe Glu Ala Arg Thr Leu Ser Pro Gly His Thr Trp Glu Glu Ala Pro
                725                 730                 735
Leu Leu Thr Leu Lys Gln Lys Gln Glu Trp Ile Cys Leu Glu Thr Leu
            740                 745                 750
Thr Pro Asp Thr Gln Tyr Glu Phe Gln Val Arg Val Lys Pro Leu Gln
        755                 760                 765


<210> 568
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 568
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu
225                 230                 235                 240
Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn
                245                 250                 255
Tyr Lys Asn Pro Lys Leu Thr Ala Met Leu Thr Ala Lys Phe Ala Met
            260                 265                 270
Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Ala
        275                 280                 285
Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe
```

```
    290                 295                 300
His Phe Asp Pro Arg Asp Val Val Ser Asn Ile Asn Val Phe Val Leu
305                 310                 315                 320
Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu
                325                 330                 335
Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln
            340                 345                 350
Ser Ile Ile Ser Thr Leu Thr
        355
```

<210> 569
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 569

```
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu
225                 230                 235                 240
Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn
                245                 250                 255
Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Lys Lys Phe Tyr Met
            260                 265                 270
```

```
Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu
        275                 280                 285
Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe
    290                 295                 300
His Phe Asp Pro Arg Asp Val Val Ser Asn Ile Asn Val Phe Val Leu
305                 310                 315                 320
Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu
                325                 330                 335
Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln
            340                 345                 350
Ser Ile Ile Ser Thr Leu Thr
        355


<210> 570
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 570
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu
225                 230                 235                 240
Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn
```

```
                245                 250                 255
Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Ala Lys Phe Ala Met
            260                 265                 270
Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu
        275                 280                 285
Leu Lys Pro Leu Glu Glu Val Leu Asn Gly Ala Gln Ser Lys Asn Phe
    290                 295                 300
His Phe Asp Pro Arg Asp Val Val Ser Asn Ile Asn Val Phe Val Leu
305                 310                 315                 320
Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu
                325                 330                 335
Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln
            340                 345                 350
Ser Ile Ile Ser Thr Leu Thr
        355


<210> 571
<211> 550
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 571
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
```

```
Pro Gly Pro Ala Glu Leu Cys Asp Asp Asp Pro Pro Glu Ile Pro His
225                 230                 235                 240
Ala Thr Phe Lys Ala Met Ala Tyr Lys Glu Gly Thr Met Leu Asn Cys
                245                 250                 255
Glu Cys Lys Arg Gly Phe Arg Arg Ile Lys Ser Gly Ser Leu Tyr Met
            260                 265                 270
Leu Cys Thr Gly Asn Ser Ser His Ser Ser Trp Asp Asn Gln Cys Gln
        275                 280                 285
Cys Thr Ser Ser Ala Thr Arg Asn Thr Thr Lys Gln Val Thr Pro Gln
    290                 295                 300
Pro Glu Glu Gln Lys Glu Arg Lys Thr Thr Glu Met Gln Ser Pro Met
305                 310                 315                 320
Gln Pro Val Asp Gln Ala Ser Leu Pro Gly His Cys Arg Glu Pro Pro
                325                 330                 335
Pro Trp Glu Asn Glu Ala Thr Glu Arg Ile Tyr His Phe Val Val Gly
            340                 345                 350
Gln Met Val Tyr Tyr Gln Cys Val Gln Gly Tyr Arg Ala Leu His Arg
        355                 360                 365
Gly Pro Ala Glu Ser Val Cys Lys Met Thr His Gly Lys Thr Arg Trp
    370                 375                 380
Thr Gln Pro Gln Leu Ile Cys Thr Gly Gly Gly Gly Ser Gly Gly Gly
385                 390                 395                 400
Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
                405                 410                 415
Ser Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu
            420                 425                 430
His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr
        435                 440                 445
Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro
    450                 455                 460
Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu
465                 470                 475                 480
Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His
                485                 490                 495
Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu
            500                 505                 510
Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr
        515                 520                 525
Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser
    530                 535                 540
Ile Ile Ser Thr Leu Thr
545                 550
```

<210> 572
<211> 555
<212> PRT
<213> Artificial Sequence

<220>
<223> Artificial Sequence

<400> 572
```
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
```

```
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Pro Ala Glu Leu Cys Asp Asp Asp Pro Pro Glu Ile Pro His
225                 230                 235                 240
Ala Thr Phe Lys Ala Met Ala Tyr Lys Glu Gly Thr Met Leu Asn Cys
                245                 250                 255
Glu Cys Lys Arg Gly Phe Arg Arg Ile Lys Ser Gly Ser Leu Tyr Met
            260                 265                 270
Leu Cys Thr Gly Asn Ser Ser His Ser Ser Trp Asp Asn Gln Cys Gln
        275                 280                 285
Cys Thr Ser Ser Ala Thr Arg Asn Thr Thr Lys Gln Val Thr Pro Gln
    290                 295                 300
Pro Glu Glu Gln Lys Glu Arg Lys Thr Thr Glu Met Gln Ser Pro Met
305                 310                 315                 320
Gln Pro Val Asp Gln Ala Ser Leu Pro Gly His Cys Arg Glu Pro Pro
                325                 330                 335
Pro Trp Glu Asn Glu Ala Thr Glu Arg Ile Tyr His Phe Val Val Gly
            340                 345                 350
Gln Met Val Tyr Tyr Gln Cys Val Gln Gly Tyr Arg Ala Leu His Arg
        355                 360                 365
Gly Pro Ala Glu Ser Val Cys Lys Met Thr His Gly Lys Thr Arg Trp
    370                 375                 380
Thr Gln Pro Gln Leu Ile Cys Thr Gly Gly Gly Gly Ser Gly Gly Gly
385                 390                 395                 400
Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
                405                 410                 415
Ser Gly Gly Gly Gly Ser Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr
            420                 425                 430
Gln Leu Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn
```

```
        435                 440                 445
Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe
    450                 455                 460
Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys
465                 470                 475                 480
Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln
                485                 490                 495
Ser Lys Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn
            500                 505                 510
Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu
        515                 520                 525
Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile
    530                 535                 540
Thr Phe Ala Gln Ser Ile Ile Ser Thr Leu Thr
545                 550                 555


<210> 573
<211> 560
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 573
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
```

```
Pro Gly Pro Ala Glu Leu Cys Asp Asp Asp Pro Pro Glu Ile Pro His
225                 230                 235                 240
Ala Thr Phe Lys Ala Met Ala Tyr Lys Glu Gly Thr Met Leu Asn Cys
                245                 250                 255
Glu Cys Lys Arg Gly Phe Arg Arg Ile Lys Ser Gly Ser Leu Tyr Met
            260                 265                 270
Leu Cys Thr Gly Asn Ser Ser His Ser Ser Trp Asp Asn Gln Cys Gln
        275                 280                 285
Cys Thr Ser Ser Ala Thr Arg Asn Thr Thr Lys Gln Val Thr Pro Gln
    290                 295                 300
Pro Glu Glu Gln Lys Glu Arg Lys Thr Thr Glu Met Gln Ser Pro Met
305                 310                 315                 320
Gln Pro Val Asp Gln Ala Ser Leu Pro Gly His Cys Arg Glu Pro Pro
                325                 330                 335
Pro Trp Glu Asn Glu Ala Thr Glu Arg Ile Tyr His Phe Val Val Gly
            340                 345                 350
Gln Met Val Tyr Tyr Gln Cys Val Gln Gly Tyr Arg Ala Leu His Arg
        355                 360                 365
Gly Pro Ala Glu Ser Val Cys Lys Met Thr His Gly Lys Thr Arg Trp
    370                 375                 380
Thr Gln Pro Gln Leu Ile Cys Thr Gly Gly Gly Gly Ser Gly Gly Gly
385                 390                 395                 400
Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
                405                 410                 415
Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Pro Thr Ser Ser
            420                 425                 430
Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His Leu Leu Leu Asp Leu
        435                 440                 445
Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr
    450                 455                 460
Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu
465                 470                 475                 480
Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu Val
                485                 490                 495
Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu Arg Pro Arg Asp Leu
            500                 505                 510
Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr
        515                 520                 525
Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu Phe
    530                 535                 540
Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser Ile Ile Ser Thr Leu Thr
545                 550                 555                 560
```

<210> 574
<211> 565
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 574
```
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
```

```
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Pro Ala Glu Leu Cys Asp Asp Asp Pro Pro Glu Ile Pro His
225                 230                 235                 240
Ala Thr Phe Lys Ala Met Ala Tyr Lys Glu Gly Thr Met Leu Asn Cys
                245                 250                 255
Glu Cys Lys Arg Gly Phe Arg Arg Ile Lys Ser Gly Ser Leu Tyr Met
            260                 265                 270
Leu Cys Thr Gly Asn Ser Ser His Ser Ser Trp Asp Asn Gln Cys Gln
        275                 280                 285
Cys Thr Ser Ser Ala Thr Arg Asn Thr Thr Lys Gln Val Thr Pro Gln
    290                 295                 300
Pro Glu Glu Gln Lys Glu Arg Lys Thr Thr Glu Met Gln Ser Pro Met
305                 310                 315                 320
Gln Pro Val Asp Gln Ala Ser Leu Pro Gly His Cys Arg Glu Pro Pro
                325                 330                 335
Pro Trp Glu Asn Glu Ala Thr Glu Arg Ile Tyr His Phe Val Val Gly
            340                 345                 350
Gln Met Val Tyr Tyr Gln Cys Val Gln Gly Tyr Arg Ala Leu His Arg
        355                 360                 365
Gly Pro Ala Glu Ser Val Cys Lys Met Thr His Gly Lys Thr Arg Trp
    370                 375                 380
Thr Gln Pro Gln Leu Ile Cys Thr Gly Gly Gly Gly Ser Gly Gly Gly
385                 390                 395                 400
Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
                405                 410                 415
Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
            420                 425                 430
Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His
```

```
        435                 440                 445
Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys
    450                 455                 460
Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys
465                 470                 475                 480
Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys
                485                 490                 495
Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu
            500                 505                 510
Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu
        515                 520                 525
Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala
    530                 535                 540
Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser Ile
545                 550                 555                 560
Ile Ser Thr Leu Thr
                565
```

<210> 575
<211> 560
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 575

```
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
```

```
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Pro Ala Glu Leu Cys Asp Asp Asp Pro Pro Glu Ile Pro His
225                 230                 235                 240
Ala Thr Phe Lys Ala Met Ala Tyr Lys Glu Gly Thr Met Leu Asn Cys
                245                 250                 255
Glu Cys Lys Arg Gly Phe Arg Arg Ile Lys Ser Gly Ser Leu Tyr Met
            260                 265                 270
Leu Cys Thr Gly Asn Ser Ser His Ser Ser Trp Asp Asn Gln Cys Gln
        275                 280                 285
Cys Thr Ser Ser Ala Thr Arg Asn Thr Thr Lys Gln Val Thr Pro Gln
    290                 295                 300
Pro Glu Glu Gln Lys Glu Arg Lys Thr Thr Glu Met Gln Ser Pro Met
305                 310                 315                 320
Gln Pro Val Asp Gln Ala Ser Leu Pro Gly His Cys Arg Glu Pro Pro
                325                 330                 335
Pro Trp Glu Asn Glu Ala Thr Glu Arg Ile Tyr His Phe Val Val Gly
            340                 345                 350
Gln Met Val Tyr Tyr Gln Cys Val Gln Gly Tyr Arg Ala Leu His Arg
        355                 360                 365
Gly Pro Ala Glu Ser Val Cys Lys Met Thr His Gly Lys Thr Arg Trp
    370                 375                 380
Thr Gln Pro Gln Leu Ile Cys Thr Gly Gly Gly Gly Gly Gly Gly Gly
385                 390                 395                 400
Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
                405                 410                 415
Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Ala Pro Thr Ser Ser
            420                 425                 430
Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His Leu Leu Leu Asp Leu
        435                 440                 445
Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr
    450                 455                 460
Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu
465                 470                 475                 480
Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu Val
                485                 490                 495
Leu Asn Leu Ala Gln Ser Lys Asn Phe His Phe Asp Pro Arg Asp Val
            500                 505                 510
Val Ser Asn Ile Asn Val Phe Val Leu Glu Leu Lys Gly Ser Glu Thr
        515                 520                 525
Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu Phe
    530                 535                 540
Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser Ile Ile Ser Thr Leu Thr
545                 550                 555                 560
```

<210> 576
<211> 550
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 576
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1   5   10   15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20   25   30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35   40   45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50   55   60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65   70   75   80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85   90   95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100   105   110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115   120   125
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130   135   140
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145   150   155   160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165   170   175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180   185   190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195   200   205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210   215   220
Pro Gly Pro Ala Glu Leu Cys Asp Asp Asp Pro Pro Glu Ile Pro His
225   230   235   240
Ala Thr Phe Lys Ala Met Ala Tyr Lys Glu Gly Thr Met Leu Asn Cys
                245   250   255
Glu Cys Lys Arg Gly Phe Arg Arg Ile Lys Ser Gly Ser Leu Tyr Met
            260   265   270
Leu Cys Thr Gly Asn Ser Ser His Ser Ser Trp Asp Asn Gln Cys Gln
        275   280   285
Cys Thr Ser Ser Ala Thr Arg Asn Thr Thr Lys Gln Val Thr Pro Gln
    290   295   300
Pro Glu Glu Gln Lys Glu Arg Lys Thr Thr Glu Met Gln Ser Pro Met
305   310   315   320
Gln Pro Val Asp Gln Ala Ser Leu Pro Gly His Cys Arg Glu Pro Pro
                325   330   335
Pro Trp Glu Asn Glu Ala Thr Glu Arg Ile Tyr His Phe Val Val Gly
            340   345   350
Gln Met Val Tyr Tyr Gln Cys Val Gln Gly Tyr Arg Ala Leu His Arg
        355   360   365
Gly Pro Ala Glu Ser Val Cys Lys Met Thr His Gly Lys Thr Arg Trp
    370   375   380
Thr Gln Pro Gln Leu Ile Cys Thr Gly Gly Gly Gly Ser Gly Gly Gly
385   390   395   400
Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
                405   410   415
Ser Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu

```
            420                 425                 430
His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr
        435                 440                 445
Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro
    450                 455                 460
Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu
465                 470                 475                 480
Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His
                485                 490                 495
Phe Asp Pro Arg Asp Val Val Ser Asn Ile Asn Val Phe Val Leu Glu
            500                 505                 510
Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr
        515                 520                 525
Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser
    530                 535                 540
Ile Ile Ser Thr Leu Thr
545                 550


<210> 577
<211> 555
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 577
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
```

```
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Pro Ala Glu Leu Cys Asp Asp Asp Pro Pro Glu Ile Pro His
225                 230                 235                 240
Ala Thr Phe Lys Ala Met Ala Tyr Lys Glu Gly Thr Met Leu Asn Cys
                245                 250                 255
Glu Cys Lys Arg Gly Phe Arg Arg Ile Lys Ser Gly Ser Leu Tyr Met
            260                 265                 270
Leu Cys Thr Gly Asn Ser Ser His Ser Ser Trp Asp Asn Gln Cys Gln
        275                 280                 285
Cys Thr Ser Ser Ala Thr Arg Asn Thr Thr Lys Gln Val Thr Pro Gln
    290                 295                 300
Pro Glu Glu Gln Lys Glu Arg Lys Thr Thr Glu Met Gln Ser Pro Met
305                 310                 315                 320
Gln Pro Val Asp Gln Ala Ser Leu Pro Gly His Cys Arg Glu Pro Pro
                325                 330                 335
Pro Trp Glu Asn Glu Ala Thr Glu Arg Ile Tyr His Phe Val Val Gly
            340                 345                 350
Gln Met Val Tyr Tyr Gln Cys Val Gln Gly Tyr Arg Ala Leu His Arg
        355                 360                 365
Gly Pro Ala Glu Ser Val Cys Lys Met Thr His Gly Lys Thr Arg Trp
    370                 375                 380
Thr Gln Pro Gln Leu Ile Cys Thr Gly Gly Gly Gly Ser Gly Gly Gly
385                 390                 395                 400
Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
                405                 410                 415
Ser Gly Gly Gly Gly Ser Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr
            420                 425                 430
Gln Leu Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn
        435                 440                 445
Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe
    450                 455                 460
Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys
465                 470                 475                 480
Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln
                485                 490                 495
Ser Lys Asn Phe His Phe Asp Pro Arg Asp Val Val Ser Asn Ile Asn
            500                 505                 510
Val Phe Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu
        515                 520                 525
Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile
    530                 535                 540
Thr Phe Ala Gln Ser Ile Ile Ser Thr Leu Thr
545                 550                 555
```

<210> 578
<211> 560
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 578
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1   5   10   15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20   25   30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35   40   45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50   55   60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65   70   75   80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85   90   95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100   105   110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115   120   125
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130   135   140
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145   150   155   160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165   170   175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180   185   190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195   200   205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210   215   220
Pro Gly Pro Ala Glu Leu Cys Asp Asp Asp Pro Pro Glu Ile Pro His
225   230   235   240
Ala Thr Phe Lys Ala Met Ala Tyr Lys Glu Gly Thr Met Leu Asn Cys
                245   250   255
Glu Cys Lys Arg Gly Phe Arg Arg Ile Lys Ser Gly Ser Leu Tyr Met
            260   265   270
Leu Cys Thr Gly Asn Ser Ser His Ser Ser Trp Asp Asn Gln Cys Gln
        275   280   285
Cys Thr Ser Ser Ala Thr Arg Asn Thr Thr Lys Gln Val Thr Pro Gln
    290   295   300
Pro Glu Glu Gln Lys Glu Arg Lys Thr Thr Glu Met Gln Ser Pro Met
305   310   315   320
Gln Pro Val Asp Gln Ala Ser Leu Pro Gly His Cys Arg Glu Pro Pro
                325   330   335
Pro Trp Glu Asn Glu Ala Thr Glu Arg Ile Tyr His Phe Val Val Gly
            340   345   350
Gln Met Val Tyr Tyr Gln Cys Val Gln Gly Tyr Arg Ala Leu His Arg
        355   360   365
Gly Pro Ala Glu Ser Val Cys Lys Met Thr His Gly Lys Thr Arg Trp
    370   375   380
Thr Gln Pro Gln Leu Ile Cys Thr Gly Gly Gly Gly Ser Gly Gly Gly
385   390   395   400
Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
                405   410   415
Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Pro Thr Ser Ser

```
            420                 425                 430
Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His Leu Leu Leu Asp Leu
        435                 440                 445
Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr
    450                 455                 460
Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu
465                 470                 475                 480
Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu Val
                485                 490                 495
Leu Asn Leu Ala Gln Ser Lys Asn Phe His Phe Asp Pro Arg Asp Val
            500                 505                 510
Val Ser Asn Ile Asn Val Phe Val Leu Glu Leu Lys Gly Ser Glu Thr
        515                 520                 525
Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu Phe
    530                 535                 540
Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser Ile Ile Ser Thr Leu Thr
545                 550                 555                 560


<210> 579
<211> 565
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 579
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
```

```
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Pro Ala Glu Leu Cys Asp Asp Asp Pro Pro Glu Ile Pro His
225                 230                 235                 240
Ala Thr Phe Lys Ala Met Ala Tyr Lys Glu Gly Thr Met Leu Asn Cys
                245                 250                 255
Glu Cys Lys Arg Gly Phe Arg Arg Ile Lys Ser Gly Ser Leu Tyr Met
            260                 265                 270
Leu Cys Thr Gly Asn Ser Ser His Ser Ser Trp Asp Asn Gln Cys Gln
        275                 280                 285
Cys Thr Ser Ser Ala Thr Arg Asn Thr Thr Lys Gln Val Thr Pro Gln
    290                 295                 300
Pro Glu Glu Gln Lys Glu Arg Lys Thr Thr Glu Met Gln Ser Pro Met
305                 310                 315                 320
Gln Pro Val Asp Gln Ala Ser Leu Pro Gly His Cys Arg Glu Pro Pro
                325                 330                 335
Pro Trp Glu Asn Glu Ala Thr Glu Arg Ile Tyr His Phe Val Val Gly
            340                 345                 350
Gln Met Val Tyr Tyr Gln Cys Val Gln Gly Tyr Arg Ala Leu His Arg
        355                 360                 365
Gly Pro Ala Glu Ser Val Cys Lys Met Thr His Gly Lys Thr Arg Trp
    370                 375                 380
Thr Gln Pro Gln Leu Ile Cys Thr Gly Gly Gly Gly Ser Gly Gly Gly
385                 390                 395                 400
Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
                405                 410                 415
Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
            420                 425                 430
Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His
        435                 440                 445
Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys
    450                 455                 460
Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys
465                 470                 475                 480
Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys
                485                 490                 495
Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His Phe
            500                 505                 510
Asp Pro Arg Asp Val Val Ser Asn Ile Asn Val Phe Val Leu Glu Leu
        515                 520                 525
Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala
    530                 535                 540
Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser Ile
545                 550                 555                 560
Ile Ser Thr Leu Thr
                565
```

<210> 580
<211> 533
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 580
Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His
 1   5   10   15
Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys
            20   25   30
Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys
        35   40   45
Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys
    50   55   60
Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu
65   70   75   80
Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu
                85   90   95
Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala
            100   105   110
Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser Ile
        115   120   125
Ile Ser Thr Leu Thr Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu
    130   135   140
Leu Cys Asp Asp Asp Pro Pro Glu Ile Pro His Ala Thr Phe Lys Ala
145   150   155   160
Met Ala Tyr Lys Glu Gly Thr Met Leu Asn Cys Glu Cys Lys Arg Gly
                165   170   175
Phe Arg Arg Ile Lys Ser Gly Ser Leu Tyr Met Leu Cys Thr Gly Asn
            180   185   190
Ser Ser His Ser Ser Trp Asp Asn Gln Cys Gln Cys Thr Ser Ser Ala
        195   200   205
Thr Arg Asn Thr Thr Lys Gln Val Thr Pro Gln Pro Glu Glu Gln Lys
    210   215   220
Glu Arg Lys Thr Thr Glu Met Gln Ser Pro Met Gln Pro Val Asp Gln
225   230   235   240
Ala Ser Leu Pro Gly His Cys Arg Glu Pro Pro Pro Trp Glu Asn Glu
                245   250   255
Ala Thr Glu Arg Ile Tyr His Phe Val Val Gly Gln Met Val Tyr Tyr
            260   265   270
Gln Cys Val Gln Gly Tyr Arg Ala Leu His Arg Gly Pro Ala Glu Ser
        275   280   285
Val Cys Lys Met Thr His Gly Lys Thr Arg Trp Thr Gln Pro Gln Leu
    290   295   300
Ile Cys Thr Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
305   310   315   320
Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
                325   330   335
Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
            340   345   350
Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
        355   360   365
Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala
    370   375   380
Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
385   390   395   400
Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro

```
                405                 410                 415
Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
            420                 425                 430
Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn
        435                 440                 445
Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
    450                 455                 460
Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
465                 470                 475                 480
Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
                485                 490                 495
Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
            500                 505                 510
Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
        515                 520                 525
Ser Leu Ser Pro Gly
    530
```

<210> 581
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 581

```
Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His
 1               5                  10                  15
Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys
            20                  25                  30
Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys
        35                  40                  45
Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys
    50                  55                  60
Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu
65                  70                  75                  80
Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu
                85                  90                  95
Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala
            100                 105                 110
Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser Ile
        115                 120                 125
Ile Ser Thr Leu Thr Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
    130                 135                 140
Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Leu Cys Asp Asp Asp Pro
145                 150                 155                 160
Pro Glu Ile Pro His Ala Thr Phe Lys Ala Met Ala Tyr Lys Glu Gly
                165                 170                 175
Thr Met Leu Asn Cys Glu Cys Lys Arg Gly Phe Arg Arg Ile Lys Ser
            180                 185                 190
Gly Ser Leu Tyr Met Leu Cys Thr Gly Asn Ser Ser His Ser Ser Trp
        195                 200                 205
```

```
Asp Asn Gln Cys Gln Cys Thr Ser Ser Ala Thr Arg Asn Thr Thr Lys
    210                 215                 220
Gln Val Thr Pro Gln Pro Glu Glu Gln Lys Glu Arg Lys Thr Thr Glu
225                 230                 235                 240
Met Gln Ser Pro Met Gln Pro Val Asp Gln Ala Ser Leu Pro Gly His
                245                 250                 255
Cys Arg Glu Pro Pro Pro Trp Glu Asn Glu Ala Thr Glu Arg Ile Tyr
            260                 265                 270
His Phe Val Val Gly Gln Met Val Tyr Tyr Gln Cys Val Gln Gly Tyr
        275                 280                 285
Arg Ala Leu His Arg Gly Pro Ala Glu Ser Val Cys Lys Met Thr His
    290                 295                 300
Gly Lys Thr Arg Trp Thr Gln Pro Gln Leu Ile Cys Thr Asp Lys Thr
305                 310                 315                 320
His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
                325                 330                 335
Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
            340                 345                 350
Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
        355                 360                 365
Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
    370                 375                 380
Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr Arg Val Val
385                 390                 395                 400
Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
                405                 410                 415
Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
            420                 425                 430
Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
        435                 440                 445
Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
    450                 455                 460
Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
465                 470                 475                 480
Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
                485                 490                 495
Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
            500                 505                 510
Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
        515                 520                 525
Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
    530                 535                 540
```

<210> 582
<211> 538
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 582
```
Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His
```

```
 1               5                  10                  15
Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys
            20                  25                  30
Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys
        35                  40                  45
Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys
    50                  55                  60
Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His Phe
65                  70                  75                  80
Asp Pro Arg Asp Val Val Ser Asn Ile Asn Val Phe Val Leu Glu Leu
                85                  90                  95
Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala
            100                 105                 110
Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser Ile
        115                 120                 125
Ile Ser Thr Leu Thr Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
    130                 135                 140
Gly Gly Gly Ser Glu Leu Cys Asp Asp Asp Pro Pro Glu Ile Pro His
145                 150                 155                 160
Ala Thr Phe Lys Ala Met Ala Tyr Lys Glu Gly Thr Met Leu Asn Cys
                165                 170                 175
Glu Cys Lys Arg Gly Phe Arg Arg Ile Lys Ser Gly Ser Leu Tyr Met
            180                 185                 190
Leu Cys Thr Gly Asn Ser Ser His Ser Ser Trp Asp Asn Gln Cys Gln
        195                 200                 205
Cys Thr Ser Ser Ala Thr Arg Asn Thr Thr Lys Gln Val Thr Pro Gln
    210                 215                 220
Pro Glu Glu Gln Lys Glu Arg Lys Thr Thr Glu Met Gln Ser Pro Met
225                 230                 235                 240
Gln Pro Val Asp Gln Ala Ser Leu Pro Gly His Cys Arg Glu Pro Pro
                245                 250                 255
Pro Trp Glu Asn Glu Ala Thr Glu Arg Ile Tyr His Phe Val Val Gly
            260                 265                 270
Gln Met Val Tyr Tyr Gln Cys Val Gln Gly Tyr Arg Ala Leu His Arg
        275                 280                 285
Gly Pro Ala Glu Ser Val Cys Lys Met Thr His Gly Lys Thr Arg Trp
    290                 295                 300
Thr Gln Pro Gln Leu Ile Cys Thr Asp Lys Thr His Thr Cys Pro Pro
305                 310                 315                 320
Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro
                325                 330                 335
Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
            340                 345                 350
Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
        355                 360                 365
Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
    370                 375                 380
Glu Glu Gln Tyr Ala Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
385                 390                 395                 400
Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
                405                 410                 415
Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
            420                 425                 430
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
```

```
        435                 440                 445
Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
    450                 455                 460
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
465                 470                 475                 480
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
                485                 490                 495
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
            500                 505                 510
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
        515                 520                 525
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
    530                 535


<210> 583
<211> 533
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 583
Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His
 1               5                  10                  15
Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys
            20                  25                  30
Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys
        35                  40                  45
Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys
    50                  55                  60
Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His Phe
65                  70                  75                  80
Asp Pro Arg Asp Val Val Ser Asn Ile Asn Val Phe Val Leu Glu Leu
                85                  90                  95
Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala
            100                 105                 110
Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser Ile
        115                 120                 125
Ile Ser Thr Leu Thr Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu
    130                 135                 140
Leu Cys Asp Asp Asp Pro Pro Glu Ile Pro His Ala Thr Phe Lys Ala
145                 150                 155                 160
Met Ala Tyr Lys Glu Gly Thr Met Leu Asn Cys Glu Cys Lys Arg Gly
                165                 170                 175
Phe Arg Arg Ile Lys Ser Gly Ser Leu Tyr Met Leu Cys Thr Gly Asn
            180                 185                 190
Ser Ser His Ser Ser Trp Asp Asn Gln Cys Gln Cys Thr Ser Ser Ala
        195                 200                 205
Thr Arg Asn Thr Thr Lys Gln Val Thr Pro Gln Pro Glu Glu Gln Lys
    210                 215                 220
Glu Arg Lys Thr Thr Glu Met Gln Ser Pro Met Gln Pro Val Asp Gln
225                 230                 235                 240
```

```
Ala Ser Leu Pro Gly His Cys Arg Glu Pro Pro Pro Trp Glu Asn Glu
                245                 250                 255
Ala Thr Glu Arg Ile Tyr His Phe Val Val Gly Gln Met Val Tyr Tyr
            260                 265                 270
Gln Cys Val Gln Gly Tyr Arg Ala Leu His Arg Gly Pro Ala Glu Ser
        275                 280                 285
Val Cys Lys Met Thr His Gly Lys Thr Arg Trp Thr Gln Pro Gln Leu
    290                 295                 300
Ile Cys Thr Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
305                 310                 315                 320
Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
                325                 330                 335
Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
            340                 345                 350
Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
        355                 360                 365
Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala
    370                 375                 380
Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
385                 390                 395                 400
Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
                405                 410                 415
Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
            420                 425                 430
Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn
        435                 440                 445
Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
    450                 455                 460
Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
465                 470                 475                 480
Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
                485                 490                 495
Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
            500                 505                 510
Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
        515                 520                 525
Ser Leu Ser Pro Gly
    530
```

<210> 584
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 584

```
Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His
 1               5                  10                  15
Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys
            20                  25                  30
Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys
```

```
        35                  40                  45
Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys
    50                  55                  60
Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His Phe
65                  70                  75                  80
Asp Pro Arg Asp Val Val Ser Asn Ile Asn Val Phe Val Leu Glu Leu
                85                  90                  95
Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala
            100                 105                 110
Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser Ile
        115                 120                 125
Ile Ser Thr Leu Thr Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
    130                 135                 140
Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Leu Cys Asp Asp Asp Pro
145                 150                 155                 160
Pro Glu Ile Pro His Ala Thr Phe Lys Ala Met Ala Tyr Lys Glu Gly
                165                 170                 175
Thr Met Leu Asn Cys Glu Cys Lys Arg Gly Phe Arg Arg Ile Lys Ser
            180                 185                 190
Gly Ser Leu Tyr Met Leu Cys Thr Gly Asn Ser Ser His Ser Ser Trp
        195                 200                 205
Asp Asn Gln Cys Gln Cys Thr Ser Ser Ala Thr Arg Asn Thr Thr Lys
    210                 215                 220
Gln Val Thr Pro Gln Pro Glu Glu Gln Lys Glu Arg Lys Thr Thr Glu
225                 230                 235                 240
Met Gln Ser Pro Met Gln Pro Val Asp Gln Ala Ser Leu Pro Gly His
                245                 250                 255
Cys Arg Glu Pro Pro Pro Trp Glu Asn Glu Ala Thr Glu Arg Ile Tyr
            260                 265                 270
His Phe Val Val Gly Gln Met Val Tyr Tyr Gln Cys Val Gln Gly Tyr
        275                 280                 285
Arg Ala Leu His Arg Gly Pro Ala Glu Ser Val Cys Lys Met Thr His
    290                 295                 300
Gly Lys Thr Arg Trp Thr Gln Pro Gln Leu Ile Cys Thr Asp Lys Thr
305                 310                 315                 320
His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
                325                 330                 335
Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
            340                 345                 350
Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
        355                 360                 365
Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
    370                 375                 380
Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr Arg Val Val
385                 390                 395                 400
Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
                405                 410                 415
Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
            420                 425                 430
Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
        435                 440                 445
Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
    450                 455                 460
Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
```

```
465                 470                 475                 480
Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
                485                 490                 495
Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
            500                 505                 510
Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
        515                 520                 525
Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
    530                 535                 540


<210> 585
<211> 568
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 585
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu
225                 230                 235                 240
Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn
                245                 250                 255
Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met
            260                 265                 270
```

```
Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu
        275                 280                 285
Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe
    290                 295                 300
His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu
305                 310                 315                 320
Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu
                325                 330                 335
Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln
            340                 345                 350
Ser Ile Ile Ser Thr Leu Thr Gly Ser Ser Gly Gly Pro Pro Gly Gly
        355                 360                 365
Met Pro Tyr Asp Leu Tyr His Pro Ser Gly Gly Gly Ala Val Asn Gly
    370                 375                 380
Thr Ser Gln Phe Thr Cys Phe Tyr Asn Ser Arg Ala Asn Ile Ser Cys
385                 390                 395                 400
Val Trp Ser Gln Asp Gly Ala Leu Gln Asp Thr Ser Cys Gln Val His
                405                 410                 415
Ala Trp Pro Asp Arg Arg Arg Trp Asn Gln Thr Cys Glu Leu Leu Pro
            420                 425                 430
Val Ser Gln Ala Ser Trp Ala Cys Asn Leu Ile Leu Gly Ala Pro Asp
        435                 440                 445
Ser Gln Lys Leu Thr Thr Val Asp Ile Val Thr Leu Arg Val Leu Cys
    450                 455                 460
Arg Glu Gly Val Arg Trp Arg Val Met Ala Ile Gln Asp Phe Lys Pro
465                 470                 475                 480
Phe Glu Asn Leu Arg Leu Met Ala Pro Ile Ser Leu Gln Val Val His
                485                 490                 495
Val Glu Thr His Arg Cys Asn Ile Ser Trp Glu Ile Ser Gln Ala Ser
            500                 505                 510
His Tyr Phe Glu Arg His Leu Glu Phe Glu Ala Arg Thr Leu Ser Pro
        515                 520                 525
Gly His Thr Trp Glu Glu Ala Pro Leu Leu Thr Leu Lys Gln Lys Gln
    530                 535                 540
Glu Trp Ile Cys Leu Glu Thr Leu Thr Pro Asp Thr Gln Tyr Glu Phe
545                 550                 555                 560
Gln Val Arg Val Lys Pro Leu Gln
                565
```

<210> 586
<211> 569
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 586

```
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
```

```
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu
225                 230                 235                 240
Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn
                245                 250                 255
Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met
            260                 265                 270
Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu
        275                 280                 285
Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe
    290                 295                 300
His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu
305                 310                 315                 320
Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu
                325                 330                 335
Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln
            340                 345                 350
Ser Ile Ile Ser Thr Leu Thr Ser Gly Ser Pro Ser Gly Ser Gly Gly
        355                 360                 365
Gly Met Pro Tyr Asp Leu Tyr His Pro Ser Gly Gly Gly Ala Val Asn
    370                 375                 380
Gly Thr Ser Gln Phe Thr Cys Phe Tyr Asn Ser Arg Ala Asn Ile Ser
385                 390                 395                 400
Cys Val Trp Ser Gln Asp Gly Ala Leu Gln Asp Thr Ser Cys Gln Val
                405                 410                 415
His Ala Trp Pro Asp Arg Arg Arg Trp Asn Gln Thr Cys Glu Leu Leu
            420                 425                 430
Pro Val Ser Gln Ala Ser Trp Ala Cys Asn Leu Ile Leu Gly Ala Pro
        435                 440                 445
Asp Ser Gln Lys Leu Thr Thr Val Asp Ile Val Thr Leu Arg Val Leu
    450                 455                 460
Cys Arg Glu Gly Val Arg Trp Arg Val Met Ala Ile Gln Asp Phe Lys
```

```
465                 470                 475                 480
Pro Phe Glu Asn Leu Arg Leu Met Ala Pro Ile Ser Leu Gln Val Val
                485                 490                 495
His Val Glu Thr His Arg Cys Asn Ile Ser Trp Glu Ile Ser Gln Ala
            500                 505                 510
Ser His Tyr Phe Glu Arg His Leu Glu Phe Glu Ala Arg Thr Leu Ser
        515                 520                 525
Pro Gly His Thr Trp Glu Glu Ala Pro Leu Leu Thr Leu Lys Gln Lys
    530                 535                 540
Gln Glu Trp Ile Cys Leu Glu Thr Leu Thr Pro Asp Thr Gln Tyr Glu
545                 550                 555                 560
Phe Gln Val Arg Val Lys Pro Leu Gln
                565
```

<210> 587
<211> 569
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 587

```
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu
225                 230                 235                 240
```

```
Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn
                245                 250                 255
Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met
            260                 265                 270
Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu
        275                 280                 285
Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe
    290                 295                 300
His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu
305                 310                 315                 320
Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu
                325                 330                 335
Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln
            340                 345                 350
Ser Ile Ile Ser Thr Leu Thr Gly Pro Pro Gly Pro Pro Gly Ser Ser
        355                 360                 365
Gly Met Pro Tyr Asp Leu Tyr His Pro Ser Gly Gly Gly Ala Val Asn
    370                 375                 380
Gly Thr Ser Gln Phe Thr Cys Phe Tyr Asn Ser Arg Ala Asn Ile Ser
385                 390                 395                 400
Cys Val Trp Ser Gln Asp Gly Ala Leu Gln Asp Thr Ser Cys Gln Val
                405                 410                 415
His Ala Trp Pro Asp Arg Arg Arg Trp Asn Gln Thr Cys Glu Leu Leu
            420                 425                 430
Pro Val Ser Gln Ala Ser Trp Ala Cys Asn Leu Ile Leu Gly Ala Pro
        435                 440                 445
Asp Ser Gln Lys Leu Thr Thr Val Asp Ile Val Thr Leu Arg Val Leu
    450                 455                 460
Cys Arg Glu Gly Val Arg Trp Arg Val Met Ala Ile Gln Asp Phe Lys
465                 470                 475                 480
Pro Phe Glu Asn Leu Arg Leu Met Ala Pro Ile Ser Leu Gln Val Val
                485                 490                 495
His Val Glu Thr His Arg Cys Asn Ile Ser Trp Glu Ile Ser Gln Ala
            500                 505                 510
Ser His Tyr Phe Glu Arg His Leu Glu Phe Glu Ala Arg Thr Leu Ser
        515                 520                 525
Pro Gly His Thr Trp Glu Glu Ala Pro Leu Leu Thr Leu Lys Gln Lys
    530                 535                 540
Gln Glu Trp Ile Cys Leu Glu Thr Leu Thr Pro Asp Thr Gln Tyr Glu
545                 550                 555                 560
Phe Gln Val Arg Val Lys Pro Leu Gln
                565
```

<210> 588
<211> 570
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 588
```
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
```

```
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu
225                 230                 235                 240
Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn
                245                 250                 255
Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met
            260                 265                 270
Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu
        275                 280                 285
Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe
    290                 295                 300
His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu
305                 310                 315                 320
Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu
                325                 330                 335
Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln
            340                 345                 350
Ser Ile Ile Ser Thr Leu Thr Gly Ser Ser Ser Gly Pro Pro Gly Pro
        355                 360                 365
Pro Ser Met Pro Tyr Asp Leu Tyr His Pro Ser Gly Gly Gly Ala Val
    370                 375                 380
Asn Gly Thr Ser Gln Phe Thr Cys Phe Tyr Asn Ser Arg Ala Asn Ile
385                 390                 395                 400
Ser Cys Val Trp Ser Gln Asp Gly Ala Leu Gln Asp Thr Ser Cys Gln
                405                 410                 415
Val His Ala Trp Pro Asp Arg Arg Arg Trp Asn Gln Thr Cys Glu Leu
            420                 425                 430
Leu Pro Val Ser Gln Ala Ser Trp Ala Cys Asn Leu Ile Leu Gly Ala
```

```
        435                 440                 445
Pro Asp Ser Gln Lys Leu Thr Thr Val Asp Ile Val Thr Leu Arg Val
    450                 455                 460
Leu Cys Arg Glu Gly Val Arg Trp Arg Val Met Ala Ile Gln Asp Phe
465                 470                 475                 480
Lys Pro Phe Glu Asn Leu Arg Leu Met Ala Pro Ile Ser Leu Gln Val
                485                 490                 495
Val His Val Glu Thr His Arg Cys Asn Ile Ser Trp Glu Ile Ser Gln
            500                 505                 510
Ala Ser His Tyr Phe Glu Arg His Leu Glu Phe Glu Ala Arg Thr Leu
        515                 520                 525
Ser Pro Gly His Thr Trp Glu Glu Ala Pro Leu Leu Thr Leu Lys Gln
    530                 535                 540
Lys Gln Glu Trp Ile Cys Leu Glu Thr Leu Thr Pro Asp Thr Gln Tyr
545                 550                 555                 560
Glu Phe Gln Val Arg Val Lys Pro Leu Gln
                565                 570


<210> 589
<211> 568
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 589
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
```

```
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu
225                 230                 235                 240
Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn
                245                 250                 255
Tyr Lys Asn Pro Lys Leu Thr Ala Met Leu Thr Ala Lys Phe Ala Met
            260                 265                 270
Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Ala
        275                 280                 285
Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe
    290                 295                 300
His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu
305                 310                 315                 320
Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu
                325                 330                 335
Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln
            340                 345                 350
Ser Ile Ile Ser Thr Leu Thr Gly Ser Ser Gly Gly Pro Pro Gly Gly
        355                 360                 365
Met Pro Tyr Asp Leu Tyr His Pro Ser Gly Gly Gly Ala Val Asn Gly
    370                 375                 380
Thr Ser Gln Phe Thr Cys Phe Tyr Asn Ser Arg Ala Asn Ile Ser Cys
385                 390                 395                 400
Val Trp Ser Gln Asp Gly Ala Leu Gln Asp Thr Ser Cys Gln Val His
                405                 410                 415
Ala Trp Pro Asp Arg Arg Arg Trp Asn Gln Thr Cys Glu Leu Leu Pro
            420                 425                 430
Val Ser Gln Ala Ser Trp Ala Cys Asn Leu Ile Leu Gly Ala Pro Asp
        435                 440                 445
Ser Gln Lys Leu Thr Thr Val Asp Ile Val Thr Leu Arg Val Leu Cys
    450                 455                 460
Arg Glu Gly Val Arg Trp Arg Val Met Ala Ile Gln Asp Phe Lys Pro
465                 470                 475                 480
Phe Glu Asn Leu Arg Leu Met Ala Pro Ile Ser Leu Gln Val Val His
                485                 490                 495
Val Glu Thr His Arg Cys Asn Ile Ser Trp Glu Ile Ser Gln Ala Ser
            500                 505                 510
His Tyr Phe Glu Arg His Leu Glu Phe Glu Ala Arg Thr Leu Ser Pro
        515                 520                 525
Gly His Thr Trp Glu Glu Ala Pro Leu Leu Thr Leu Lys Gln Lys Gln
    530                 535                 540
Glu Trp Ile Cys Leu Glu Thr Leu Thr Pro Asp Thr Gln Tyr Glu Phe
545                 550                 555                 560
Gln Val Arg Val Lys Pro Leu Gln
                565
```

<210> 590
<211> 569
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 590
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1   5   10   15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20   25   30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35   40   45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50   55   60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65   70   75   80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85   90   95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100   105   110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115   120   125
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130   135   140
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145   150   155   160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165   170   175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180   185   190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195   200   205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210   215   220
Pro Gly Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu
225   230   235   240
Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn
                245   250   255
Tyr Lys Asn Pro Lys Leu Thr Ala Met Leu Thr Ala Lys Phe Ala Met
            260   265   270
Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Ala
        275   280   285
Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe
    290   295   300
His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu
305   310   315   320
Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu
                325   330   335
Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln
            340   345   350
Ser Ile Ile Ser Thr Leu Thr Ser Gly Ser Pro Ser Gly Ser Gly Gly
        355   360   365
Gly Met Pro Tyr Asp Leu Tyr His Pro Ser Gly Gly Gly Ala Val Asn
    370   375   380
Gly Thr Ser Gln Phe Thr Cys Phe Tyr Asn Ser Arg Ala Asn Ile Ser
385   390   395   400
Cys Val Trp Ser Gln Asp Gly Ala Leu Gln Asp Thr Ser Cys Gln Val

```
                405                 410                 415
His Ala Trp Pro Asp Arg Arg Arg Trp Asn Gln Thr Cys Glu Leu Leu
            420                 425                 430
Pro Val Ser Gln Ala Ser Trp Ala Cys Asn Leu Ile Leu Gly Ala Pro
        435                 440                 445
Asp Ser Gln Lys Leu Thr Thr Val Asp Ile Val Thr Leu Arg Val Leu
    450                 455                 460
Cys Arg Glu Gly Val Arg Trp Arg Val Met Ala Ile Gln Asp Phe Lys
465                 470                 475                 480
Pro Phe Glu Asn Leu Arg Leu Met Ala Pro Ile Ser Leu Gln Val Val
                485                 490                 495
His Val Glu Thr His Arg Cys Asn Ile Ser Trp Glu Ile Ser Gln Ala
            500                 505                 510
Ser His Tyr Phe Glu Arg His Leu Glu Phe Glu Ala Arg Thr Leu Ser
        515                 520                 525
Pro Gly His Thr Trp Glu Glu Ala Pro Leu Leu Thr Leu Lys Gln Lys
    530                 535                 540
Gln Glu Trp Ile Cys Leu Glu Thr Leu Thr Pro Asp Thr Gln Tyr Glu
545                 550                 555                 560
Phe Gln Val Arg Val Lys Pro Leu Gln
                565
```

<210> 591
<211> 569
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 591

```
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
```

```
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu
225                 230                 235                 240
Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn
                245                 250                 255
Tyr Lys Asn Pro Lys Leu Thr Ala Met Leu Thr Ala Lys Phe Ala Met
            260                 265                 270
Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Ala
        275                 280                 285
Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe
    290                 295                 300
His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu
305                 310                 315                 320
Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu
                325                 330                 335
Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln
            340                 345                 350
Ser Ile Ile Ser Thr Leu Thr Gly Pro Pro Gly Pro Pro Gly Ser Ser
        355                 360                 365
Gly Met Pro Tyr Asp Leu Tyr His Pro Ser Gly Gly Gly Ala Val Asn
    370                 375                 380
Gly Thr Ser Gln Phe Thr Cys Phe Tyr Asn Ser Arg Ala Asn Ile Ser
385                 390                 395                 400
Cys Val Trp Ser Gln Asp Gly Ala Leu Gln Asp Thr Ser Cys Gln Val
                405                 410                 415
His Ala Trp Pro Asp Arg Arg Arg Trp Asn Gln Thr Cys Glu Leu Leu
            420                 425                 430
Pro Val Ser Gln Ala Ser Trp Ala Cys Asn Leu Ile Leu Gly Ala Pro
        435                 440                 445
Asp Ser Gln Lys Leu Thr Thr Val Asp Ile Val Thr Leu Arg Val Leu
    450                 455                 460
Cys Arg Glu Gly Val Arg Trp Arg Val Met Ala Ile Gln Asp Phe Lys
465                 470                 475                 480
Pro Phe Glu Asn Leu Arg Leu Met Ala Pro Ile Ser Leu Gln Val Val
                485                 490                 495
His Val Glu Thr His Arg Cys Asn Ile Ser Trp Glu Ile Ser Gln Ala
            500                 505                 510
Ser His Tyr Phe Glu Arg His Leu Glu Phe Glu Ala Arg Thr Leu Ser
        515                 520                 525
Pro Gly His Thr Trp Glu Glu Ala Pro Leu Leu Thr Leu Lys Gln Lys
    530                 535                 540
Gln Glu Trp Ile Cys Leu Glu Thr Leu Thr Pro Asp Thr Gln Tyr Glu
545                 550                 555                 560
Phe Gln Val Arg Val Lys Pro Leu Gln
                565
```

<210> 592
<211> 570

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 592
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1   5   10   15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20   25   30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35   40   45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50   55   60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65   70   75   80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85   90   95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100   105   110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115   120   125
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130   135   140
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145   150   155   160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165   170   175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180   185   190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195   200   205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210   215   220
Pro Gly Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu
225   230   235   240
Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn
                245   250   255
Tyr Lys Asn Pro Lys Leu Thr Ala Met Leu Thr Ala Lys Phe Ala Met
            260   265   270
Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Ala
        275   280   285
Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe
    290   295   300
His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu
305   310   315   320
Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu
                325   330   335
Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln
            340   345   350
Ser Ile Ile Ser Thr Leu Thr Gly Ser Ser Ser Gly Pro Pro Gly Pro
        355   360   365
Pro Ser Met Pro Tyr Asp Leu Tyr His Pro Ser Gly Gly Gly Ala Val

```
    370                 375                 380
Asn Gly Thr Ser Gln Phe Thr Cys Phe Tyr Asn Ser Arg Ala Asn Ile
385                 390                 395                 400
Ser Cys Val Trp Ser Gln Asp Gly Ala Leu Gln Asp Thr Ser Cys Gln
                405                 410                 415
Val His Ala Trp Pro Asp Arg Arg Arg Trp Asn Gln Thr Cys Glu Leu
            420                 425                 430
Leu Pro Val Ser Gln Ala Ser Trp Ala Cys Asn Leu Ile Leu Gly Ala
        435                 440                 445
Pro Asp Ser Gln Lys Leu Thr Thr Val Asp Ile Val Thr Leu Arg Val
    450                 455                 460
Leu Cys Arg Glu Gly Val Arg Trp Arg Val Met Ala Ile Gln Asp Phe
465                 470                 475                 480
Lys Pro Phe Glu Asn Leu Arg Leu Met Ala Pro Ile Ser Leu Gln Val
                485                 490                 495
Val His Val Glu Thr His Arg Cys Asn Ile Ser Trp Glu Ile Ser Gln
            500                 505                 510
Ala Ser His Tyr Phe Glu Arg His Leu Glu Phe Glu Ala Arg Thr Leu
        515                 520                 525
Ser Pro Gly His Thr Trp Glu Glu Ala Pro Leu Leu Thr Leu Lys Gln
    530                 535                 540
Lys Gln Glu Trp Ile Cys Leu Glu Thr Leu Thr Pro Asp Thr Gln Tyr
545                 550                 555                 560
Glu Phe Gln Val Arg Val Lys Pro Leu Gln
                565                 570
```

<210> 593
<211> 567
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 593

```
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
```

```
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu
225                 230                 235                 240
Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn
                245                 250                 255
Tyr Lys Asn Pro Lys Leu Thr Ala Met Leu Thr Ala Lys Phe Ala Met
            260                 265                 270
Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Ala
        275                 280                 285
Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe
    290                 295                 300
His Phe Asp Pro Arg Asp Val Val Ser Asn Ile Asn Val Phe Val Leu
305                 310                 315                 320
Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu
                325                 330                 335
Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln
            340                 345                 350
Ser Ile Ile Ser Thr Leu Thr Gly Pro Pro Ser Gly Ser Ser Pro Met
        355                 360                 365
Pro Tyr Asp Leu Tyr His Pro Ser Gly Gly Gly Ala Val Asn Gly Thr
    370                 375                 380
Ser Gln Phe Thr Cys Phe Tyr Asn Ser Arg Ala Asn Ile Ser Cys Val
385                 390                 395                 400
Trp Ser Gln Asp Gly Ala Leu Gln Asp Thr Ser Cys Gln Val His Ala
                405                 410                 415
Trp Pro Asp Arg Arg Arg Trp Asn Gln Thr Cys Glu Leu Leu Pro Val
            420                 425                 430
Ser Gln Ala Ser Trp Ala Cys Asn Leu Ile Leu Gly Ala Pro Asp Ser
        435                 440                 445
Gln Lys Leu Thr Thr Val Asp Ile Val Thr Leu Arg Val Leu Cys Arg
    450                 455                 460
Glu Gly Val Arg Trp Arg Val Met Ala Ile Gln Asp Phe Lys Pro Phe
465                 470                 475                 480
Glu Asn Leu Arg Leu Met Ala Pro Ile Ser Leu Gln Val Val His Val
                485                 490                 495
Glu Thr His Arg Cys Asn Ile Ser Trp Glu Ile Ser Gln Ala Ser His
            500                 505                 510
Tyr Phe Glu Arg His Leu Glu Phe Glu Ala Arg Thr Leu Ser Pro Gly
        515                 520                 525
His Thr Trp Glu Glu Ala Pro Leu Leu Thr Leu Lys Gln Lys Gln Glu
    530                 535                 540
Trp Ile Cys Leu Glu Thr Leu Thr Pro Asp Thr Gln Tyr Glu Phe Gln
545                 550                 555                 560
Val Arg Val Lys Pro Leu Gln
                565
```

<210> 594
<211> 568
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 594
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1   5   10   15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20   25   30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35   40   45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50   55   60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65   70   75   80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85   90   95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100   105   110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115   120   125
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130   135   140
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145   150   155   160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165   170   175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180   185   190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195   200   205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210   215   220
Pro Gly Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu
225   230   235   240
Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn
                245   250   255
Tyr Lys Asn Pro Lys Leu Thr Ala Met Leu Thr Ala Lys Phe Ala Met
            260   265   270
Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Ala
        275   280   285
Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe
    290   295   300
His Phe Asp Pro Arg Asp Val Val Ser Asn Ile Asn Val Phe Val Leu
305   310   315   320
Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu
                325   330   335
Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln

```
            340                 345                 350
Ser Ile Ile Ser Thr Leu Thr Gly Ser Ser Gly Gly Pro Pro Gly Gly
        355                 360                 365
Met Pro Tyr Asp Leu Tyr His Pro Ser Gly Gly Gly Ala Val Asn Gly
    370                 375                 380
Thr Ser Gln Phe Thr Cys Phe Tyr Asn Ser Arg Ala Asn Ile Ser Cys
385                 390                 395                 400
Val Trp Ser Gln Asp Gly Ala Leu Gln Asp Thr Ser Cys Gln Val His
                405                 410                 415
Ala Trp Pro Asp Arg Arg Arg Trp Asn Gln Thr Cys Glu Leu Leu Pro
            420                 425                 430
Val Ser Gln Ala Ser Trp Ala Cys Asn Leu Ile Leu Gly Ala Pro Asp
        435                 440                 445
Ser Gln Lys Leu Thr Thr Val Asp Ile Val Thr Leu Arg Val Leu Cys
    450                 455                 460
Arg Glu Gly Val Arg Trp Arg Val Met Ala Ile Gln Asp Phe Lys Pro
465                 470                 475                 480
Phe Glu Asn Leu Arg Leu Met Ala Pro Ile Ser Leu Gln Val Val His
                485                 490                 495
Val Glu Thr His Arg Cys Asn Ile Ser Trp Glu Ile Ser Gln Ala Ser
            500                 505                 510
His Tyr Phe Glu Arg His Leu Glu Phe Glu Ala Arg Thr Leu Ser Pro
        515                 520                 525
Gly His Thr Trp Glu Glu Ala Pro Leu Leu Thr Leu Lys Gln Lys Gln
    530                 535                 540
Glu Trp Ile Cys Leu Glu Thr Leu Thr Pro Asp Thr Gln Tyr Glu Phe
545                 550                 555                 560
Gln Val Arg Val Lys Pro Leu Gln
                565
```

<210> 595
<211> 569
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 595

```
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
```

```
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu
225                 230                 235                 240
Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn
                245                 250                 255
Tyr Lys Asn Pro Lys Leu Thr Ala Met Leu Thr Ala Lys Phe Ala Met
            260                 265                 270
Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Ala
        275                 280                 285
Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe
    290                 295                 300
His Phe Asp Pro Arg Asp Val Val Ser Asn Ile Asn Val Phe Val Leu
305                 310                 315                 320
Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu
                325                 330                 335
Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln
            340                 345                 350
Ser Ile Ile Ser Thr Leu Thr Ser Gly Ser Pro Ser Gly Ser Gly Gly
        355                 360                 365
Gly Met Pro Tyr Asp Leu Tyr His Pro Ser Gly Gly Gly Ala Val Asn
    370                 375                 380
Gly Thr Ser Gln Phe Thr Cys Phe Tyr Asn Ser Arg Ala Asn Ile Ser
385                 390                 395                 400
Cys Val Trp Ser Gln Asp Gly Ala Leu Gln Asp Thr Ser Cys Gln Val
                405                 410                 415
His Ala Trp Pro Asp Arg Arg Arg Trp Asn Gln Thr Cys Glu Leu Leu
            420                 425                 430
Pro Val Ser Gln Ala Ser Trp Ala Cys Asn Leu Ile Leu Gly Ala Pro
        435                 440                 445
Asp Ser Gln Lys Leu Thr Thr Val Asp Ile Val Thr Leu Arg Val Leu
    450                 455                 460
Cys Arg Glu Gly Val Arg Trp Arg Val Met Ala Ile Gln Asp Phe Lys
465                 470                 475                 480
Pro Phe Glu Asn Leu Arg Leu Met Ala Pro Ile Ser Leu Gln Val Val
                485                 490                 495
His Val Glu Thr His Arg Cys Asn Ile Ser Trp Glu Ile Ser Gln Ala
            500                 505                 510
Ser His Tyr Phe Glu Arg His Leu Glu Phe Glu Ala Arg Thr Leu Ser
        515                 520                 525
Pro Gly His Thr Trp Glu Glu Ala Pro Leu Leu Thr Leu Lys Gln Lys
    530                 535                 540
```

```
Gln Glu Trp Ile Cys Leu Glu Thr Leu Thr Pro Asp Thr Gln Tyr Glu
545                 550                 555                 560
Phe Gln Val Arg Val Lys Pro Leu Gln
                565
```

<210> 596
<211> 569
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 596

```
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu
225                 230                 235                 240
Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn
                245                 250                 255
Tyr Lys Asn Pro Lys Leu Thr Ala Met Leu Thr Ala Lys Phe Ala Met
            260                 265                 270
Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Ala
        275                 280                 285
Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe
    290                 295                 300
His Phe Asp Pro Arg Asp Val Val Ser Asn Ile Asn Val Phe Val Leu
```

305 310 315 320
Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu
325 330 335
Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln
340 345 350
Ser Ile Ile Ser Thr Leu Thr Gly Pro Pro Gly Pro Pro Gly Ser Ser
355 360 365
Gly Met Pro Tyr Asp Leu Tyr His Pro Ser Gly Gly Gly Ala Val Asn
370 375 380
Gly Thr Ser Gln Phe Thr Cys Phe Tyr Asn Ser Arg Ala Asn Ile Ser
385 390 395 400
Cys Val Trp Ser Gln Asp Gly Ala Leu Gln Asp Thr Ser Cys Gln Val
405 410 415
His Ala Trp Pro Asp Arg Arg Arg Trp Asn Gln Thr Cys Glu Leu Leu
420 425 430
Pro Val Ser Gln Ala Ser Trp Ala Cys Asn Leu Ile Leu Gly Ala Pro
435 440 445
Asp Ser Gln Lys Leu Thr Thr Val Asp Ile Val Thr Leu Arg Val Leu
450 455 460
Cys Arg Glu Gly Val Arg Trp Arg Val Met Ala Ile Gln Asp Phe Lys
465 470 475 480
Pro Phe Glu Asn Leu Arg Leu Met Ala Pro Ile Ser Leu Gln Val Val
485 490 495
His Val Glu Thr His Arg Cys Asn Ile Ser Trp Glu Ile Ser Gln Ala
500 505 510
Ser His Tyr Phe Glu Arg His Leu Glu Phe Glu Ala Arg Thr Leu Ser
515 520 525
Pro Gly His Thr Trp Glu Glu Ala Pro Leu Leu Thr Leu Lys Gln Lys
530 535 540
Gln Glu Trp Ile Cys Leu Glu Thr Leu Thr Pro Asp Thr Gln Tyr Glu
545 550 555 560
Phe Gln Val Arg Val Lys Pro Leu Gln
565

<210> 597
<211> 570
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 597
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
1 5 10 15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
20 25 30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
35 40 45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
50 55 60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65 70 75 80

```
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu
225                 230                 235                 240
Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn
                245                 250                 255
Tyr Lys Asn Pro Lys Leu Thr Ala Met Leu Thr Ala Lys Phe Ala Met
            260                 265                 270
Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Ala
        275                 280                 285
Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe
    290                 295                 300
His Phe Asp Pro Arg Asp Val Val Ser Asn Ile Asn Val Phe Val Leu
305                 310                 315                 320
Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu
                325                 330                 335
Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln
            340                 345                 350
Ser Ile Ile Ser Thr Leu Thr Gly Ser Ser Ser Gly Pro Pro Gly Pro
        355                 360                 365
Pro Ser Met Pro Tyr Asp Leu Tyr His Pro Ser Gly Gly Gly Ala Val
    370                 375                 380
Asn Gly Thr Ser Gln Phe Thr Cys Phe Tyr Asn Ser Arg Ala Asn Ile
385                 390                 395                 400
Ser Cys Val Trp Ser Gln Asp Gly Ala Leu Gln Asp Thr Ser Cys Gln
                405                 410                 415
Val His Ala Trp Pro Asp Arg Arg Arg Trp Asn Gln Thr Cys Glu Leu
            420                 425                 430
Leu Pro Val Ser Gln Ala Ser Trp Ala Cys Asn Leu Ile Leu Gly Ala
        435                 440                 445
Pro Asp Ser Gln Lys Leu Thr Thr Val Asp Ile Val Thr Leu Arg Val
    450                 455                 460
Leu Cys Arg Glu Gly Val Arg Trp Arg Val Met Ala Ile Gln Asp Phe
465                 470                 475                 480
Lys Pro Phe Glu Asn Leu Arg Leu Met Ala Pro Ile Ser Leu Gln Val
                485                 490                 495
Val His Val Glu Thr His Arg Cys Asn Ile Ser Trp Glu Ile Ser Gln
            500                 505                 510
```

```
Ala Ser His Tyr Phe Glu Arg His Leu Glu Phe Glu Ala Arg Thr Leu
        515                 520                 525
Ser Pro Gly His Thr Trp Glu Glu Ala Pro Leu Leu Thr Leu Lys Gln
    530                 535                 540
Lys Gln Glu Trp Ile Cys Leu Glu Thr Leu Thr Pro Asp Thr Gln Tyr
545                 550                 555                 560
Glu Phe Gln Val Arg Val Lys Pro Leu Gln
                565                 570
```

<210> 598
<211> 769
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 598

```
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Pro Ala Glu Leu Cys Asp Asp Asp Pro Pro Glu Ile Pro His
225                 230                 235                 240
Ala Thr Phe Lys Ala Met Ala Tyr Lys Glu Gly Thr Met Leu Asn Cys
                245                 250                 255
Glu Cys Lys Arg Gly Phe Arg Arg Ile Lys Ser Gly Ser Leu Tyr Met
            260                 265                 270
Leu Cys Thr Gly Asn Ser Ser His Ser Ser Trp Asp Asn Gln Cys Gln
```

```
        275                 280                 285
Cys Thr Ser Ser Ala Thr Arg Asn Thr Thr Lys Gln Val Thr Pro Gln
    290                 295                 300
Pro Glu Glu Gln Lys Glu Arg Lys Thr Thr Glu Met Gln Ser Pro Met
305                 310                 315                 320
Gln Pro Val Asp Gln Ala Ser Leu Pro Gly His Cys Arg Glu Pro Pro
                325                 330                 335
Pro Trp Glu Asn Glu Ala Thr Glu Arg Ile Tyr His Phe Val Val Gly
            340                 345                 350
Gln Met Val Tyr Tyr Gln Cys Val Gln Gly Tyr Arg Ala Leu His Arg
        355                 360                 365
Gly Pro Ala Glu Ser Val Cys Lys Met Thr His Gly Lys Thr Arg Trp
    370                 375                 380
Thr Gln Pro Gln Leu Ile Cys Thr Gly Gly Gly Gly Gly Gly Gly Gly
385                 390                 395                 400
Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
                405                 410                 415
Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Ala Pro Thr Ser Ser
            420                 425                 430
Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His Leu Leu Leu Asp Leu
        435                 440                 445
Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr
    450                 455                 460
Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu
465                 470                 475                 480
Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu Val
                485                 490                 495
Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu Arg Pro Arg Asp Leu
            500                 505                 510
Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr
        515                 520                 525
Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu Phe
    530                 535                 540
Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser Ile Ile Ser Thr Leu Thr
545                 550                 555                 560
Gly Ser Ser Gly Gly Pro Pro Gly Gly Met Pro Tyr Asp Leu Tyr His
                565                 570                 575
Pro Ser Gly Gly Gly Ala Val Asn Gly Thr Ser Gln Phe Thr Cys Phe
            580                 585                 590
Tyr Asn Ser Arg Ala Asn Ile Ser Cys Val Trp Ser Gln Asp Gly Ala
        595                 600                 605
Leu Gln Asp Thr Ser Cys Gln Val His Ala Trp Pro Asp Arg Arg Arg
    610                 615                 620
Trp Asn Gln Thr Cys Glu Leu Leu Pro Val Ser Gln Ala Ser Trp Ala
625                 630                 635                 640
Cys Asn Leu Ile Leu Gly Ala Pro Asp Ser Gln Lys Leu Thr Thr Val
                645                 650                 655
Asp Ile Val Thr Leu Arg Val Leu Cys Arg Glu Gly Val Arg Trp Arg
            660                 665                 670
Val Met Ala Ile Gln Asp Phe Lys Pro Phe Glu Asn Leu Arg Leu Met
        675                 680                 685
Ala Pro Ile Ser Leu Gln Val Val His Val Glu Thr His Arg Cys Asn
    690                 695                 700
Ile Ser Trp Glu Ile Ser Gln Ala Ser His Tyr Phe Glu Arg His Leu
```

705 710 715 720
Glu Phe Glu Ala Arg Thr Leu Ser Pro Gly His Thr Trp Glu Glu Ala
725 730 735
Pro Leu Leu Thr Leu Lys Gln Lys Gln Glu Trp Ile Cys Leu Glu Thr
740 745 750
Leu Thr Pro Asp Thr Gln Tyr Glu Phe Gln Val Arg Val Lys Pro Leu
755 760 765
Gln

<210> 599
<211> 770
<212> PRT
<213> Synthetic Construct

<220>
<223> Synthetic Construct

<400> 599
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
1 5 10 15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
20 25 30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
35 40 45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
50 55 60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65 70 75 80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
85 90 95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
100 105 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
115 120 125
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
130 135 140
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145 150 155 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
165 170 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
180 185 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
195 200 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
210 215 220
Pro Gly Pro Ala Glu Leu Cys Asp Asp Pro Pro Glu Ile Pro His
225 230 235 240
Ala Thr Phe Lys Ala Met Ala Tyr Lys Glu Gly Thr Met Leu Asn Cys
245 250 255
Glu Cys Lys Arg Gly Phe Arg Arg Ile Lys Ser Gly Ser Leu Tyr Met
260 265 270

```
Leu Cys Thr Gly Asn Ser Ser His Ser Ser Trp Asp Asn Gln Cys Gln
        275                 280                 285
Cys Thr Ser Ser Ala Thr Arg Asn Thr Thr Lys Gln Val Thr Pro Gln
    290                 295                 300
Pro Glu Glu Gln Lys Glu Arg Lys Thr Thr Glu Met Gln Ser Pro Met
305                 310                 315                 320
Gln Pro Val Asp Gln Ala Ser Leu Pro Gly His Cys Arg Glu Pro Pro
                325                 330                 335
Pro Trp Glu Asn Glu Ala Thr Glu Arg Ile Tyr His Phe Val Val Gly
            340                 345                 350
Gln Met Val Tyr Tyr Gln Cys Val Gln Gly Tyr Arg Ala Leu His Arg
        355                 360                 365
Gly Pro Ala Glu Ser Val Cys Lys Met Thr His Gly Lys Thr Arg Trp
    370                 375                 380
Thr Gln Pro Gln Leu Ile Cys Thr Gly Gly Gly Gly Gly Gly Gly Gly
385                 390                 395                 400
Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
                405                 410                 415
Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Ala Pro Thr Ser Ser
            420                 425                 430
Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His Leu Leu Leu Asp Leu
        435                 440                 445
Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr
    450                 455                 460
Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu
465                 470                 475                 480
Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu Val
                485                 490                 495
Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu Arg Pro Arg Asp Leu
            500                 505                 510
Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr
        515                 520                 525
Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu Phe
    530                 535                 540
Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser Ile Ile Ser Thr Leu Thr
545                 550                 555                 560
Ser Gly Ser Pro Ser Gly Ser Gly Gly Gly Met Pro Tyr Asp Leu Tyr
                565                 570                 575
His Pro Ser Gly Gly Gly Ala Val Asn Gly Thr Ser Gln Phe Thr Cys
            580                 585                 590
Phe Tyr Asn Ser Arg Ala Asn Ile Ser Cys Val Trp Ser Gln Asp Gly
        595                 600                 605
Ala Leu Gln Asp Thr Ser Cys Gln Val His Ala Trp Pro Asp Arg Arg
    610                 615                 620
Arg Trp Asn Gln Thr Cys Glu Leu Leu Pro Val Ser Gln Ala Ser Trp
625                 630                 635                 640
Ala Cys Asn Leu Ile Leu Gly Ala Pro Asp Ser Gln Lys Leu Thr Thr
                645                 650                 655
Val Asp Ile Val Thr Leu Arg Val Leu Cys Arg Glu Gly Val Arg Trp
            660                 665                 670
Arg Val Met Ala Ile Gln Asp Phe Lys Pro Phe Glu Asn Leu Arg Leu
        675                 680                 685
Met Ala Pro Ile Ser Leu Gln Val Val His Val Glu Thr His Arg Cys
    690                 695                 700
```

```
Asn Ile Ser Trp Glu Ile Ser Gln Ala Ser His Tyr Phe Glu Arg His
705                 710                 715                 720
Leu Glu Phe Glu Ala Arg Thr Leu Ser Pro Gly His Thr Trp Glu Glu
                725                 730                 735
Ala Pro Leu Leu Thr Leu Lys Gln Lys Gln Glu Trp Ile Cys Leu Glu
            740                 745                 750
Thr Leu Thr Pro Asp Thr Gln Tyr Glu Phe Gln Val Arg Val Lys Pro
        755                 760                 765
Leu Gln
    770
```

<210> 600
<211> 770
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 600

```
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Pro Ala Glu Leu Cys Asp Asp Asp Pro Pro Glu Ile Pro His
225                 230                 235                 240
Ala Thr Phe Lys Ala Met Ala Tyr Lys Glu Gly Thr Met Leu Asn Cys
                245                 250                 255
Glu Cys Lys Arg Gly Phe Arg Arg Ile Lys Ser Gly Ser Leu Tyr Met
```

```
            260                 265                 270
Leu Cys Thr Gly Asn Ser Ser His Ser Ser Trp Asp Asn Gln Cys Gln
        275                 280                 285
Cys Thr Ser Ser Ala Thr Arg Asn Thr Thr Lys Gln Val Thr Pro Gln
    290                 295                 300
Pro Glu Glu Gln Lys Glu Arg Lys Thr Thr Glu Met Gln Ser Pro Met
305                 310                 315                 320
Gln Pro Val Asp Gln Ala Ser Leu Pro Gly His Cys Arg Glu Pro Pro
                325                 330                 335
Pro Trp Glu Asn Glu Ala Thr Glu Arg Ile Tyr His Phe Val Val Gly
            340                 345                 350
Gln Met Val Tyr Tyr Gln Cys Val Gln Gly Tyr Arg Ala Leu His Arg
        355                 360                 365
Gly Pro Ala Glu Ser Val Cys Lys Met Thr His Gly Lys Thr Arg Trp
    370                 375                 380
Thr Gln Pro Gln Leu Ile Cys Thr Gly Gly Gly Gly Gly Gly Gly Gly
385                 390                 395                 400
Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
                405                 410                 415
Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Ala Pro Thr Ser Ser
            420                 425                 430
Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His Leu Leu Leu Asp Leu
        435                 440                 445
Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr
    450                 455                 460
Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu
465                 470                 475                 480
Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu Val
                485                 490                 495
Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu Arg Pro Arg Asp Leu
            500                 505                 510
Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr
        515                 520                 525
Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu Phe
    530                 535                 540
Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser Ile Ile Ser Thr Leu Thr
545                 550                 555                 560
Gly Pro Pro Gly Pro Pro Gly Ser Ser Gly Met Pro Tyr Asp Leu Tyr
                565                 570                 575
His Pro Ser Gly Gly Gly Ala Val Asn Gly Thr Ser Gln Phe Thr Cys
            580                 585                 590
Phe Tyr Asn Ser Arg Ala Asn Ile Ser Cys Val Trp Ser Gln Asp Gly
        595                 600                 605
Ala Leu Gln Asp Thr Ser Cys Gln Val His Ala Trp Pro Asp Arg Arg
    610                 615                 620
Arg Trp Asn Gln Thr Cys Glu Leu Leu Pro Val Ser Gln Ala Ser Trp
625                 630                 635                 640
Ala Cys Asn Leu Ile Leu Gly Ala Pro Asp Ser Gln Lys Leu Thr Thr
                645                 650                 655
Val Asp Ile Val Thr Leu Arg Val Leu Cys Arg Glu Gly Val Arg Trp
            660                 665                 670
Arg Val Met Ala Ile Gln Asp Phe Lys Pro Phe Glu Asn Leu Arg Leu
        675                 680                 685
Met Ala Pro Ile Ser Leu Gln Val Val His Val Glu Thr His Arg Cys
```

```
    690                 695                 700
Asn Ile Ser Trp Glu Ile Ser Gln Ala Ser His Tyr Phe Glu Arg His
705                 710                 715                 720
Leu Glu Phe Glu Ala Arg Thr Leu Ser Pro Gly His Thr Trp Glu Glu
                725                 730                 735
Ala Pro Leu Leu Thr Leu Lys Gln Lys Gln Glu Trp Ile Cys Leu Glu
            740                 745                 750
Thr Leu Thr Pro Asp Thr Gln Tyr Glu Phe Gln Val Arg Val Lys Pro
        755                 760                 765
Leu Gln
    770
```

<210> 601
<211> 771
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 601

```
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Pro Ala Glu Leu Cys Asp Asp Asp Pro Pro Glu Ile Pro His
225                 230                 235                 240
Ala Thr Phe Lys Ala Met Ala Tyr Lys Glu Gly Thr Met Leu Asn Cys
                245                 250                 255
```

```
Glu Cys Lys Arg Gly Phe Arg Arg Ile Lys Ser Gly Ser Leu Tyr Met
            260                 265                 270
Leu Cys Thr Gly Asn Ser Ser His Ser Ser Trp Asp Asn Gln Cys Gln
        275                 280                 285
Cys Thr Ser Ser Ala Thr Arg Asn Thr Thr Lys Gln Val Thr Pro Gln
    290                 295                 300
Pro Glu Glu Gln Lys Glu Arg Lys Thr Thr Glu Met Gln Ser Pro Met
305                 310                 315                 320
Gln Pro Val Asp Gln Ala Ser Leu Pro Gly His Cys Arg Glu Pro Pro
                325                 330                 335
Pro Trp Glu Asn Glu Ala Thr Glu Arg Ile Tyr His Phe Val Val Gly
            340                 345                 350
Gln Met Val Tyr Tyr Gln Cys Val Gln Gly Tyr Arg Ala Leu His Arg
        355                 360                 365
Gly Pro Ala Glu Ser Val Cys Lys Met Thr His Gly Lys Thr Arg Trp
    370                 375                 380
Thr Gln Pro Gln Leu Ile Cys Thr Gly Gly Gly Gly Gly Gly Gly Gly
385                 390                 395                 400
Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
                405                 410                 415
Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Ala Pro Thr Ser Ser
            420                 425                 430
Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His Leu Leu Leu Asp Leu
        435                 440                 445
Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr
    450                 455                 460
Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu
465                 470                 475                 480
Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu Val
                485                 490                 495
Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu Arg Pro Arg Asp Leu
            500                 505                 510
Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr
        515                 520                 525
Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu Phe
    530                 535                 540
Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser Ile Ile Ser Thr Leu Thr
545                 550                 555                 560
Gly Ser Ser Ser Gly Pro Pro Gly Pro Pro Ser Met Pro Tyr Asp Leu
                565                 570                 575
Tyr His Pro Ser Gly Gly Gly Ala Val Asn Gly Thr Ser Gln Phe Thr
            580                 585                 590
Cys Phe Tyr Asn Ser Arg Ala Asn Ile Ser Cys Val Trp Ser Gln Asp
        595                 600                 605
Gly Ala Leu Gln Asp Thr Ser Cys Gln Val His Ala Trp Pro Asp Arg
    610                 615                 620
Arg Arg Trp Asn Gln Thr Cys Glu Leu Leu Pro Val Ser Gln Ala Ser
625                 630                 635                 640
Trp Ala Cys Asn Leu Ile Leu Gly Ala Pro Asp Ser Gln Lys Leu Thr
                645                 650                 655
Thr Val Asp Ile Val Thr Leu Arg Val Leu Cys Arg Glu Gly Val Arg
            660                 665                 670
Trp Arg Val Met Ala Ile Gln Asp Phe Lys Pro Phe Glu Asn Leu Arg
        675                 680                 685
```

```
Leu Met Ala Pro Ile Ser Leu Gln Val Val His Val Glu Thr His Arg
    690                 695                 700
Cys Asn Ile Ser Trp Glu Ile Ser Gln Ala Ser His Tyr Phe Glu Arg
705                 710                 715                 720
His Leu Glu Phe Glu Ala Arg Thr Leu Ser Pro Gly His Thr Trp Glu
                725                 730                 735
Glu Ala Pro Leu Leu Thr Leu Lys Gln Lys Gln Glu Trp Ile Cys Leu
            740                 745                 750
Glu Thr Leu Thr Pro Asp Thr Gln Tyr Glu Phe Gln Val Arg Val Lys
        755                 760                 765
Pro Leu Gln
    770
```

<210> 602
<211> 592
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 602

```
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu
225                 230                 235                 240
Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn
```

```
                245                 250                 255
Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met
            260                 265                 270
Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu
        275                 280                 285
Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe
    290                 295                 300
His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu
305                 310                 315                 320
Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu
                325                 330                 335
Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln
            340                 345                 350
Ser Ile Ile Ser Thr Leu Thr Gly Pro Pro Ser Gly Ser Ser Pro Met
        355                 360                 365
Pro Tyr Asp Leu Tyr His Pro Ser Gly Gly Gly Ala Val Asn Gly Thr
    370                 375                 380
Ser Gln Phe Thr Cys Phe Tyr Asn Ser Arg Ala Asn Ile Ser Cys Val
385                 390                 395                 400
Trp Ser Gln Asp Gly Ala Leu Gln Asp Thr Ser Cys Gln Val His Ala
                405                 410                 415
Trp Pro Asp Arg Arg Arg Trp Asn Gln Thr Cys Glu Leu Leu Pro Val
            420                 425                 430
Ser Gln Ala Ser Trp Ala Cys Asn Leu Ile Leu Gly Ala Pro Asp Ser
        435                 440                 445
Gln Lys Leu Thr Thr Val Asp Ile Val Thr Leu Arg Val Leu Cys Arg
    450                 455                 460
Glu Gly Val Arg Trp Arg Val Met Ala Ile Gln Asp Phe Lys Pro Phe
465                 470                 475                 480
Glu Asn Leu Arg Leu Met Ala Pro Ile Ser Leu Gln Val Val His Val
                485                 490                 495
Glu Thr His Arg Cys Asn Ile Ser Trp Glu Ile Ser Gln Ala Ser His
            500                 505                 510
Tyr Phe Glu Arg His Leu Glu Phe Glu Ala Arg Thr Leu Ser Pro Gly
        515                 520                 525
His Thr Trp Glu Glu Ala Pro Leu Leu Thr Leu Lys Gln Lys Gln Glu
    530                 535                 540
Trp Ile Cys Leu Glu Thr Leu Thr Pro Asp Thr Gln Tyr Glu Phe Gln
545                 550                 555                 560
Val Arg Val Lys Pro Leu Gln Gly Glu Phe Thr Thr Trp Ser Pro Trp
                565                 570                 575
Ser Gln Pro Leu Ala Phe Arg Thr Lys Pro Ala Ala Leu Gly Lys Asp
            580                 585                 590
```

<210> 603
<211> 418
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 603

```
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Pro Gly Ser Gly Ala Val Asn Gly Thr Ser Gln Phe Thr Cys
225                 230                 235                 240
Phe Tyr Asn Ser Arg Ala Asn Ile Ser Cys Val Trp Ser Gln Asp Gly
                245                 250                 255
Ala Leu Gln Asp Thr Ser Cys Gln Val His Ala Trp Pro Asp Arg Arg
            260                 265                 270
Arg Trp Asn Gln Thr Cys Glu Leu Leu Pro Val Ser Gln Ala Ser Trp
        275                 280                 285
Ala Cys Asn Leu Ile Leu Gly Ala Pro Asp Ser Gln Lys Leu Thr Thr
    290                 295                 300
Val Asp Ile Val Thr Leu Arg Val Leu Cys Arg Glu Gly Val Arg Trp
305                 310                 315                 320
Arg Val Met Ala Ile Gln Asp Phe Lys Pro Phe Glu Asn Leu Arg Leu
                325                 330                 335
Met Ala Pro Ile Ser Leu Gln Val Val His Val Glu Thr His Arg Cys
            340                 345                 350
Asn Ile Ser Trp Glu Ile Ser Gln Ala Ser His Tyr Phe Glu Arg His
        355                 360                 365
Leu Glu Phe Glu Ala Arg Thr Leu Ser Pro Gly His Thr Trp Glu Glu
    370                 375                 380
Ala Pro Leu Leu Thr Leu Lys Gln Lys Gln Glu Trp Ile Cys Leu Glu
385                 390                 395                 400
Thr Leu Thr Pro Asp Thr Gln Tyr Glu Phe Gln Val Arg Val Lys Pro
                405                 410                 415
Leu Gln
```

<210> 604
<211> 370
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 604
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1   5   10   15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20   25   30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35   40   45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50   55   60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65   70   75   80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85   90   95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100   105   110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115   120   125
Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130   135   140
Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145   150   155   160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165   170   175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180   185   190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195   200   205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210   215   220
Pro Gly Gly Ser Pro Met Pro Tyr Asp Leu Tyr His Pro Ala Pro Thr
225   230   235   240
Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His Leu Leu Leu
                245   250   255
Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys Asn Pro Lys
            260   265   270
Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys Lys Ala Thr
        275   280   285
Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys Pro Leu Glu
    290   295   300
Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu Arg Pro Arg
305   310   315   320
Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu Lys Gly Ser
                325   330   335
Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala Thr Ile Val

```
            340                 345                 350
Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser Ile Ile Ser Thr
        355                 360                 365
Leu Thr
    370
```

<210> 605
<211> 374
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 605

```
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Gly Ser Pro Pro Met Pro Tyr Asp Leu Tyr His Pro Ser Gly
225                 230                 235                 240
Pro Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu
                245                 250                 255
His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr
            260                 265                 270
Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro
        275                 280                 285
Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu
    290                 295                 300
```

Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His
305 310 315 320
Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu
325 330 335
Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr
340 345 350
Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser
355 360 365
Ile Ile Ser Thr Leu Thr
370

<210> 606
<211> 374
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 606
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
1 5 10 15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
20 25 30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
35 40 45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
50 55 60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65 70 75 80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
85 90 95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
100 105 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
115 120 125
Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
130 135 140
Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145 150 155 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
165 170 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
180 185 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
195 200 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
210 215 220
Pro Gly Gly Ser Pro Ser Met Pro Tyr Asp Leu Tyr His Pro Ser Gly
225 230 235 240
Pro Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu
245 250 255
His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr

```
            260                 265                 270
Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro
        275                 280                 285
Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu
    290                 295                 300
Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His
305                 310                 315                 320
Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu
                325                 330                 335
Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr
            340                 345                 350
Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser
        355                 360                 365
Ile Ile Ser Thr Leu Thr
    370
```

<210> 607
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 607

```
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
```

```
Pro Gly Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu
225                 230                 235                 240
Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn
                245                 250                 255
Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met
            260                 265                 270
Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu
        275                 280                 285
Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe
    290                 295                 300
His Phe Asp Pro Arg Asp Val Val Ser Asn Ile Asn Val Phe Val Leu
305                 310                 315                 320
Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu
                325                 330                 335
Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln
            340                 345                 350
Ser Ile Ile Ser Thr Leu Thr
        355
```

<210> 608
<211> 376
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 608

```
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
```

```
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Gly Gly Ser Ser Pro Pro Met Pro Tyr Asp Leu Tyr His Pro
225                 230                 235                 240
Ser Gly Pro Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln
                245                 250                 255
Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn
            260                 265                 270
Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr
        275                 280                 285
Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu
    290                 295                 300
Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn
305                 310                 315                 320
Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val
                325                 330                 335
Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp
            340                 345                 350
Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala
        355                 360                 365
Gln Ser Ile Ile Ser Thr Leu Thr
    370                 375


<210> 609
<211> 419
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 609
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
```

```
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Pro Gly Ser Gly Ser Ala Val Asn Gly Thr Ser Gln Phe Thr
225                 230                 235                 240
Cys Phe Tyr Asn Ser Arg Ala Asn Ile Ser Cys Val Trp Ser Gln Asp
                245                 250                 255
Gly Ala Leu Gln Asp Thr Ser Cys Gln Val His Ala Trp Pro Asp Arg
            260                 265                 270
Arg Arg Trp Asn Gln Thr Cys Glu Leu Leu Pro Val Ser Gln Ala Ser
        275                 280                 285
Trp Ala Cys Asn Leu Ile Leu Gly Ala Pro Asp Ser Gln Lys Leu Thr
    290                 295                 300
Thr Val Asp Ile Val Thr Leu Arg Val Leu Cys Arg Glu Gly Val Arg
305                 310                 315                 320
Trp Arg Val Met Ala Ile Gln Asp Phe Lys Pro Phe Glu Asn Leu Arg
                325                 330                 335
Leu Met Ala Pro Ile Ser Leu Gln Val Val His Val Glu Thr His Arg
            340                 345                 350
Cys Asn Ile Ser Trp Glu Ile Ser Gln Ala Ser His Tyr Phe Glu Arg
        355                 360                 365
His Leu Glu Phe Glu Ala Arg Thr Leu Ser Pro Gly His Thr Trp Glu
    370                 375                 380
Glu Ala Pro Leu Leu Thr Leu Lys Gln Lys Gln Glu Trp Ile Cys Leu
385                 390                 395                 400
Glu Thr Leu Thr Pro Asp Thr Gln Tyr Glu Phe Gln Val Arg Val Lys
                405                 410                 415
Pro Leu Gln
```

<210> 610
<211> 477
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 610

```
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
```

```
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu
225                 230                 235                 240
Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn
                245                 250                 255
Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met
            260                 265                 270
Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu
        275                 280                 285
Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe
    290                 295                 300
His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu
305                 310                 315                 320
Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu
                325                 330                 335
Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln
            340                 345                 350
Ser Ile Ile Ser Thr Leu Thr Gly Pro Pro Ser Gly Ser Ser Pro Met
        355                 360                 365
Pro Tyr Asp Leu Tyr His Pro Ser Gly Gly Gly Ala Val Asn Gly Thr
    370                 375                 380
Ser Gln Phe Thr Cys Phe Tyr Asn Ser Arg Ala Asn Ile Ser Cys Val
385                 390                 395                 400
Trp Ser Gln Asp Gly Ala Leu Gln Asp Thr Ser Cys Gln Val His Ala
                405                 410                 415
Trp Pro Asp Arg Arg Arg Trp Asn Gln Thr Cys Glu Leu Leu Pro Val
            420                 425                 430
Ser Gln Ala Ser Trp Ala Cys Asn Leu Ile Leu Gly Ala Pro Asp Ser
        435                 440                 445
Gln Lys Leu Thr Thr Val Asp Ile Val Thr Leu Arg Val Leu Cys Arg
    450                 455                 460
Glu Gly Val Arg Trp Arg Val Met Ala Ile Gln Asp Phe
465                 470                 475
```

<210> 611

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

<220>
<223> Synthetic Construct

<400> 611
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1   5   10   15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20   25   30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35   40   45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50   55   60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65   70   75   80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85   90   95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100   105   110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115   120   125
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130   135   140
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145   150   155   160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165   170   175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180   185   190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195   200   205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210   215   220
Pro Gly Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu
225   230   235   240
Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn
                245   250   255
Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met
            260   265   270
Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu
        275   280   285
Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe
    290   295   300
His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu
305   310   315   320
Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu
                325   330   335
Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln
            340   345   350
Ser Ile Ile Ser Thr Leu Thr Gly Ser Ser Gly Gly Pro Pro Gly Gly
        355   360   365

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Met Pro Tyr Asp Leu Tyr His Pro Ser Gly Gly Gly Ala Val Asn Gly
    370                 375                 380
Thr Ser Gln Phe Thr Cys Phe Tyr Asn Ser Arg Ala Asn Ile Ser Cys
385                 390                 395                 400
Val Trp Ser Gln Asp Gly Ala Leu Gln Asp Thr Ser Cys Gln Val His
                405                 410                 415
Ala Trp Pro Asp Arg Arg Arg Trp Asn Gln Thr Cys Glu Leu Leu Pro
            420                 425                 430
Val Ser Gln Ala Ser Trp Ala Cys Asn Leu Ile Leu Gly Ala Pro Asp
        435                 440                 445
Ser Gln Lys Leu Thr Thr Val Asp Ile Val Thr Leu Arg Val Leu Cys
    450                 455                 460
Arg Glu Gly Val Arg Trp Arg Val Met Ala Ile Gln Asp Phe
465                 470                 475


<210> 612
<211> 479
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 612
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu
```

225 230 235 240
Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn
245 250 255
Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met
260 265 270
Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu
275 280 285
Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe
290 295 300
His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu
305 310 315 320
Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu
325 330 335
Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln
340 345 350
Ser Ile Ile Ser Thr Leu Thr Ser Gly Ser Pro Ser Gly Ser Gly Gly
355 360 365
Gly Met Pro Tyr Asp Leu Tyr His Pro Ser Gly Gly Gly Ala Val Asn
370 375 380
Gly Thr Ser Gln Phe Thr Cys Phe Tyr Asn Ser Arg Ala Asn Ile Ser
385 390 395 400
Cys Val Trp Ser Gln Asp Gly Ala Leu Gln Asp Thr Ser Cys Gln Val
405 410 415
His Ala Trp Pro Asp Arg Arg Arg Trp Asn Gln Thr Cys Glu Leu Leu
420 425 430
Pro Val Ser Gln Ala Ser Trp Ala Cys Asn Leu Ile Leu Gly Ala Pro
435 440 445
Asp Ser Gln Lys Leu Thr Thr Val Asp Ile Val Thr Leu Arg Val Leu
450 455 460
Cys Arg Glu Gly Val Arg Trp Arg Val Met Ala Ile Gln Asp Phe
465 470 475

<210> 613
<211> 479
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 613
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
1 5 10 15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
20 25 30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
35 40 45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
50 55 60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65 70 75 80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
85 90 95

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Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu
225                 230                 235                 240
Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn
                245                 250                 255
Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met
            260                 265                 270
Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu
        275                 280                 285
Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe
    290                 295                 300
His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu
305                 310                 315                 320
Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu
                325                 330                 335
Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln
            340                 345                 350
Ser Ile Ile Ser Thr Leu Thr Gly Pro Pro Gly Pro Pro Gly Ser Ser
        355                 360                 365
Gly Met Pro Tyr Asp Leu Tyr His Pro Ser Gly Gly Gly Ala Val Asn
    370                 375                 380
Gly Thr Ser Gln Phe Thr Cys Phe Tyr Asn Ser Arg Ala Asn Ile Ser
385                 390                 395                 400
Cys Val Trp Ser Gln Asp Gly Ala Leu Gln Asp Thr Ser Cys Gln Val
                405                 410                 415
His Ala Trp Pro Asp Arg Arg Arg Trp Asn Gln Thr Cys Glu Leu Leu
            420                 425                 430
Pro Val Ser Gln Ala Ser Trp Ala Cys Asn Leu Ile Leu Gly Ala Pro
        435                 440                 445
Asp Ser Gln Lys Leu Thr Thr Val Asp Ile Val Thr Leu Arg Val Leu
    450                 455                 460
Cys Arg Glu Gly Val Arg Trp Arg Val Met Ala Ile Gln Asp Phe
465                 470                 475
```

<210> 614
<211> 480
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 614
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1   5   10   15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20   25   30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35   40   45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50   55   60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65   70   75   80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85   90   95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100   105   110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115   120   125
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130   135   140
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145   150   155   160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165   170   175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180   185   190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195   200   205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210   215   220
Pro Gly Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu
225   230   235   240
Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn
                245   250   255
Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met
            260   265   270
Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu
        275   280   285
Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe
    290   295   300
His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu
305   310   315   320
Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu
                325   330   335
Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln
            340   345   350
Ser Ile Ile Ser Thr Leu Thr Gly Ser Ser Ser Gly Pro Pro Gly Pro
        355   360   365
Pro Ser Met Pro Tyr Asp Leu Tyr His Pro Ser Gly Gly Gly Ala Val
    370   375   380
Asn Gly Thr Ser Gln Phe Thr Cys Phe Tyr Asn Ser Arg Ala Asn Ile

385 390 395 400
Ser Cys Val Trp Ser Gln Asp Gly Ala Leu Gln Asp Thr Ser Cys Gln
405 410 415
Val His Ala Trp Pro Asp Arg Arg Arg Trp Asn Gln Thr Cys Glu Leu
420 425 430
Leu Pro Val Ser Gln Ala Ser Trp Ala Cys Asn Leu Ile Leu Gly Ala
435 440 445
Pro Asp Ser Gln Lys Leu Thr Thr Val Asp Ile Val Thr Leu Arg Val
450 455 460
Leu Cys Arg Glu Gly Val Arg Trp Arg Val Met Ala Ile Gln Asp Phe
465 470 475 480

<210> 615
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 615
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
1 5 10 15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
20 25 30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
35 40 45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
50 55 60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65 70 75 80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
85 90 95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
100 105 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
115 120 125
Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
130 135 140
Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145 150 155 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
165 170 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val
180 185 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
195 200 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
210 215 220
Pro Gly Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu
225 230 235 240
Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn
245 250 255

Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met
            260   265   270
Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu
        275   280   285
Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe
    290   295   300
His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu
305   310   315   320
Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu
                325   330   335
Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln
            340   345   350
Ser Ile Ile Ser Thr Leu Thr
        355

<210> 616
<211> 227
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 616
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1   5   10   15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20   25   30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35   40   45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50   55   60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65   70   75   80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85   90   95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100   105   110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115   120   125
Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130   135   140
Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145   150   155   160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165   170   175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180   185   190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195   200   205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210   215   220
Pro Gly Lys

225

<210> 617
<211> 434
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 617
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1   5   10   15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20   25   30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35   40   45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50   55   60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65   70   75   80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85   90   95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100   105   110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115   120   125
Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130   135   140
Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145   150   155   160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165   170   175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180   185   190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195   200   205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210   215   220
Pro Gly Gly Pro Pro Ser Gly Ser Ser Pro Met Pro Tyr Asp Leu Tyr
225   230   235   240
His Pro Ser Gly Gly Gly Ala Val Asn Gly Thr Ser Gln Phe Thr Cys
                245   250   255
Phe Tyr Asn Ser Arg Ala Asn Ile Ser Cys Val Trp Ser Gln Asp Gly
            260   265   270
Ala Leu Gln Asp Thr Ser Cys Gln Val His Ala Trp Pro Asp Arg Arg
        275   280   285
Arg Trp Asn Gln Thr Cys Glu Leu Leu Pro Val Ser Gln Ala Ser Trp
    290   295   300
Ala Cys Asn Leu Ile Leu Gly Ala Pro Asp Ser Gln Lys Leu Thr Thr
305   310   315   320
Val Asp Ile Val Thr Leu Arg Val Leu Cys Arg Glu Gly Val Arg Trp
                325   330   335

Arg Val Met Ala Ile Gln Asp Phe Lys Pro Phe Glu Asn Leu Arg Leu
            340   345   350
Met Ala Pro Ile Ser Leu Gln Val Val His Val Glu Thr His Arg Cys
        355   360   365
Asn Ile Ser Trp Glu Ile Ser Gln Ala Ser His Tyr Phe Glu Arg His
    370   375   380
Leu Glu Phe Glu Ala Arg Thr Leu Ser Pro Gly His Thr Trp Glu Glu
385   390   395   400
Ala Pro Leu Leu Thr Leu Lys Gln Lys Gln Glu Trp Ile Cys Leu Glu
                405   410   415
Thr Leu Thr Pro Asp Thr Gln Tyr Glu Phe Gln Val Arg Val Lys Pro
            420   425   430
Leu Gln

<210> 618
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 618
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1   5   10   15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20   25   30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35   40   45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50   55   60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65   70   75   80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85   90   95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100   105   110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115   120   125
Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130   135   140
Leu Thr Cys Leu Val Glu Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145   150   155   160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165   170   175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180   185   190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195   200   205
His Glu Ala Leu His Asn His Tyr Thr Gln Glu Ser Leu Ser Leu Ser
    210   215   220
Pro Gly Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu

225 230 235 240
Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn
245 250 255
Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met
260 265 270
Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu
275 280 285
Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe
290 295 300
His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu
305 310 315 320
Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu
325 330 335
Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln
340 345 350
Ser Ile Ile Ser Thr Leu Thr
355

<210> 619
<211> 227
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 619
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
1 5 10 15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
20 25 30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
35 40 45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
50 55 60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65 70 75 80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
85 90 95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
100 105 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
115 120 125
Tyr Thr Leu Pro Pro Cys Arg Lys Lys Leu Thr Lys Asn Gln Val Ser
130 135 140
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145 150 155 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
165 170 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
180 185 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
195 200 205

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
210 215 220
Pro Gly Lys
225

<210> 620
<211> 434
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 620
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
1 5 10 15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
20 25 30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
35 40 45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
50 55 60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65 70 75 80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
85 90 95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
100 105 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
115 120 125
Tyr Thr Leu Pro Pro Cys Arg Lys Lys Leu Thr Lys Asn Gln Val Ser
130 135 140
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145 150 155 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
165 170 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
180 185 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
195 200 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
210 215 220
Pro Gly Gly Pro Pro Ser Gly Ser Ser Pro Met Pro Tyr Asp Leu Tyr
225 230 235 240
His Pro Ser Gly Gly Gly Ala Val Asn Gly Thr Ser Gln Phe Thr Cys
245 250 255
Phe Tyr Asn Ser Arg Ala Asn Ile Ser Cys Val Trp Ser Gln Asp Gly
260 265 270
Ala Leu Gln Asp Thr Ser Cys Gln Val His Ala Trp Pro Asp Arg Arg
275 280 285
Arg Trp Asn Gln Thr Cys Glu Leu Leu Pro Val Ser Gln Ala Ser Trp
290 295 300
Ala Cys Asn Leu Ile Leu Gly Ala Pro Asp Ser Gln Lys Leu Thr Thr

305 310 315 320
Val Asp Ile Val Thr Leu Arg Val Leu Cys Arg Glu Gly Val Arg Trp
325 330 335
Arg Val Met Ala Ile Gln Asp Phe Lys Pro Phe Glu Asn Leu Arg Leu
340 345 350
Met Ala Pro Ile Ser Leu Gln Val Val His Val Glu Thr His Arg Cys
355 360 365
Asn Ile Ser Trp Glu Ile Ser Gln Ala Ser His Tyr Phe Glu Arg His
370 375 380
Leu Glu Phe Glu Ala Arg Thr Leu Ser Pro Gly His Thr Trp Glu Glu
385 390 395 400
Ala Pro Leu Leu Thr Leu Lys Gln Lys Gln Glu Trp Ile Cys Leu Glu
405 410 415
Thr Leu Thr Pro Asp Thr Gln Tyr Glu Phe Gln Val Arg Val Lys Pro
420 425 430
Leu Gln

<210> 621
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 621
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
1 5 10 15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
20 25 30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
35 40 45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
50 55 60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65 70 75 80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
85 90 95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
100 105 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
115 120 125
Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
130 135 140
Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145 150 155 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Asp Thr Thr Pro Pro
165 170 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Asp Leu Thr Val
180 185 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
195 200 205

```
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu
225                 230                 235                 240
Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn
                245                 250                 255
Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met
            260                 265                 270
Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu
        275                 280                 285
Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe
    290                 295                 300
His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu
305                 310                 315                 320
Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu
                325                 330                 335
Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln
            340                 345                 350
Ser Ile Ile Ser Thr Leu Thr
        355


<210> 622
<211> 227
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 622
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Tyr Thr Leu Pro Pro Cys Arg Lys Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Lys Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
```

```
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Lys
225
```

<210> 623
<211> 434
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 623

```
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Tyr Thr Leu Pro Pro Cys Arg Lys Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Lys Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Gly Pro Pro Ser Gly Ser Ser Pro Met Pro Tyr Asp Leu Tyr
225                 230                 235                 240
His Pro Ser Gly Gly Gly Ala Val Asn Gly Thr Ser Gln Phe Thr Cys
                245                 250                 255
Phe Tyr Asn Ser Arg Ala Asn Ile Ser Cys Val Trp Ser Gln Asp Gly
            260                 265                 270
Ala Leu Gln Asp Thr Ser Cys Gln Val His Ala Trp Pro Asp Arg Arg
        275                 280                 285
```

```
Arg Trp Asn Gln Thr Cys Glu Leu Leu Pro Val Ser Gln Ala Ser Trp
    290                 295                 300
Ala Cys Asn Leu Ile Leu Gly Ala Pro Asp Ser Gln Lys Leu Thr Thr
305                 310                 315                 320
Val Asp Ile Val Thr Leu Arg Val Leu Cys Arg Glu Gly Val Arg Trp
                325                 330                 335
Arg Val Met Ala Ile Gln Asp Phe Lys Pro Phe Glu Asn Leu Arg Leu
            340                 345                 350
Met Ala Pro Ile Ser Leu Gln Val Val His Val Glu Thr His Arg Cys
        355                 360                 365
Asn Ile Ser Trp Glu Ile Ser Gln Ala Ser His Tyr Phe Glu Arg His
    370                 375                 380
Leu Glu Phe Glu Ala Arg Thr Leu Ser Pro Gly His Thr Trp Glu Glu
385                 390                 395                 400
Ala Pro Leu Leu Thr Leu Lys Gln Lys Gln Glu Trp Ile Cys Leu Glu
                405                 410                 415
Thr Leu Thr Pro Asp Thr Gln Tyr Glu Phe Gln Val Arg Val Lys Pro
            420                 425                 430
Leu Gln
```

<210> 624
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 624

```
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Ser Cys Ala Val Glu Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val
```

```
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Glu Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu
225                 230                 235                 240
Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn
                245                 250                 255
Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met
            260                 265                 270
Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu
        275                 280                 285
Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe
    290                 295                 300
His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu
305                 310                 315                 320
Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu
                325                 330                 335
Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln
            340                 345                 350
Ser Ile Ile Ser Thr Leu Thr
        355
```

<210> 625
<211> 227
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 625

```
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Tyr Thr Leu Pro Pro Cys Arg Lys Lys Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
```

```
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Lys
225
```

<210> 626
<211> 434
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 626

```
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Tyr Thr Leu Pro Pro Cys Arg Lys Lys Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Gly Pro Pro Ser Gly Ser Ser Pro Met Pro Tyr Asp Leu Tyr
225                 230                 235                 240
His Pro Ser Gly Gly Gly Ala Val Asn Gly Thr Ser Gln Phe Thr Cys
                245                 250                 255
Phe Tyr Asn Ser Arg Ala Asn Ile Ser Cys Val Trp Ser Gln Asp Gly
```

```
            260                 265                 270
Ala Leu Gln Asp Thr Ser Cys Gln Val His Ala Trp Pro Asp Arg Arg
        275                 280                 285
Arg Trp Asn Gln Thr Cys Glu Leu Leu Pro Val Ser Gln Ala Ser Trp
    290                 295                 300
Ala Cys Asn Leu Ile Leu Gly Ala Pro Asp Ser Gln Lys Leu Thr Thr
305                 310                 315                 320
Val Asp Ile Val Thr Leu Arg Val Leu Cys Arg Glu Gly Val Arg Trp
                325                 330                 335
Arg Val Met Ala Ile Gln Asp Phe Lys Pro Phe Glu Asn Leu Arg Leu
            340                 345                 350
Met Ala Pro Ile Ser Leu Gln Val Val His Val Glu Thr His Arg Cys
        355                 360                 365
Asn Ile Ser Trp Glu Ile Ser Gln Ala Ser His Tyr Phe Glu Arg His
    370                 375                 380
Leu Glu Phe Glu Ala Arg Thr Leu Ser Pro Gly His Thr Trp Glu Glu
385                 390                 395                 400
Ala Pro Leu Leu Thr Leu Lys Gln Lys Gln Glu Trp Ile Cys Leu Glu
                405                 410                 415
Thr Leu Thr Pro Asp Thr Gln Tyr Glu Phe Gln Val Arg Val Lys Pro
            420                 425                 430
Leu Gln
```

<210> 627
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 627

```
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
```

```
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu
225                 230                 235                 240
Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn
                245                 250                 255
Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met
            260                 265                 270
Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu
        275                 280                 285
Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe
    290                 295                 300
His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu
305                 310                 315                 320
Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu
                325                 330                 335
Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln
            340                 345                 350
Ser Ile Ile Ser Thr Leu Thr Pro Gly Pro Gly Pro Met Pro Tyr Asp
        355                 360                 365
Leu Tyr His Pro Ser Gly Gly Cys Gly Gly His Gln Tyr Glu Arg Arg
    370                 375                 380
Gly Gly Cys
385
```

<210> 628
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 628

```
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
```

```
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu
225                 230                 235                 240
Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn
                245                 250                 255
Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met
            260                 265                 270
Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu
        275                 280                 285
Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe
    290                 295                 300
His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu
305                 310                 315                 320
Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu
                325                 330                 335
Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln
            340                 345                 350
Ser Ile Ile Ser Thr Leu Thr Pro Gly Pro Gly Pro Met Pro Tyr Asp
        355                 360                 365
Leu Tyr His Pro Ser Gly Gly Cys Ser Gly His Gln Tyr Glu Arg Arg
    370                 375                 380
Glu Gly Cys
385
```

<210> 629
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 629

```
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
```

```
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu
225                 230                 235                 240
Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn
                245                 250                 255
Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met
            260                 265                 270
Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu
        275                 280                 285
Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe
    290                 295                 300
His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu
305                 310                 315                 320
Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu
                325                 330                 335
Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln
            340                 345                 350
Ser Ile Ile Ser Thr Leu Thr Pro Gly Pro Gly Pro Met Pro Tyr Asp
        355                 360                 365
Leu Tyr His Pro Ser Gly Gly Cys Gly Gly His Tyr Phe Glu Arg His
    370                 375                 380
Gly Gly Cys
385
```

<210> 630
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 630
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1   5   10   15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20   25   30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35   40   45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50   55   60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65   70   75   80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85   90   95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100   105   110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115   120   125
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130   135   140
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145   150   155   160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165   170   175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180   185   190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195   200   205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210   215   220
Pro Gly Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu
225   230   235   240
Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn
                245   250   255
Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met
            260   265   270
Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu
        275   280   285
Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe
    290   295   300
His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu
305   310   315   320
Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu
                325   330   335
Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln
            340   345   350
Ser Ile Ile Ser Thr Leu Thr Pro Gly Pro Gly Pro Met Pro Tyr Asp
        355   360   365
Leu Tyr His Pro Ser Gly Gly Cys Ser Gly His Tyr Phe Glu Arg His
    370   375   380
Glu Gly Cys
385

<210> 631

<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 631
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1   5   10   15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20   25   30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35   40   45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50   55   60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65   70   75   80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85   90   95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100   105   110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115   120   125
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130   135   140
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145   150   155   160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165   170   175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180   185   190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195   200   205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210   215   220
Pro Gly Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu
225   230   235   240
Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn
                245   250   255
Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met
            260   265   270
Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu
        275   280   285
Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe
    290   295   300
His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu
305   310   315   320
Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu
                325   330   335
Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln
            340   345   350
Ser Ile Ile Ser Thr Leu Thr Pro Gly Pro Gly Pro Met Pro Tyr Asp
        355   360   365

```
Leu Tyr His Pro Ser Gly Gly Cys Ser Phe His Gln Tyr Glu Arg His
    370                 375                 380
Glu Gly Cys
385
```

<210> 632
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 632

```
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu
225                 230                 235                 240
Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn
                245                 250                 255
Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met
            260                 265                 270
Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu
        275                 280                 285
Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe
    290                 295                 300
His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu
```

305 310 315 320
Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu
325 330 335
Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln
340 345 350
Ser Ile Ile Ser Thr Leu Thr Pro Ser Gly Ser Ser Met Pro Tyr Asp
355 360 365
Leu Tyr His Pro Ser Gly Gly Cys Gly Gly His Gln Tyr Glu Arg Arg
370 375 380
Gly Gly Cys
385

<210> 633
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 633
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
1 5 10 15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
20 25 30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
35 40 45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
50 55 60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65 70 75 80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
85 90 95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
100 105 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
115 120 125
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
130 135 140
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145 150 155 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
165 170 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
180 185 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
195 200 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
210 215 220
Pro Gly Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu
225 230 235 240
Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn
245 250 255

```
Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met
            260                 265                 270
Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu
        275                 280                 285
Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe
    290                 295                 300
His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu
305                 310                 315                 320
Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu
                325                 330                 335
Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln
            340                 345                 350
Ser Ile Ile Ser Thr Leu Thr Pro Ser Gly Ser Ser Met Pro Tyr Asp
        355                 360                 365
Leu Tyr His Pro Ser Gly Gly Cys Ser Gly His Gln Tyr Glu Arg Arg
    370                 375                 380
Glu Gly Cys
385
```

<210> 634
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 634

```
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
```

```
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu
225                 230                 235                 240
Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn
                245                 250                 255
Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met
            260                 265                 270
Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu
        275                 280                 285
Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe
    290                 295                 300
His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu
305                 310                 315                 320
Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu
                325                 330                 335
Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln
            340                 345                 350
Ser Ile Ile Ser Thr Leu Thr Pro Ser Gly Ser Ser Met Pro Tyr Asp
        355                 360                 365
Leu Tyr His Pro Ser Gly Gly Cys Gly Gly His Tyr Phe Glu Arg His
    370                 375                 380
Gly Gly Cys
385
```

<210> 635
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 635

```
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
```

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145 150 155 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
165 170 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
180 185 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
195 200 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
210 215 220
Pro Gly Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu
225 230 235 240
Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn
245 250 255
Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met
260 265 270
Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu
275 280 285
Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe
290 295 300
His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu
305 310 315 320
Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu
325 330 335
Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln
340 345 350
Ser Ile Ile Ser Thr Leu Thr Pro Ser Gly Ser Ser Met Pro Tyr Asp
355 360 365
Leu Tyr His Pro Ser Gly Gly Cys Ser Gly His Tyr Phe Glu Arg His
370 375 380
Glu Gly Cys
385

<210> 636
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 636
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
1 5 10 15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
20 25 30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
35 40 45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
50 55 60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65 70 75 80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly

```
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu
225                 230                 235                 240
Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn
                245                 250                 255
Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met
            260                 265                 270
Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu
        275                 280                 285
Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe
    290                 295                 300
His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu
305                 310                 315                 320
Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu
                325                 330                 335
Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln
            340                 345                 350
Ser Ile Ile Ser Thr Leu Thr Pro Ser Gly Ser Ser Met Pro Tyr Asp
        355                 360                 365
Leu Tyr His Pro Ser Gly Gly Cys Ser Phe His Gln Tyr Glu Arg His
    370                 375                 380
Glu Gly Cys
385
```

<210> 637
<211> 444
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 637

```
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
```

```
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Pro Gly Ser Gly Ser Ala Val Asn Gly Thr Ser Gln Phe Thr
225                 230                 235                 240
Cys Phe Tyr Asn Ser Arg Ala Asn Ile Ser Cys Val Trp Ser Gln Asp
                245                 250                 255
Gly Ala Leu Gln Asp Thr Ser Cys Gln Val His Ala Trp Pro Asp Arg
            260                 265                 270
Arg Arg Trp Asn Gln Thr Cys Glu Leu Leu Pro Val Ser Gln Ala Ser
        275                 280                 285
Trp Ala Cys Asn Leu Ile Leu Gly Ala Pro Asp Ser Gln Lys Leu Thr
    290                 295                 300
Thr Val Asp Ile Val Thr Leu Arg Val Leu Cys Arg Glu Gly Val Arg
305                 310                 315                 320
Trp Arg Val Met Ala Ile Gln Asp Phe Lys Pro Phe Glu Asn Leu Arg
                325                 330                 335
Leu Met Ala Pro Ile Ser Leu Gln Val Val His Val Glu Thr His Arg
            340                 345                 350
Cys Asn Ile Ser Trp Glu Ile Ser Gln Ala Ser His Tyr Phe Glu Arg
        355                 360                 365
His Leu Glu Phe Glu Ala Arg Thr Leu Ser Pro Gly His Thr Trp Glu
    370                 375                 380
Glu Ala Pro Leu Leu Thr Leu Lys Gln Lys Gln Glu Trp Ile Cys Leu
385                 390                 395                 400
Glu Thr Leu Thr Pro Asp Thr Gln Tyr Glu Phe Gln Val Arg Val Lys
                405                 410                 415
Pro Leu Gln Gly Glu Phe Thr Thr Trp Ser Pro Trp Ser Gln Pro Leu
            420                 425                 430
Ala Phe Arg Thr Lys Pro Ala Ala Leu Gly Lys Asp
        435                 440
```

<210> 638
<211> 459
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 638
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1   5   10   15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20   25   30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35   40   45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50   55   60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65   70   75   80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85   90   95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100   105   110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115   120   125
Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130   135   140
Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145   150   155   160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165   170   175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180   185   190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195   200   205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210   215   220
Pro Gly Gly Pro Pro Ser Gly Ser Ser Pro Met Pro Tyr Asp Leu Tyr
225   230   235   240
His Pro Ser Gly Gly Gly Ala Val Asn Gly Thr Ser Gln Phe Thr Cys
                245   250   255
Phe Tyr Asn Ser Arg Ala Asn Ile Ser Cys Val Trp Ser Gln Asp Gly
            260   265   270
Ala Leu Gln Asp Thr Ser Cys Gln Val His Ala Trp Pro Asp Arg Arg
        275   280   285
Arg Trp Asn Gln Thr Cys Glu Leu Leu Pro Val Ser Gln Ala Ser Trp
    290   295   300
Ala Cys Asn Leu Ile Leu Gly Ala Pro Asp Ser Gln Lys Leu Thr Thr
305   310   315   320
Val Asp Ile Val Thr Leu Arg Val Leu Cys Arg Glu Gly Val Arg Trp
                325   330   335
Arg Val Met Ala Ile Gln Asp Phe Lys Pro Phe Glu Asn Leu Arg Leu
            340   345   350
Met Ala Pro Ile Ser Leu Gln Val Val His Val Glu Thr His Arg Cys

```
        355                 360                 365
Asn Ile Ser Trp Glu Ile Ser Gln Ala Ser His Tyr Phe Glu Arg His
    370                 375                 380
Leu Glu Phe Glu Ala Arg Thr Leu Ser Pro Gly His Thr Trp Glu Glu
385                 390                 395                 400
Ala Pro Leu Leu Thr Leu Lys Gln Lys Gln Glu Trp Ile Cys Leu Glu
                405                 410                 415
Thr Leu Thr Pro Asp Thr Gln Tyr Glu Phe Gln Val Arg Val Lys Pro
            420                 425                 430
Leu Gln Gly Glu Phe Thr Thr Trp Ser Pro Trp Ser Gln Pro Leu Ala
        435                 440                 445
Phe Arg Thr Lys Pro Ala Ala Leu Gly Lys Asp
    450                 455


<210> 639
<211> 459
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 639
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Tyr Thr Leu Pro Pro Cys Arg Lys Lys Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Gly Pro Pro Ser Gly Ser Ser Pro Met Pro Tyr Asp Leu Tyr
225                 230                 235                 240
```

```
His Pro Ser Gly Gly Gly Ala Val Asn Gly Thr Ser Gln Phe Thr Cys
                245                 250                 255
Phe Tyr Asn Ser Arg Ala Asn Ile Ser Cys Val Trp Ser Gln Asp Gly
            260                 265                 270
Ala Leu Gln Asp Thr Ser Cys Gln Val His Ala Trp Pro Asp Arg Arg
        275                 280                 285
Arg Trp Asn Gln Thr Cys Glu Leu Leu Pro Val Ser Gln Ala Ser Trp
    290                 295                 300
Ala Cys Asn Leu Ile Leu Gly Ala Pro Asp Ser Gln Lys Leu Thr Thr
305                 310                 315                 320
Val Asp Ile Val Thr Leu Arg Val Leu Cys Arg Glu Gly Val Arg Trp
                325                 330                 335
Arg Val Met Ala Ile Gln Asp Phe Lys Pro Phe Glu Asn Leu Arg Leu
            340                 345                 350
Met Ala Pro Ile Ser Leu Gln Val Val His Val Glu Thr His Arg Cys
        355                 360                 365
Asn Ile Ser Trp Glu Ile Ser Gln Ala Ser His Tyr Phe Glu Arg His
    370                 375                 380
Leu Glu Phe Glu Ala Arg Thr Leu Ser Pro Gly His Thr Trp Glu Glu
385                 390                 395                 400
Ala Pro Leu Leu Thr Leu Lys Gln Lys Gln Glu Trp Ile Cys Leu Glu
                405                 410                 415
Thr Leu Thr Pro Asp Thr Gln Tyr Glu Phe Gln Val Arg Val Lys Pro
            420                 425                 430
Leu Gln Gly Glu Phe Thr Thr Trp Ser Pro Trp Ser Gln Pro Leu Ala
        435                 440                 445
Phe Arg Thr Lys Pro Ala Ala Leu Gly Lys Asp
    450                 455
```

<210> 640
<211> 459
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 640

```
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
```

```
        115                 120                 125
Tyr Thr Leu Pro Pro Cys Arg Lys Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Lys Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Gly Pro Pro Ser Gly Ser Ser Pro Met Pro Tyr Asp Leu Tyr
225                 230                 235                 240
His Pro Ser Gly Gly Gly Ala Val Asn Gly Thr Ser Gln Phe Thr Cys
                245                 250                 255
Phe Tyr Asn Ser Arg Ala Asn Ile Ser Cys Val Trp Ser Gln Asp Gly
            260                 265                 270
Ala Leu Gln Asp Thr Ser Cys Gln Val His Ala Trp Pro Asp Arg Arg
        275                 280                 285
Arg Trp Asn Gln Thr Cys Glu Leu Leu Pro Val Ser Gln Ala Ser Trp
    290                 295                 300
Ala Cys Asn Leu Ile Leu Gly Ala Pro Asp Ser Gln Lys Leu Thr Thr
305                 310                 315                 320
Val Asp Ile Val Thr Leu Arg Val Leu Cys Arg Glu Gly Val Arg Trp
                325                 330                 335
Arg Val Met Ala Ile Gln Asp Phe Lys Pro Phe Glu Asn Leu Arg Leu
            340                 345                 350
Met Ala Pro Ile Ser Leu Gln Val Val His Val Glu Thr His Arg Cys
        355                 360                 365
Asn Ile Ser Trp Glu Ile Ser Gln Ala Ser His Tyr Phe Glu Arg His
    370                 375                 380
Leu Glu Phe Glu Ala Arg Thr Leu Ser Pro Gly His Thr Trp Glu Glu
385                 390                 395                 400
Ala Pro Leu Leu Thr Leu Lys Gln Lys Gln Glu Trp Ile Cys Leu Glu
                405                 410                 415
Thr Leu Thr Pro Asp Thr Gln Tyr Glu Phe Gln Val Arg Val Lys Pro
            420                 425                 430
Leu Gln Gly Glu Phe Thr Thr Trp Ser Pro Trp Ser Gln Pro Leu Ala
        435                 440                 445
Phe Arg Thr Lys Pro Ala Ala Leu Gly Lys Asp
    450                 455
```

<210> 641
<211> 459
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 641

```
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Tyr Thr Leu Pro Pro Cys Arg Lys Lys Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Gly Pro Pro Ser Gly Ser Ser Pro Met Pro Tyr Asp Leu Tyr
225                 230                 235                 240
His Pro Ser Gly Gly Gly Ala Val Asn Gly Thr Ser Gln Phe Thr Cys
                245                 250                 255
Phe Tyr Asn Ser Arg Ala Asn Ile Ser Cys Val Trp Ser Gln Asp Gly
            260                 265                 270
Ala Leu Gln Asp Thr Ser Cys Gln Val His Ala Trp Pro Asp Arg Arg
        275                 280                 285
Arg Trp Asn Gln Thr Cys Glu Leu Leu Pro Val Ser Gln Ala Ser Trp
    290                 295                 300
Ala Cys Asn Leu Ile Leu Gly Ala Pro Asp Ser Gln Lys Leu Thr Thr
305                 310                 315                 320
Val Asp Ile Val Thr Leu Arg Val Leu Cys Arg Glu Gly Val Arg Trp
                325                 330                 335
Arg Val Met Ala Ile Gln Asp Phe Lys Pro Phe Glu Asn Leu Arg Leu
            340                 345                 350
Met Ala Pro Ile Ser Leu Gln Val Val His Val Glu Thr His Arg Cys
        355                 360                 365
Asn Ile Ser Trp Glu Ile Ser Gln Ala Ser His Tyr Phe Glu Arg His
    370                 375                 380
Leu Glu Phe Glu Ala Arg Thr Leu Ser Pro Gly His Thr Trp Glu Glu
385                 390                 395                 400
Ala Pro Leu Leu Thr Leu Lys Gln Lys Gln Glu Trp Ile Cys Leu Glu
                405                 410                 415
Thr Leu Thr Pro Asp Thr Gln Tyr Glu Phe Gln Val Arg Val Lys Pro
            420                 425                 430
```

Leu Gln Gly Glu Phe Thr Thr Trp Ser Pro Trp Ser Gln Pro Leu Ala
435 440 445
Phe Arg Thr Lys Pro Ala Ala Leu Gly Lys Asp
450 455

<210> 642
<211> 592
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 642
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
1 5 10 15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
20 25 30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
35 40 45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
50 55 60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65 70 75 80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
85 90 95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
100 105 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
115 120 125
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
130 135 140
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145 150 155 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
165 170 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
180 185 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
195 200 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
210 215 220
Pro Gly Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu
225 230 235 240
Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn
245 250 255
Tyr Lys Asn Pro Lys Leu Thr Ala Met Leu Thr Ala Lys Phe Ala Met
260 265 270
Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Ala
275 280 285
Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe
290 295 300
His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu

305 310 315 320
Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu
325 330 335
Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln
340 345 350
Ser Ile Ile Ser Thr Leu Thr Gly Pro Pro Ser Gly Ser Ser Pro Met
355 360 365
Pro Tyr Asp Leu Tyr His Pro Ser Gly Gly Gly Ala Val Asn Gly Thr
370 375 380
Ser Gln Phe Thr Cys Phe Tyr Asn Ser Arg Ala Asn Ile Ser Cys Val
385 390 395 400
Trp Ser Gln Asp Gly Ala Leu Gln Asp Thr Ser Cys Gln Val His Ala
405 410 415
Trp Pro Asp Arg Arg Arg Trp Asn Gln Thr Cys Glu Leu Leu Pro Val
420 425 430
Ser Gln Ala Ser Trp Ala Cys Asn Leu Ile Leu Gly Ala Pro Asp Ser
435 440 445
Gln Lys Leu Thr Thr Val Asp Ile Val Thr Leu Arg Val Leu Cys Arg
450 455 460
Glu Gly Val Arg Trp Arg Val Met Ala Ile Gln Asp Phe Lys Pro Phe
465 470 475 480
Glu Asn Leu Arg Leu Met Ala Pro Ile Ser Leu Gln Val Val His Val
485 490 495
Glu Thr His Arg Cys Asn Ile Ser Trp Glu Ile Ser Gln Ala Ser His
500 505 510
Tyr Phe Glu Arg His Leu Glu Phe Glu Ala Arg Thr Leu Ser Pro Gly
515 520 525
His Thr Trp Glu Glu Ala Pro Leu Leu Thr Leu Lys Gln Lys Gln Glu
530 535 540
Trp Ile Cys Leu Glu Thr Leu Thr Pro Asp Thr Gln Tyr Glu Phe Gln
545 550 555 560
Val Arg Val Lys Pro Leu Gln Gly Glu Phe Thr Thr Trp Ser Pro Trp
565 570 575
Ser Gln Pro Leu Ala Phe Arg Thr Lys Pro Ala Ala Leu Gly Lys Asp
580 585 590

<210> 643
<211> 592
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 643
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
1 5 10 15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
20 25 30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
35 40 45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
50 55 60

```
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu
225                 230                 235                 240
Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn
                245                 250                 255
Tyr Lys Asn Pro Lys Leu Thr Ala Met Leu Thr Ala Lys Phe Ala Met
            260                 265                 270
Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Ala
        275                 280                 285
Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe
    290                 295                 300
His Phe Asp Pro Arg Asp Val Val Ser Asn Ile Asn Val Phe Val Leu
305                 310                 315                 320
Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu
                325                 330                 335
Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln
            340                 345                 350
Ser Ile Ile Ser Thr Leu Thr Gly Pro Pro Ser Gly Ser Ser Pro Met
        355                 360                 365
Pro Tyr Asp Leu Tyr His Pro Ser Gly Gly Gly Ala Val Asn Gly Thr
    370                 375                 380
Ser Gln Phe Thr Cys Phe Tyr Asn Ser Arg Ala Asn Ile Ser Cys Val
385                 390                 395                 400
Trp Ser Gln Asp Gly Ala Leu Gln Asp Thr Ser Cys Gln Val His Ala
                405                 410                 415
Trp Pro Asp Arg Arg Arg Trp Asn Gln Thr Cys Glu Leu Leu Pro Val
            420                 425                 430
Ser Gln Ala Ser Trp Ala Cys Asn Leu Ile Leu Gly Ala Pro Asp Ser
        435                 440                 445
Gln Lys Leu Thr Thr Val Asp Ile Val Thr Leu Arg Val Leu Cys Arg
    450                 455                 460
Glu Gly Val Arg Trp Arg Val Met Ala Ile Gln Asp Phe Lys Pro Phe
465                 470                 475                 480
Glu Asn Leu Arg Leu Met Ala Pro Ile Ser Leu Gln Val Val His Val
                485                 490                 495
```

```
Glu Thr His Arg Cys Asn Ile Ser Trp Glu Ile Ser Gln Ala Ser His
            500                 505                 510
Tyr Phe Glu Arg His Leu Glu Phe Glu Ala Arg Thr Leu Ser Pro Gly
        515                 520                 525
His Thr Trp Glu Glu Ala Pro Leu Leu Thr Leu Lys Gln Lys Gln Glu
    530                 535                 540
Trp Ile Cys Leu Glu Thr Leu Thr Pro Asp Thr Gln Tyr Glu Phe Gln
545                 550                 555                 560
Val Arg Val Lys Pro Leu Gln Gly Glu Phe Thr Thr Trp Ser Pro Trp
                565                 570                 575
Ser Gln Pro Leu Ala Phe Arg Thr Lys Pro Ala Ala Leu Gly Lys Asp
            580                 585                 590


<210> 644
<211> 419
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 644
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Pro Gly Ser Gly Ser Ala Val Asn Gly Thr Ser Gln Phe Thr
225                 230                 235                 240
Cys Phe Tyr Asn Ser Arg Ala Asn Ile Ser Cys Val Trp Ser Gln Asp
```

```
                245                 250                 255
Gly Ala Leu Gln Asp Thr Ser Cys Gln Val His Ala Trp Pro Asp Arg
            260                 265                 270
Arg Arg Trp Asn Gln Thr Cys Glu Leu Leu Pro Val Ser Gln Ala Ser
        275                 280                 285
Trp Ala Cys Asn Leu Ile Leu Gly Ala Pro Asp Ser Gln Lys Leu Thr
    290                 295                 300
Thr Val Asp Ile Val Thr Leu Arg Val Leu Cys Arg Glu Gly Val Arg
305                 310                 315                 320
Trp Arg Val Met Ala Ile Gln Asp Phe Lys Pro Phe Glu Asn Leu Arg
                325                 330                 335
Leu Met Ala Pro Ile Ser Leu Gln Val Val His Val Glu Thr His Arg
            340                 345                 350
Cys Asn Ile Ser Trp Glu Ile Ser Gln Ala Ser His Tyr Phe Glu Arg
        355                 360                 365
His Leu Glu Phe Glu Ala Arg Thr Leu Ser Pro Gly His Thr Trp Glu
    370                 375                 380
Glu Ala Pro Leu Leu Thr Leu Lys Gln Lys Gln Glu Trp Ile Cys Leu
385                 390                 395                 400
Glu Thr Leu Thr Pro Asp Thr Gln Tyr Glu Phe Gln Val Arg Val Lys
                405                 410                 415
Pro Leu Gln
```

<210> 645
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 645

```
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
```

```
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu
225                 230                 235                 240
Glu Ile Leu Cys Leu Leu Leu Gln Met Ile Leu Asn Gly Ile Leu Asn
                245                 250                 255
Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met
            260                 265                 270
Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu
        275                 280                 285
Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe
    290                 295                 300
His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu
305                 310                 315                 320
Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu
                325                 330                 335
Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Cys Gln
            340                 345                 350
Ser Ile Ile Ser Thr Leu Thr
        355
```

<210> 646
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 646

```
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
```

```
    130                 135                 140
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu
225                 230                 235                 240
Glu Ile Leu Leu Leu Leu Leu Gln Met Ile Leu Asn Gly Ile Leu Asn
                245                 250                 255
Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met
            260                 265                 270
Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu
        275                 280                 285
Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe
    290                 295                 300
His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu
305                 310                 315                 320
Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu
                325                 330                 335
Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ile Gln
            340                 345                 350
Ser Ile Ile Ser Thr Leu Thr
        355
```

<210> 647
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 647

```
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
```

```
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu
225                 230                 235                 240
Glu Ile Leu Cys Leu Phe Leu Gln Met Ile Leu Asn Gly Ile Leu Asn
                245                 250                 255
Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met
            260                 265                 270
Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu
        275                 280                 285
Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe
    290                 295                 300
His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu
305                 310                 315                 320
Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu
                325                 330                 335
Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Cys Gln
            340                 345                 350
Ser Ile Ile Ser Thr Leu Thr
        355
```

<210> 648
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 648

```
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
```

```
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu
225                 230                 235                 240
Glu Ile Leu Leu Leu Phe Leu Gln Met Ile Leu Asn Gly Ile Leu Asn
                245                 250                 255
Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met
            260                 265                 270
Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu
        275                 280                 285
Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe
    290                 295                 300
His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu
305                 310                 315                 320
Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu
                325                 330                 335
Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ile Gln
            340                 345                 350
Ser Ile Ile Ser Thr Leu Thr
        355
```

<210> 649
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 649

```
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
```

```
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu
225                 230                 235                 240
Glu His Leu Cys Leu Leu Leu Gln Met Ile Leu Asn Gly Ile Leu Asn
                245                 250                 255
Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met
            260                 265                 270
Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu
        275                 280                 285
Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe
    290                 295                 300
His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu
305                 310                 315                 320
Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu
                325                 330                 335
Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Cys Gln
            340                 345                 350
Ser Ile Ile Ser Thr Leu Thr
        355
```

<210> 650
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 650

```
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
```

```
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu
225                 230                 235                 240
Glu His Leu Leu Leu Leu Leu Gln Met Ile Leu Asn Gly Ile Leu Asn
                245                 250                 255
Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met
            260                 265                 270
Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu
        275                 280                 285
Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe
    290                 295                 300
His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu
305                 310                 315                 320
Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu
                325                 330                 335
Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ile Gln
            340                 345                 350
Ser Ile Ile Ser Thr Leu Thr
        355
```

<210> 651
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 651

```
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
```

```
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu
225                 230                 235                 240
Glu Ile Leu Leu Leu Leu Leu Gln Met Ile Leu Asn Gly Ile Leu Asn
                245                 250                 255
Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met
            260                 265                 270
Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu
        275                 280                 285
Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe
    290                 295                 300
His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu
305                 310                 315                 320
Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu
                325                 330                 335
Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln
            340                 345                 350
Ser Ile Ile Ser Thr Leu Thr
        355
```

<210> 652
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 652
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1   5   10   15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20   25   30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35   40   45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50   55   60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65   70   75   80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85   90   95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100   105   110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115   120   125
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130   135   140
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145   150   155   160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165   170   175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180   185   190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195   200   205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210   215   220
Pro Gly Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu
225   230   235   240
Glu Ile Leu Leu Leu Phe Leu Gln Met Ile Leu Asn Gly Ile Leu Asn
                245   250   255
Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met
            260   265   270
Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu
        275   280   285
Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe
    290   295   300
His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu
305   310   315   320
Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu
                325   330   335
Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln
            340   345   350
Ser Ile Ile Ser Thr Leu Thr
        355

<210> 653
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 653
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1   5   10   15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20   25   30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35   40   45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50   55   60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65   70   75   80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85   90   95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100   105   110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115   120   125
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130   135   140
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145   150   155   160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165   170   175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180   185   190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195   200   205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210   215   220
Pro Gly Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu
225   230   235   240
Glu His Leu Leu Leu Leu Leu Gln Met Ile Leu Asn Gly Ile Leu Asn
                245   250   255
Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met
            260   265   270
Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu
        275   280   285
Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe
    290   295   300
His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu
305   310   315   320
Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu
                325   330   335
Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln
            340   345   350
Ser Ile Ile Ser Thr Leu Thr
        355

<210> 654
<211> 359

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 654
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1   5   10   15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20   25   30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35   40   45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50   55   60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65   70   75   80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85   90   95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100   105   110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115   120   125
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130   135   140
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145   150   155   160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165   170   175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180   185   190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195   200   205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210   215   220
Pro Gly Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu
225   230   235   240
Glu His Leu Cys Leu Phe Leu Gln Met Ile Leu Asn Gly Ile Leu Asn
                245   250   255
Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met
            260   265   270
Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu
        275   280   285
Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe
    290   295   300
His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu
305   310   315   320
Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu
                325   330   335
Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Cys Gln
            340   345   350
Ser Ile Ile Ser Thr Leu Thr
        355

<210> 655
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 655
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1   5   10   15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20   25   30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35   40   45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50   55   60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65   70   75   80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85   90   95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100   105   110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115   120   125
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130   135   140
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145   150   155   160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165   170   175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180   185   190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195   200   205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210   215   220
Pro Gly Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu
225   230   235   240
Glu His Leu Leu Leu Phe Leu Gln Met Ile Leu Asn Gly Ile Leu Asn
                245   250   255
Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met
            260   265   270
Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu
        275   280   285
Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe
    290   295   300
His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu
305   310   315   320
Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu
                325   330   335
Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ile Gln
            340   345   350

Ser Ile Ile Ser Thr Leu Thr
355

<210> 656
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 656
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
1 5 10 15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
20 25 30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
35 40 45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
50 55 60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65 70 75 80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
85 90 95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
100 105 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
115 120 125
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
130 135 140
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145 150 155 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
165 170 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
180 185 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
195 200 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
210 215 220
Pro Gly Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu
225 230 235 240
Glu His Leu Leu Leu Phe Leu Gln Met Ile Leu Asn Gly Ile Leu Asn
245 250 255
Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met
260 265 270
Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu
275 280 285
Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe
290 295 300
His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu
305 310 315 320
Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu

```
                325                 330                 335
Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln
            340                 345                 350
Ser Ile Ile Ser Thr Leu Thr
        355
```

<210> 657
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 657

```
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu
225                 230                 235                 240
Glu Ile Leu Cys Leu Leu Leu Gln Met Ile Leu Asn Gly Ile Asn Asn
                245                 250                 255
Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met
            260                 265                 270
Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu
        275                 280                 285
Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe
    290                 295                 300
```

```
His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu
305                 310                 315                 320
Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu
                325                 330                 335
Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Cys Gln
            340                 345                 350
Ser Ile Ile Ser Thr Leu Thr
        355
```

<210> 658
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 658

```
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu
225                 230                 235                 240
Glu Ile Leu Leu Leu Leu Leu Gln Met Ile Leu Asn Gly Ile Asn Asn
                245                 250                 255
Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met
            260                 265                 270
Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu
```

```
        275                 280                 285
Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe
    290                 295                 300
His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu
305                 310                 315                 320
Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu
                325                 330                 335
Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ile Gln
            340                 345                 350
Ser Ile Ile Ser Thr Leu Thr
        355


<210> 659
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 659
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu
225                 230                 235                 240
Glu Ile Leu Leu Leu Leu Leu Gln Met Ile Leu Asn Gly Ile Asn Asn
                245                 250                 255
```

```
Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met
            260                 265                 270
Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu
        275                 280                 285
Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe
    290                 295                 300
His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu
305                 310                 315                 320
Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu
                325                 330                 335
Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln
            340                 345                 350
Ser Ile Ile Ser Thr Leu Thr
        355


<210> 660
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 660
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu
```

225 230 235 240
Glu Ile Leu Cys Leu Phe Leu Gln Met Ile Leu Asn Gly Ile Asn Asn
245 250 255
Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met
260 265 270
Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu
275 280 285
Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe
290 295 300
His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu
305 310 315 320
Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu
325 330 335
Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Cys Gln
340 345 350
Ser Ile Ile Ser Thr Leu Thr
355

<210> 661
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 661
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
1 5 10 15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
20 25 30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
35 40 45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
50 55 60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65 70 75 80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
85 90 95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
100 105 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
115 120 125
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
130 135 140
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145 150 155 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
165 170 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
180 185 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
195 200 205

```
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu
225                 230                 235                 240
Glu Ile Leu Leu Leu Phe Leu Gln Met Ile Leu Asn Gly Ile Asn Asn
                245                 250                 255
Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met
            260                 265                 270
Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu
        275                 280                 285
Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe
    290                 295                 300
His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu
305                 310                 315                 320
Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu
                325                 330                 335
Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ile Gln
            340                 345                 350
Ser Ile Ile Ser Thr Leu Thr
        355
```

<210> 662
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 662

```
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
```

```
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu
225                 230                 235                 240
Glu Ile Leu Leu Leu Phe Leu Gln Met Ile Leu Asn Gly Ile Asn Asn
                245                 250                 255
Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met
            260                 265                 270
Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu
        275                 280                 285
Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe
    290                 295                 300
His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu
305                 310                 315                 320
Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu
                325                 330                 335
Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln
            340                 345                 350
Ser Ile Ile Ser Thr Leu Thr
        355
```

<210> 663
<211> 376
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 663

```
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
```

```
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Asp Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Asp Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Gly Gly Ser Ser Pro Pro Met Pro Tyr Asp Leu Tyr His Pro
225                 230                 235                 240
Ser Gly Pro Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln
                245                 250                 255
Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn
            260                 265                 270
Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr
        275                 280                 285
Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu
    290                 295                 300
Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn
305                 310                 315                 320
Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val
                325                 330                 335
Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp
            340                 345                 350
Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala
        355                 360                 365
Gln Ser Ile Ile Ser Thr Leu Thr
    370                 375
```

<210> 664
<211> 443
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 664

```
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
```

```
        115                 120                 125
Tyr Thr Leu Pro Pro Cys Arg Lys Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Lys Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Pro Gly Ser Gly Ala Val Asn Gly Thr Ser Gln Phe Thr Cys
225                 230                 235                 240
Phe Tyr Asn Ser Arg Ala Asn Ile Ser Cys Val Trp Ser Gln Asp Gly
                245                 250                 255
Ala Leu Gln Asp Thr Ser Cys Gln Val His Ala Trp Pro Asp Arg Arg
            260                 265                 270
Arg Trp Asn Gln Thr Cys Glu Leu Leu Pro Val Ser Gln Ala Ser Trp
        275                 280                 285
Ala Cys Asn Leu Ile Leu Gly Ala Pro Asp Ser Gln Lys Leu Thr Thr
    290                 295                 300
Val Asp Ile Val Thr Leu Arg Val Leu Cys Arg Glu Gly Val Arg Trp
305                 310                 315                 320
Arg Val Met Ala Ile Gln Asp Phe Lys Pro Phe Glu Asn Leu Arg Leu
                325                 330                 335
Met Ala Pro Ile Ser Leu Gln Val Val His Val Glu Thr His Arg Cys
            340                 345                 350
Asn Ile Ser Trp Glu Ile Ser Gln Ala Ser His Tyr Phe Glu Arg His
        355                 360                 365
Leu Glu Phe Glu Ala Arg Thr Leu Ser Pro Gly His Thr Trp Glu Glu
    370                 375                 380
Ala Pro Leu Leu Thr Leu Lys Gln Lys Gln Glu Trp Ile Cys Leu Glu
385                 390                 395                 400
Thr Leu Thr Pro Asp Thr Gln Tyr Glu Phe Gln Val Arg Val Lys Pro
                405                 410                 415
Leu Gln Gly Glu Phe Thr Thr Trp Ser Pro Trp Ser Gln Pro Leu Ala
            420                 425                 430
Phe Arg Thr Lys Pro Ala Ala Leu Gly Lys Asp
        435                 440
```

<210> 665
<211> 376
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 665

```
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
```

```
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Ser Cys Ala Val Glu Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Glu Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Gly Gly Ser Ser Pro Pro Met Pro Tyr Asp Leu Tyr His Pro
225                 230                 235                 240
Ser Gly Pro Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln
                245                 250                 255
Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn
            260                 265                 270
Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr
        275                 280                 285
Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu
    290                 295                 300
Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn
305                 310                 315                 320
Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val
                325                 330                 335
Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp
            340                 345                 350
Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala
        355                 360                 365
Gln Ser Ile Ile Ser Thr Leu Thr
    370                 375
```

<210> 666
<211> 443
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 666
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1   5   10   15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20   25   30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35   40   45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50   55   60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65   70   75   80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85   90   95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100   105   110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115   120   125
Tyr Thr Leu Pro Pro Cys Arg Lys Lys Leu Thr Lys Asn Gln Val Ser
    130   135   140
Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145   150   155   160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165   170   175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180   185   190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195   200   205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210   215   220
Pro Gly Pro Gly Ser Gly Ala Val Asn Gly Thr Ser Gln Phe Thr Cys
225   230   235   240
Phe Tyr Asn Ser Arg Ala Asn Ile Ser Cys Val Trp Ser Gln Asp Gly
                245   250   255
Ala Leu Gln Asp Thr Ser Cys Gln Val His Ala Trp Pro Asp Arg Arg
            260   265   270
Arg Trp Asn Gln Thr Cys Glu Leu Leu Pro Val Ser Gln Ala Ser Trp
        275   280   285
Ala Cys Asn Leu Ile Leu Gly Ala Pro Asp Ser Gln Lys Leu Thr Thr
    290   295   300
Val Asp Ile Val Thr Leu Arg Val Leu Cys Arg Glu Gly Val Arg Trp
305   310   315   320
Arg Val Met Ala Ile Gln Asp Phe Lys Pro Phe Glu Asn Leu Arg Leu
                325   330   335
Met Ala Pro Ile Ser Leu Gln Val Val His Val Glu Thr His Arg Cys
            340   345   350
Asn Ile Ser Trp Glu Ile Ser Gln Ala Ser His Tyr Phe Glu Arg His
        355   360   365
Leu Glu Phe Glu Ala Arg Thr Leu Ser Pro Gly His Thr Trp Glu Glu
    370   375   380
Ala Pro Leu Leu Thr Leu Lys Gln Lys Gln Glu Trp Ile Cys Leu Glu
385   390   395   400
Thr Leu Thr Pro Asp Thr Gln Tyr Glu Phe Gln Val Arg Val Lys Pro

```
                405                 410                 415
Leu Gln Gly Glu Phe Thr Thr Trp Ser Pro Trp Ser Gln Pro Leu Ala
            420                 425                 430
Phe Arg Thr Lys Pro Ala Ala Leu Gly Lys Asp
        435                 440
```

<210> 667
<211> 376
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 667

```
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Gly Gly Ser Ser Pro Pro Met Pro Tyr Asp Leu Tyr His Pro
225                 230                 235                 240
Ser Gly Pro Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln
                245                 250                 255
Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn
            260                 265                 270
Asn Tyr Lys Asn Pro Lys Leu Thr Ala Met Leu Thr Ala Lys Phe Ala
        275                 280                 285
Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu
    290                 295                 300
```

Ala Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn
305 310 315 320
Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val
325 330 335
Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp
340 345 350
Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala
355 360 365
Gln Ser Ile Ile Ser Thr Leu Thr
370 375

<210> 668
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 668
Gly Gly Ser Ser Pro Pro Met Pro Tyr Asp Leu Tyr His Pro Ser Gly
1 5 10 15
Pro Gly Ser Gly Ser
20

<210> 669
<211> 376
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 669
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
1 5 10 15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
20 25 30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
35 40 45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
50 55 60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65 70 75 80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
85 90 95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
100 105 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
115 120 125
Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
130 135 140

```
Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Gly Gly Ser Ser Pro Pro Met Pro Tyr Asp Leu Tyr His Pro
225                 230                 235                 240
Ser Gly Pro Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln
                245                 250                 255
Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn
            260                 265                 270
Asn Tyr Lys Asn Pro Lys Leu Thr Ala Met Leu Thr Ala Lys Phe Ala
        275                 280                 285
Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu
    290                 295                 300
Ala Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn
305                 310                 315                 320
Phe His Phe Asp Pro Arg Asp Val Val Ser Asn Ile Asn Val Phe Val
                325                 330                 335
Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp
            340                 345                 350
Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala
        355                 360                 365
Gln Ser Ile Ile Ser Thr Leu Thr
    370                 375
```

<210> 670
<211> 376
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 670

```
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
```

```
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Gly Gly Ser Ser Pro Pro Met Pro Tyr Asp Leu Tyr His Pro
225                 230                 235                 240
Ser Gly Pro Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln
                245                 250                 255
Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn
            260                 265                 270
Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr
        275                 280                 285
Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu
    290                 295                 300
Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn
305                 310                 315                 320
Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val
                325                 330                 335
Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp
            340                 345                 350
Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala
        355                 360                 365
Gln Ser Ile Ile Ser Thr Leu Thr
    370                 375


<210> 671
<211> 443
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 671
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
```

```
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Pro Gly Ser Gly Ala Val Asn Gly Thr Ser Gln Phe Thr Cys
225                 230                 235                 240
Phe Tyr Asn Ser Arg Ala Asn Ile Ser Cys Val Trp Ser Gln Asp Gly
                245                 250                 255
Ala Leu Gln Asp Thr Ser Cys Gln Val His Ala Trp Pro Asp Arg Arg
            260                 265                 270
Arg Trp Asn Gln Thr Cys Glu Leu Leu Pro Val Ser Gln Ala Ser Trp
        275                 280                 285
Ala Cys Asn Leu Ile Leu Gly Ala Pro Asp Ser Gln Lys Leu Thr Thr
    290                 295                 300
Val Asp Ile Val Thr Leu Arg Val Leu Cys Arg Glu Gly Val Arg Trp
305                 310                 315                 320
Arg Val Met Ala Ile Gln Asp Phe Lys Pro Phe Glu Asn Leu Arg Leu
                325                 330                 335
Met Ala Pro Ile Ser Leu Gln Val Val His Val Glu Thr His Arg Cys
            340                 345                 350
Asn Ile Ser Trp Glu Ile Ser Gln Ala Ser His Tyr Phe Glu Arg His
        355                 360                 365
Leu Glu Phe Glu Ala Arg Thr Leu Ser Pro Gly His Thr Trp Glu Glu
    370                 375                 380
Ala Pro Leu Leu Thr Leu Lys Gln Lys Gln Glu Trp Ile Cys Leu Glu
385                 390                 395                 400
Thr Leu Thr Pro Asp Thr Gln Tyr Glu Phe Gln Val Arg Val Lys Pro
                405                 410                 415
Leu Gln Gly Glu Phe Thr Thr Trp Ser Pro Trp Ser Gln Pro Leu Ala
            420                 425                 430
Phe Arg Thr Lys Pro Ala Ala Leu Gly Lys Asp
        435                 440
```

<210> 672
<211> 376
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 672
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1   5   10   15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20   25   30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35   40   45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50   55   60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65   70   75   80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85   90   95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100   105   110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115   120   125
Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130   135   140
Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145   150   155   160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165   170   175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180   185   190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195   200   205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210   215   220
Pro Gly Gly Ile Ser Ser Gly Leu Leu Ser Gly Arg Ser Asp Asn His
225   230   235   240
Ser Gly Pro Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln
                245   250   255
Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn
            260   265   270
Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr
        275   280   285
Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu
    290   295   300
Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn
305   310   315   320
Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val
                325   330   335
Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp
            340   345   350
Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala
        355   360   365
Gln Ser Ile Ile Ser Thr Leu Thr
    370   375

<210> 673
<211> 382
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 673
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1   5   10   15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20   25   30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35   40   45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50   55   60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65   70   75   80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85   90   95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100   105   110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115   120   125
Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130   135   140
Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145   150   155   160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165   170   175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180   185   190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195   200   205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210   215   220
Pro Gly Gly Gly Ala Val Gly Leu Leu Ala Pro Pro Gly Gly Leu Ser
225   230   235   240
Gly Arg Ser Asp Asn His Ser Gly Pro Ala Pro Thr Ser Ser Ser Thr
                245   250   255
Lys Lys Thr Gln Leu Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met
            260   265   270
Ile Leu Asn Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met
        275   280   285
Leu Thr Phe Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His
    290   295   300
Leu Gln Cys Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn
305   310   315   320
Leu Ala Gln Ser Lys Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser
                325   330   335
Asn Ile Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe
            340   345   350

Met Cys Glu Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn
        355   360   365
Arg Trp Ile Thr Phe Ala Gln Ser Ile Ile Ser Thr Leu Thr
    370   375   380

<210> 674
<211> 372
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 674
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1   5   10   15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20   25   30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35   40   45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50   55   60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65   70   75   80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85   90   95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100   105   110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115   120   125
Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130   135   140
Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145   150   155   160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165   170   175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180   185   190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195   200   205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210   215   220
Pro Gly Gly Ser Pro Gly Val Pro Leu Ser Leu Tyr Ser Gly Pro Ala
225   230   235   240
Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His Leu
                245   250   255
Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys Asn
            260   265   270
Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys Lys
        275   280   285
Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys Pro
    290   295   300
Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu Arg

305 310 315 320
Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu Lys
325 330 335
Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala Thr
340 345 350
Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser Ile Ile
355 360 365
Ser Thr Leu Thr
370

<210> 675
<211> 374
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 675
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
1 5 10 15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
20 25 30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
35 40 45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
50 55 60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65 70 75 80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
85 90 95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
100 105 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
115 120 125
Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
130 135 140
Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145 150 155 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
165 170 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
180 185 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
195 200 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
210 215 220
Pro Gly Gly Gly Ser Ser Pro Pro Val Pro Leu Ser Leu Tyr Ser Gly
225 230 235 240
Pro Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu
245 250 255
His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr
260 265 270

```
Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro
        275                 280                 285
Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu
    290                 295                 300
Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His
305                 310                 315                 320
Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu
                325                 330                 335
Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr
            340                 345                 350
Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser
        355                 360                 365
Ile Ile Ser Thr Leu Thr
    370
```

<210> 676
<211> 374
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 676

```
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Gly Gly Ser Pro Gly Gly Val Pro Leu Ser Leu Tyr Ser Gly
```

225 230 235 240
Pro Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu
245 250 255
His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr
260 265 270
Lys Asn Pro Lys Leu Thr Ala Met Leu Thr Ala Lys Phe Ala Met Pro
275 280 285
Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Ala Leu
290 295 300
Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His
305 310 315 320
Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu
325 330 335
Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr
340 345 350
Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser
355 360 365
Ile Ile Ser Thr Leu Thr
370

<210> 677
<211> 376
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 677
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
1 5 10 15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
20 25 30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
35 40 45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
50 55 60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65 70 75 80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
85 90 95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
100 105 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
115 120 125
Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
130 135 140
Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145 150 155 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
165 170 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
180 185 190

```
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Gly Gly Ser Ser Pro Pro Arg Ala Ala Ala Val Lys Ser Pro
225                 230                 235                 240
Ser Gly Pro Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln
                245                 250                 255
Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn
            260                 265                 270
Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr
        275                 280                 285
Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu
    290                 295                 300
Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn
305                 310                 315                 320
Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val
                325                 330                 335
Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp
            340                 345                 350
Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala
        355                 360                 365
Gln Ser Ile Ile Ser Thr Leu Thr
    370                 375
```

<210> 678
<211> 376
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 678

```
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
```

145 150 155 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
165 170 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
180 185 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
195 200 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
210 215 220
Pro Gly Gly Gly Pro Gly Gly Pro Arg Ala Ala Ala Val Lys Ser Pro
225 230 235 240
Ser Gly Pro Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln
245 250 255
Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn
260 265 270
Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr
275 280 285
Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu
290 295 300
Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn
305 310 315 320
Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val
325 330 335
Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp
340 345 350
Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala
355 360 365
Gln Ser Ile Ile Ser Thr Leu Thr
370 375

<210> 679
<211> 374
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 679
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
1 5 10 15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
20 25 30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
35 40 45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
50 55 60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65 70 75 80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
85 90 95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
100 105 110

```
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Gly Gly Ser Gly Arg Ala Ala Ala Val Lys Ser Pro Ser Gly
225                 230                 235                 240
Pro Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu
                245                 250                 255
His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr
            260                 265                 270
Lys Asn Pro Lys Leu Thr Ala Met Leu Thr Ala Lys Phe Ala Met Pro
        275                 280                 285
Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Ala Leu
    290                 295                 300
Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His
305                 310                 315                 320
Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu
                325                 330                 335
Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr
            340                 345                 350
Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser
        355                 360                 365
Ile Ile Ser Thr Leu Thr
    370
```

<210> 680
<211> 376
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 680

```
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
```

65 70 75 80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
85 90 95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
100 105 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
115 120 125
Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
130 135 140
Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145 150 155 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
165 170 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
180 185 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
195 200 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
210 215 220
Pro Gly Gly Gly Ser Ser Pro Pro Arg Ala Ala Ala Val Lys Ser Pro
225 230 235 240
Ser Gly Pro Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln
245 250 255
Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn
260 265 270
Asn Tyr Lys Asn Pro Lys Leu Thr Ala Met Leu Thr Ala Lys Phe Ala
275 280 285
Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu
290 295 300
Ala Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn
305 310 315 320
Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val
325 330 335
Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp
340 345 350
Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala
355 360 365
Gln Ser Ile Ile Ser Thr Leu Thr
370 375

<210> 681
<211> 376
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 681
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
1 5 10 15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
20 25 30

```
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Gly Gly Pro Gly Gly Pro Arg Ala Ala Ala Val Lys Ser Pro
225                 230                 235                 240
Ser Gly Pro Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln
                245                 250                 255
Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn
            260                 265                 270
Asn Tyr Lys Asn Pro Lys Leu Thr Ala Met Leu Thr Ala Lys Phe Ala
        275                 280                 285
Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu
    290                 295                 300
Ala Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn
305                 310                 315                 320
Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val
                325                 330                 335
Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp
            340                 345                 350
Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala
        355                 360                 365
Gln Ser Ile Ile Ser Thr Leu Thr
    370                 375
```

<210> 682
<211> 372
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 682
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1   5   10   15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20   25   30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35   40   45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50   55   60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65   70   75   80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85   90   95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100   105   110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115   120   125
Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130   135   140
Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145   150   155   160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165   170   175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180   185   190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195   200   205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210   215   220
Pro Gly Gly Gly Ser Gly His Glu Gln Leu Thr Val Ser Gly Pro Ala
225   230   235   240
Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His Leu
                245   250   255
Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys Asn
            260   265   270
Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys Lys
        275   280   285
Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys Pro
    290   295   300
Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu Arg
305   310   315   320
Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu Lys
                325   330   335
Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala Thr
            340   345   350
Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser Ile Ile
        355   360   365
Ser Thr Leu Thr
    370

<210> 683
<211> 374
<212> PRT

<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 683
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1   5   10   15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20   25   30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35   40   45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50   55   60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65   70   75   80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85   90   95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100   105   110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115   120   125
Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130   135   140
Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145   150   155   160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165   170   175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180   185   190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195   200   205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210   215   220
Pro Gly Gly Gly Ser Ser Pro Pro His Glu Gln Leu Thr Val Ser Gly
225   230   235   240
Pro Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu
                245   250   255
His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr
            260   265   270
Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro
        275   280   285
Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu
    290   295   300
Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His
305   310   315   320
Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu
                325   330   335
Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr
            340   345   350
Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser
        355   360   365
Ile Ile Ser Thr Leu Thr
    370

<210> 684
<211> 374
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 684
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1   5   10   15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20   25   30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35   40   45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50   55   60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65   70   75   80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85   90   95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100   105   110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115   120   125
Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130   135   140
Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145   150   155   160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165   170   175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180   185   190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195   200   205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210   215   220
Pro Gly Gly Ser Pro Pro Gly Gly His Glu Gln Leu Thr Val Ser Gly
225   230   235   240
Pro Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu
                245   250   255
His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr
            260   265   270
Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro
        275   280   285
Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu
    290   295   300
Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His
305   310   315   320
Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu
                325   330   335
Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr

```
            340                 345                 350
Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser
        355                 360                 365
Ile Ile Ser Thr Leu Thr
    370
```

<210> 685
<211> 372
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 685

```
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Gly Gly Ser Gly His Glu Gln Leu Thr Val Ser Gly Pro Ala
225                 230                 235                 240
Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His Leu
                245                 250                 255
Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys Asn
            260                 265                 270
Pro Lys Leu Thr Ala Met Leu Thr Ala Lys Phe Ala Met Pro Lys Lys
        275                 280                 285
Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Ala Leu Lys Pro
    290                 295                 300
```

Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu Arg
305 310 315 320
Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu Lys
325 330 335
Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala Thr
340 345 350
Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser Ile Ile
355 360 365
Ser Thr Leu Thr
370

<210> 686
<211> 374
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 686
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
1 5 10 15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
20 25 30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
35 40 45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
50 55 60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65 70 75 80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
85 90 95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
100 105 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
115 120 125
Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
130 135 140
Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145 150 155 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
165 170 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
180 185 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
195 200 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
210 215 220
Pro Gly Gly Gly Ser Ser Pro Pro His Glu Gln Leu Thr Val Ser Gly
225 230 235 240
Pro Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu
245 250 255
His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr

```
            260                 265                 270
Lys Asn Pro Lys Leu Thr Ala Met Leu Thr Ala Lys Phe Ala Met Pro
        275                 280                 285
Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Ala Leu
    290                 295                 300
Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His
305                 310                 315                 320
Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu
                325                 330                 335
Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr
            340                 345                 350
Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser
        355                 360                 365
Ile Ile Ser Thr Leu Thr
    370


<210> 687
<211> 374
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 687
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
```

```
Pro Gly Gly Ser Pro Pro Gly Gly His Glu Gln Leu Thr Val Ser Gly
225                 230                 235                 240
Pro Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu
                245                 250                 255
His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr
            260                 265                 270
Lys Asn Pro Lys Leu Thr Ala Met Leu Thr Ala Lys Phe Ala Met Pro
        275                 280                 285
Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Ala Leu
    290                 295                 300
Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His
305                 310                 315                 320
Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu
                325                 330                 335
Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr
            340                 345                 350
Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser
        355                 360                 365
Ile Ile Ser Thr Leu Thr
    370
```

<210> 688
<211> 374
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 688

```
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
```

```
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Gly Ser Gly Pro Asp Ser Gly Gly Phe Met Leu Thr Ser Gly
225                 230                 235                 240
Pro Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu
                245                 250                 255
His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr
            260                 265                 270
Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro
        275                 280                 285
Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu
    290                 295                 300
Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His
305                 310                 315                 320
Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu
                325                 330                 335
Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr
            340                 345                 350
Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser
        355                 360                 365
Ile Ile Ser Thr Leu Thr
    370
```

<210> 689
<211> 376
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 689

```
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
```

```
Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Gly Pro Gly Ser Pro Gly Asp Ser Gly Gly Phe Met Leu Thr
225                 230                 235                 240
Ser Gly Pro Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln
                245                 250                 255
Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn
            260                 265                 270
Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr
        275                 280                 285
Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu
    290                 295                 300
Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn
305                 310                 315                 320
Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val
                325                 330                 335
Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp
            340                 345                 350
Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala
        355                 360                 365
Gln Ser Ile Ile Ser Thr Leu Thr
    370                 375


<210> 690
<211> 376
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 690
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
```

```
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Gly Ser Ser Pro Pro Gly Asp Ser Gly Gly Phe Met Leu Thr
225                 230                 235                 240
Ser Gly Pro Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln
                245                 250                 255
Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn
            260                 265                 270
Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr
        275                 280                 285
Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu
    290                 295                 300
Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn
305                 310                 315                 320
Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val
                325                 330                 335
Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp
            340                 345                 350
Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala
        355                 360                 365
Gln Ser Ile Ile Ser Thr Leu Thr
    370                 375
```

<210> 691
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 691
```
Gly Ile Ser Ser Gly Leu Leu Ser Gly Arg Ser Asp Asn His Gly Gly
 1               5                  10                  15
Pro
```

<210> 692
<211> 376

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 692
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1   5   10   15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20   25   30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35   40   45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50   55   60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65   70   75   80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85   90   95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100   105   110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115   120   125
Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130   135   140
Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145   150   155   160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165   170   175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180   185   190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195   200   205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210   215   220
Pro Gly Gly Pro Gly Ser Pro Gly Asp Ser Gly Gly Phe Met Leu Thr
225   230   235   240
Ser Gly Pro Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln
                245   250   255
Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn
            260   265   270
Asn Tyr Lys Asn Pro Lys Leu Thr Ala Met Leu Thr Ala Lys Phe Ala
        275   280   285
Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu
    290   295   300
Ala Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn
305   310   315   320
Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val
                325   330   335
Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp
            340   345   350
Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala
        355   360   365
Gln Ser Ile Ile Ser Thr Leu Thr

370 375

<210> 693
<211> 376
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 693
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
1 5 10 15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
20 25 30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
35 40 45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
50 55 60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65 70 75 80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
85 90 95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
100 105 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
115 120 125
Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
130 135 140
Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145 150 155 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
165 170 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
180 185 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
195 200 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
210 215 220
Pro Gly Gly Ser Ser Pro Pro Gly Asp Ser Gly Gly Phe Met Leu Thr
225 230 235 240
Ser Gly Pro Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln
245 250 255
Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn
260 265 270
Asn Tyr Lys Asn Pro Lys Leu Thr Ala Met Leu Thr Ala Lys Phe Ala
275 280 285
Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu
290 295 300
Ala Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn
305 310 315 320
Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val
325 330 335

```
Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp
            340                 345                 350
Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala
        355                 360                 365
Gln Ser Ile Ile Ser Thr Leu Thr
    370                 375


<210> 694
<211> 376
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 694
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Gly Ile Ser Ser Gly Leu Leu Ser Gly Arg Ser Asp Asn His
225                 230                 235                 240
Ser Gly Pro Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln
                245                 250                 255
Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn
            260                 265                 270
Asn Tyr Lys Asn Pro Lys Leu Thr Ala Met Leu Thr Ala Lys Phe Ala
        275                 280                 285
Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu
```

```
    290                 295                 300
Ala Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn
305                 310                 315                 320
Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val
                325                 330                 335
Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp
            340                 345                 350
Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala
        355                 360                 365
Gln Ser Ile Ile Ser Thr Leu Thr
    370                 375


<210> 695
<211> 382
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 695
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Gly Gly Ala Val Gly Leu Leu Ala Pro Pro Gly Gly Leu Ser
225                 230                 235                 240
Gly Arg Ser Asp Asn His Ser Gly Pro Ala Pro Thr Ser Ser Ser Thr
                245                 250                 255
```

Lys Lys Thr Gln Leu Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met
            260   265   270
Ile Leu Asn Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr Ala Met
        275   280   285
Leu Thr Ala Lys Phe Ala Met Pro Lys Lys Ala Thr Glu Leu Lys His
    290   295   300
Leu Gln Cys Leu Glu Glu Ala Leu Lys Pro Leu Glu Glu Val Leu Asn
305   310   315   320
Leu Ala Gln Ser Lys Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser
                325   330   335
Asn Ile Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe
            340   345   350
Met Cys Glu Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn
        355   360   365
Arg Trp Ile Thr Phe Ala Gln Ser Ile Ile Ser Thr Leu Thr
    370   375   380

<210> 696
<211> 374
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 696
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1   5   10   15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20   25   30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35   40   45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50   55   60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65   70   75   80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85   90   95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100   105   110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115   120   125
Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130   135   140
Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145   150   155   160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165   170   175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180   185   190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195   200   205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser

```
    210                 215                 220
Pro Gly Gly Gly Ser Pro Gly Gly Val Pro Leu Ser Leu Tyr Ser Gly
225                 230                 235                 240
Pro Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu
                245                 250                 255
His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr
            260                 265                 270
Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro
        275                 280                 285
Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu
    290                 295                 300
Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His
305                 310                 315                 320
Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu
                325                 330                 335
Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr
            340                 345                 350
Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser
        355                 360                 365
Ile Ile Ser Thr Leu Thr
    370
```

<210> 697
<211> 372
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 697

```
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
```

```
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Gly Ser Pro Gly Val Pro Leu Ser Leu Tyr Ser Gly Pro Ala
225                 230                 235                 240
Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His Leu
                245                 250                 255
Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys Asn
            260                 265                 270
Pro Lys Leu Thr Ala Met Leu Thr Ala Lys Phe Ala Met Pro Lys Lys
        275                 280                 285
Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Ala Leu Lys Pro
    290                 295                 300
Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu Arg
305                 310                 315                 320
Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu Lys
                325                 330                 335
Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala Thr
            340                 345                 350
Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser Ile Ile
        355                 360                 365
Ser Thr Leu Thr
    370
```

<210> 698
<211> 374
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 698

```
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
```

```
    130                 135                 140
Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Gly Gly Ser Gly Arg Ala Ala Ala Val Lys Ser Pro Ser Gly
225                 230                 235                 240
Pro Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu
                245                 250                 255
His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr
            260                 265                 270
Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro
        275                 280                 285
Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu
    290                 295                 300
Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His
305                 310                 315                 320
Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu
                325                 330                 335
Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr
            340                 345                 350
Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser
        355                 360                 365
Ile Ile Ser Thr Leu Thr
    370
```

<210> 699
<211> 376
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 699

```
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
```

```
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Gly Gly Ser Ser Pro Pro Gly Gly Gly Ser Ser Gly Gly Gly
225                 230                 235                 240
Ser Gly Pro Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln
                245                 250                 255
Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn
            260                 265                 270
Asn Tyr Lys Asn Pro Lys Leu Thr Ala Met Leu Thr Ala Lys Phe Ala
        275                 280                 285
Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu
    290                 295                 300
Ala Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn
305                 310                 315                 320
Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val
                325                 330                 335
Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp
            340                 345                 350
Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala
        355                 360                 365
Gln Ser Ile Ile Ser Thr Leu Thr
    370                 375


<210> 700
<211> 376
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 700
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
```

```
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Gly Gly Ser Ser Pro Pro Gly Gly Gly Ser Ser Gly Gly Gly
225                 230                 235                 240
Ser Gly Pro Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln
                245                 250                 255
Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn
            260                 265                 270
Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr
        275                 280                 285
Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu
    290                 295                 300
Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn
305                 310                 315                 320
Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val
                325                 330                 335
Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp
            340                 345                 350
Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala
        355                 360                 365
Gln Ser Ile Ile Ser Thr Leu Thr
    370                 375


<210> 701
<211> 376
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 701
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
```

```
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Gly Gly Ser Ser Pro Pro Met Pro Tyr Asp Leu Tyr His Pro
225                 230                 235                 240
Ser Gly Pro Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln
                245                 250                 255
Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn
            260                 265                 270
Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr
        275                 280                 285
Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu
    290                 295                 300
Arg Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn
305                 310                 315                 320
Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val
                325                 330                 335
Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp
            340                 345                 350
Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala
        355                 360                 365
Gln Ser Ile Ile Ser Thr Leu Thr
    370                 375
```

<210> 702
<211> 376
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 702
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1   5   10   15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20   25   30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35   40   45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50   55   60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65   70   75   80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85   90   95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100   105   110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115   120   125
Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130   135   140
Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145   150   155   160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165   170   175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180   185   190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195   200   205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210   215   220
Pro Gly Gly Gly Ser Ser Pro Pro Met Pro Tyr Asp Leu Tyr His Pro
225   230   235   240
Ser Gly Pro Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln
                245   250   255
Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn
            260   265   270
Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Glu Lys Phe Tyr
        275   280   285
Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu
    290   295   300
Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn
305   310   315   320
Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val
                325   330   335
Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp
            340   345   350
Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala
        355   360   365
Gln Ser Ile Ile Ser Thr Leu Thr
    370   375

<210> 703

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

<220>
<223> Synthetic Construct

<400> 703
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1   5   10   15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20   25   30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35   40   45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50   55   60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65   70   75   80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85   90   95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100   105   110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115   120   125
Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130   135   140
Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145   150   155   160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165   170   175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180   185   190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195   200   205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210   215   220
Pro Gly Gly Gly Ser Ser Pro Pro Met Pro Tyr Asp Leu Tyr His Pro
225   230   235   240
Ser Gly Pro Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln
                245   250   255
Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn
            260   265   270
Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Asn
        275   280   285
Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu
    290   295   300
Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn
305   310   315   320
Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val
                325   330   335
Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp
            340   345   350
Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala
        355   360   365

Gln Ser Ile Ile Ser Thr Leu Thr
370 375

<210> 704
<211> 376
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 704
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
1 5 10 15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
20 25 30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
35 40 45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
50 55 60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65 70 75 80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
85 90 95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
100 105 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
115 120 125
Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
130 135 140
Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145 150 155 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
165 170 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
180 185 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
195 200 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
210 215 220
Pro Gly Gly Gly Ser Ser Pro Pro Met Pro Tyr Asp Leu Tyr His Pro
225 230 235 240
Ser Gly Pro Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln
245 250 255
Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn
260 265 270
Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr
275 280 285
Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu
290 295 300
Ser Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn
305 310 315 320
Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val

```
                325                 330                 335
Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp
            340                 345                 350
Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala
        355                 360                 365
Gln Ser Ile Ile Ser Thr Leu Thr
    370                 375


<210> 705
<211> 376
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 705
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Gly Gly Ser Ser Pro Pro Met Pro Tyr Asp Leu Tyr His Pro
225                 230                 235                 240
Ser Gly Pro Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln
                245                 250                 255
Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn
            260                 265                 270
Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Ala Lys Phe Tyr
        275                 280                 285
```

```
Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu
    290                 295                 300
Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn
305                 310                 315                 320
Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val
                325                 330                 335
Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp
            340                 345                 350
Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala
        355                 360                 365
Gln Ser Ile Ile Ser Thr Leu Thr
    370                 375


<210> 706
<211> 376
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 706
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Gly Gly Ser Ser Pro Pro Met Pro Tyr Asp Leu Tyr His Pro
225                 230                 235                 240
Ser Gly Pro Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln
```

```
                245                 250                 255
Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn
            260                 265                 270
Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Arg
        275                 280                 285
Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu
    290                 295                 300
Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn
305                 310                 315                 320
Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val
                325                 330                 335
Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp
            340                 345                 350
Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala
        355                 360                 365
Gln Ser Ile Ile Ser Thr Leu Thr
    370                 375


<210> 707
<211> 376
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 707
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
```

```
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Gly Gly Ser Ser Pro Pro Met Pro Tyr Asp Leu Tyr His Pro
225                 230                 235                 240
Ser Gly Pro Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln
                245                 250                 255
Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn
            260                 265                 270
Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Ala Phe Tyr
        275                 280                 285
Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu
    290                 295                 300
Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn
305                 310                 315                 320
Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val
                325                 330                 335
Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp
            340                 345                 350
Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala
        355                 360                 365
Gln Ser Ile Ile Ser Thr Leu Thr
    370                 375
```

<210> 708
<211> 376
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 708

```
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
```

```
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Gly Gly Ser Ser Pro Pro Met Pro Tyr Asp Leu Tyr His Pro
225                 230                 235                 240
Ser Gly Pro Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln
                245                 250                 255
Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn
            260                 265                 270
Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Ala
        275                 280                 285
Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu
    290                 295                 300
Ser Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn
305                 310                 315                 320
Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val
                325                 330                 335
Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp
            340                 345                 350
Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala
        355                 360                 365
Gln Ser Ile Ile Ser Thr Leu Thr
    370                 375


<210> 709
<211> 376
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 709
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
```

```
Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Gly Gly Ser Ser Pro Pro Met Pro Tyr Asp Leu Tyr His Pro
225                 230                 235                 240
Ser Gly Pro Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln
                245                 250                 255
Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn
            260                 265                 270
Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Ser Lys Phe Tyr
        275                 280                 285
Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu
    290                 295                 300
Ser Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn
305                 310                 315                 320
Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val
                325                 330                 335
Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp
            340                 345                 350
Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala
        355                 360                 365
Gln Ser Ile Ile Ser Thr Leu Thr
    370                 375


<210> 710
<211> 376
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 710
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
```

```
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Gly Gly Ser Ser Pro Pro Met Pro Tyr Asp Leu Tyr His Pro
225                 230                 235                 240
Ser Gly Pro Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln
                245                 250                 255
Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn
            260                 265                 270
Asn Tyr Lys Asn Pro Lys Leu Thr Gly Met Leu Thr Phe Lys Phe Ala
        275                 280                 285
Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu
    290                 295                 300
Ser Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn
305                 310                 315                 320
Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val
                325                 330                 335
Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp
            340                 345                 350
Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala
        355                 360                 365
Gln Ser Ile Ile Ser Thr Leu Thr
    370                 375
```

<210> 711
<211> 374
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 711

```
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
```

```
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Gly Gly Ser Ser Pro Pro Val Pro Leu Ser Leu Tyr Ser Gly
225                 230                 235                 240
Pro Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu
                245                 250                 255
His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr
            260                 265                 270
Lys Asn Pro Lys Leu Thr Ala Met Leu Thr Ala Lys Phe Ala Met Pro
        275                 280                 285
Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Ala Leu
    290                 295                 300
Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His
305                 310                 315                 320
Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu
                325                 330                 335
Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr
            340                 345                 350
Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser
        355                 360                 365
Ile Ile Ser Thr Leu Thr
    370
```

<210> 712
<211> 443
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 712
```
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
```

```
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Pro Gly Ser Gly Ala Val Asn Gly Thr Ser Gln Phe Thr Cys
225                 230                 235                 240
Phe Tyr Asn Ser Arg Ala Asn Ile Ser Cys Val Trp Ser Gln Asp Gly
                245                 250                 255
Ala Leu Gln Asp Thr Ser Cys Gln Val His Ala Trp Pro Asp Arg Arg
            260                 265                 270
Arg Trp Asn Gln Thr Cys Glu Leu Leu Pro Val Ser Gln Ala Ser Trp
        275                 280                 285
Ala Cys Asn Leu Ile Leu Gly Ala Pro Asp Ser Gln Lys Leu Thr Thr
    290                 295                 300
Val Asp Ile Val Thr Leu Arg Val Leu Cys Arg Glu Gly Val Arg Trp
305                 310                 315                 320
Arg Val Met Ala Ile Gln Asp Phe Lys Pro Phe Glu Asn Leu Arg Leu
                325                 330                 335
Met Ala Pro Ile Ser Leu Gln Val Val His Val Glu Thr His Arg Cys
            340                 345                 350
Asn Ile Ser Trp Glu Ile Ser Gln Ala Ser His Tyr Phe Glu Arg His
        355                 360                 365
Leu Glu Phe Glu Ala Arg Thr Leu Ser Pro Gly His Thr Trp Glu Glu
    370                 375                 380
Ala Pro Leu Leu Thr Leu Lys Gln Lys Gln Glu Trp Ile Cys Leu Glu
385                 390                 395                 400
Thr Leu Thr Pro Asp Thr Gln Tyr Glu Phe Gln Val Arg Val Lys Pro
                405                 410                 415
Leu Gln Gly Glu Phe Thr Thr Trp Ser Pro Trp Ser Gln Pro Leu Ala
            420                 425                 430
Phe Arg Thr Lys Pro Ala Ala Leu Gly Lys Asp
```

435 440

<210> 713
<211> 376
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 713
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
1 5 10 15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
20 25 30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
35 40 45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
50 55 60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65 70 75 80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
85 90 95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
100 105 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
115 120 125
Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
130 135 140
Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145 150 155 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
165 170 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
180 185 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
195 200 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
210 215 220
Pro Gly Gly Ile Ser Ser Gly Leu Leu Ser Gly Arg Ser Asp Asn His
225 230 235 240
Gly Gly Pro Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln
245 250 255
Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn
260 265 270
Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr
275 280 285
Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu
290 295 300
Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn
305 310 315 320
Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val
325 330 335

```
Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp
            340                 345                 350
Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala
        355                 360                 365
Gln Ser Ile Ile Ser Thr Leu Thr
    370                 375
```

<210> 714
<211> 376
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 714

```
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Gly Ile Ser Ser Gly Leu Leu Ser Gly Arg Ser Asp Asn His
225                 230                 235                 240
Gly Gly Pro Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln
                245                 250                 255
Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn
            260                 265                 270
Asn Tyr Lys Asn Pro Lys Leu Thr Ala Met Leu Thr Ala Lys Phe Ala
        275                 280                 285
Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu
```

```
    290                 295                 300
Ala Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn
305                 310                 315                 320
Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val
                325                 330                 335
Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp
            340                 345                 350
Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala
        355                 360                 365
Gln Ser Ile Ile Ser Thr Leu Thr
    370                 375


<210> 715
<211> 361
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 715
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Gly Gly Ser Ser Pro Pro Met Pro Tyr Asp Leu Tyr His Pro
225                 230                 235                 240
Ser Gly Pro Gly Ser Gly Ser Asn Trp Val Asn Val Ile Ser Asp Leu
                245                 250                 255
```

```
Lys Lys Ile Glu Asp Leu Ile Gln Ser Met His Ile Asp Ala Thr Leu
            260                 265                 270
Tyr Thr Glu Ser Asp Val His Pro Ser Cys Lys Val Thr Ala Met Lys
        275                 280                 285
Cys Phe Leu Leu Glu Leu Gln Val Ile Ser Leu Glu Ser Gly Asp Ala
    290                 295                 300
Ser Ile His Asp Thr Val Glu Asn Leu Ile Ile Leu Ala Asn Asn Ser
305                 310                 315                 320
Leu Ser Ser Asn Gly Asn Val Thr Glu Ser Gly Cys Lys Glu Cys Glu
                325                 330                 335
Glu Leu Glu Glu Lys Asn Ile Lys Glu Phe Leu Gln Ser Phe Val His
            340                 345                 350
Ile Val Gln Met Phe Ile Asn Thr Ser
        355                 360
```

<210> 716
<211> 459
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 716

```
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Gly Pro Pro Ser Gly Ser Ser Pro Met Pro Tyr Asp Leu Tyr
```

225 230 235 240
His Pro Ser Gly Gly Gly Ala Val Asn Gly Thr Ser Gln Phe Thr Cys
245 250 255
Phe Tyr Asn Ser Arg Ala Asn Ile Ser Cys Val Trp Ser Gln Asp Gly
260 265 270
Ala Leu Gln Asp Thr Ser Cys Gln Val His Ala Trp Pro Asp Arg Arg
275 280 285
Arg Trp Asn Gln Thr Cys Glu Leu Leu Pro Val Ser Gln Ala Ser Trp
290 295 300
Ala Cys Asn Leu Ile Leu Gly Ala Pro Asp Ser Gln Lys Leu Thr Thr
305 310 315 320
Val Asp Ile Val Thr Leu Arg Val Leu Cys Arg Glu Gly Val Arg Trp
325 330 335
Arg Val Met Ala Ile Gln Asp Phe Lys Pro Phe Glu Asn Leu Arg Leu
340 345 350
Met Ala Pro Ile Ser Leu Gln Val Val His Val Glu Thr His Arg Cys
355 360 365
Asn Ile Ser Trp Glu Ile Ser Gln Ala Ser His Tyr Phe Glu Arg His
370 375 380
Leu Glu Phe Glu Ala Arg Thr Leu Ser Pro Gly His Thr Trp Glu Glu
385 390 395 400
Ala Pro Leu Leu Thr Leu Lys Gln Lys Gln Glu Trp Ile Cys Leu Glu
405 410 415
Thr Leu Thr Pro Asp Thr Gln Tyr Glu Phe Gln Val Arg Val Lys Pro
420 425 430
Leu Gln Gly Glu Phe Thr Thr Trp Ser Pro Trp Ser Gln Pro Leu Ala
435 440 445
Phe Arg Thr Lys Pro Ala Ala Leu Gly Lys Asp
450 455

<210> 717
<211> 372
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 717
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
1 5 10 15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
20 25 30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
35 40 45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
50 55 60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65 70 75 80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
85 90 95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
100 105 110

```
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Gly Ser Pro Gly Val Pro Leu Ser Leu Tyr Ser Gly Pro Ala
225                 230                 235                 240
Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His Leu
                245                 250                 255
Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys Asn
            260                 265                 270
Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys Lys
        275                 280                 285
Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Arg Leu Lys Pro
    290                 295                 300
Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu Arg
305                 310                 315                 320
Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu Lys
                325                 330                 335
Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala Thr
            340                 345                 350
Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser Ile Ile
        355                 360                 365
Ser Thr Leu Thr
    370


<210> 718
<211> 372
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 718
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
```

65 70 75 80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
85 90 95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
100 105 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
115 120 125
Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
130 135 140
Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145 150 155 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
165 170 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
180 185 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
195 200 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
210 215 220
Pro Gly Gly Ser Pro Gly Val Pro Leu Ser Leu Tyr Ser Gly Pro Ala
225 230 235 240
Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His Leu
245 250 255
Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys Asn
260 265 270
Pro Lys Leu Thr Arg Met Leu Thr Glu Lys Phe Tyr Met Pro Lys Lys
275 280 285
Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys Pro
290 295 300
Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu Arg
305 310 315 320
Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu Lys
325 330 335
Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala Thr
340 345 350
Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser Ile Ile
355 360 365
Ser Thr Leu Thr
370

<210> 719
<211> 372
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 719
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
1 5 10 15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
20 25 30

```
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Gly Ser Pro Gly Val Pro Leu Ser Leu Tyr Ser Gly Pro Ala
225                 230                 235                 240
Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His Leu
                245                 250                 255
Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys Asn
            260                 265                 270
Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys Lys
        275                 280                 285
Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Ser Leu Lys Pro
    290                 295                 300
Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu Arg
305                 310                 315                 320
Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu Lys
                325                 330                 335
Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala Thr
            340                 345                 350
Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser Ile Ile
        355                 360                 365
Ser Thr Leu Thr
    370
```

<210> 720
<211> 372
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 720
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1   5   10   15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20   25   30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35   40   45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50   55   60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65   70   75   80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85   90   95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100   105   110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115   120   125
Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130   135   140
Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145   150   155   160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165   170   175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180   185   190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195   200   205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210   215   220
Pro Gly Gly Ser Pro Gly Val Pro Leu Ser Leu Tyr Ser Gly Pro Ala
225   230   235   240
Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His Leu
                245   250   255
Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys Asn
            260   265   270
Pro Lys Leu Thr Arg Met Leu Thr Ala Lys Phe Tyr Met Pro Lys Lys
        275   280   285
Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys Pro
    290   295   300
Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu Arg
305   310   315   320
Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu Lys
                325   330   335
Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala Thr
            340   345   350
Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser Ile Ile
        355   360   365
Ser Thr Leu Thr
    370

<210> 721
<211> 226
<212> PRT

<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 721
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1   5   10   15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20   25   30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35   40   45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50   55   60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65   70   75   80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85   90   95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100   105   110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115   120   125
Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130   135   140
Leu Thr Cys Leu Val Glu Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145   150   155   160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165   170   175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180   185   190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195   200   205
His Glu Ala Leu His Asn His Tyr Thr Gln Glu Ser Leu Ser Leu Ser
    210   215   220
Pro Gly
225

<210> 722
<211> 372
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 722
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1   5   10   15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20   25   30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35   40   45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val

```
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Gly Ser Pro Gly Val Pro Leu Ser Leu Tyr Ser Gly Pro Ala
225                 230                 235                 240
Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His Leu
                245                 250                 255
Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys Asn
            260                 265                 270
Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Arg Met Pro Lys Lys
        275                 280                 285
Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys Pro
    290                 295                 300
Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu Arg
305                 310                 315                 320
Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu Lys
                325                 330                 335
Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala Thr
            340                 345                 350
Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser Ile Ile
        355                 360                 365
Ser Thr Leu Thr
    370


<210> 723
<211> 372
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 723
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
```

```
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Gly Ser Pro Gly Val Pro Leu Ser Leu Tyr Ser Gly Pro Ala
225                 230                 235                 240
Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His Leu
                245                 250                 255
Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys Asn
            260                 265                 270
Pro Lys Leu Thr Arg Met Leu Thr Ser Lys Phe Tyr Met Pro Lys Lys
        275                 280                 285
Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Ser Leu Lys Pro
    290                 295                 300
Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu Arg
305                 310                 315                 320
Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu Lys
                325                 330                 335
Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala Thr
            340                 345                 350
Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser Ile Ile
        355                 360                 365
Ser Thr Leu Thr
    370
```

<210> 724
<211> 17
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 724
Gly Ile Ser Ser Gly Leu Leu Ser Gly Arg Ser Asp Asn Pro Ser Gly
 1   5   10   15
Pro

<210> 725
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 725
Gly Gly Ser Gly Ile Ser Ser Gly Leu Leu Ser Gly Arg Ser Asp Asn
 1   5   10   15
Pro Ser Gly Pro
            20

<210> 726
<211> 372
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 726
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1   5   10   15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20   25   30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35   40   45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50   55   60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65   70   75   80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85   90   95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100   105   110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115   120   125
Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130   135   140
Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145   150   155   160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro

```
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Gly Ser Pro Gly Val Pro Leu Ser Leu Tyr Ser Gly Pro Ala
225                 230                 235                 240
Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His Leu
                245                 250                 255
Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys Asn
            260                 265                 270
Pro Lys Leu Thr Ala Met Leu Thr Ala Lys Phe Ala Met Pro Lys Lys
        275                 280                 285
Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Ala Leu Lys Pro
    290                 295                 300
Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu Arg
305                 310                 315                 320
Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu Lys
                325                 330                 335
Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala Thr
            340                 345                 350
Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser Ile Ile
        355                 360                 365
Ser Thr Leu Thr
    370
```

<210> 727
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 727
Ser Gly Ser
 1

<210> 728
<211> 374
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 728
```
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
```

```
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Gly Gly Ser Gly Arg Ala Ala Ala Val Lys Ser Pro Ser Gly
225                 230                 235                 240
Pro Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu
                245                 250                 255
His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr
            260                 265                 270
Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Ser Lys Phe Tyr Met Pro
        275                 280                 285
Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Ser Leu
    290                 295                 300
Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His
305                 310                 315                 320
Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu
                325                 330                 335
Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr
            340                 345                 350
Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser
        355                 360                 365
Ile Ile Ser Thr Leu Thr
    370
```

<210> 729
<211> 373
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 729
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1   5   10   15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20   25   30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35   40   45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50   55   60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65   70   75   80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85   90   95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100   105   110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115   120   125
Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130   135   140
Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145   150   155   160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165   170   175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180   185   190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195   200   205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210   215   220
Pro Gly Gly Ile Ser Ser Gly Leu Leu Ser Gly Arg Ser Ser Gly Pro
225   230   235   240
Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His
                245   250   255
Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys
            260   265   270
Asn Pro Lys Leu Thr Arg Met Leu Thr Ser Lys Phe Tyr Met Pro Lys
        275   280   285
Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Ser Leu Lys
    290   295   300
Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu
305   310   315   320
Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu
                325   330   335
Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala
            340   345   350
Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser Ile
        355   360   365
Ile Ser Thr Leu Thr
    370

<210> 730
<211> 376

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 730
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1   5   10   15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20   25   30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35   40   45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50   55   60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65   70   75   80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85   90   95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100   105   110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115   120   125
Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130   135   140
Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145   150   155   160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165   170   175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180   185   190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195   200   205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210   215   220
Pro Gly Gly Gly Ser Gly Ile Ser Ser Gly Leu Leu Ser Gly Arg Ser
225   230   235   240
Ser Gly Pro Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln
                245   250   255
Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn
            260   265   270
Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Ser Lys Phe Tyr
        275   280   285
Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu
    290   295   300
Ser Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn
305   310   315   320
Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val
                325   330   335
Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp
            340   345   350
Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala
        355   360   365
Gln Ser Ile Ile Ser Thr Leu Thr

370 375

<210> 731
<211> 376
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 731
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
1 5 10 15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
20 25 30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
35 40 45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
50 55 60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65 70 75 80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
85 90 95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
100 105 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
115 120 125
Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
130 135 140
Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145 150 155 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
165 170 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
180 185 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
195 200 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
210 215 220
Pro Gly Gly Ile Ser Ser Gly Leu Leu Ser Gly Arg Ser Asp Asn Pro
225 230 235 240
Ser Gly Pro Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln
245 250 255
Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn
260 265 270
Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Ser Lys Phe Tyr
275 280 285
Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu
290 295 300
Ser Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn
305 310 315 320
Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val
325 330 335

```
Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp
            340                 345                 350
Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala
        355                 360                 365
Gln Ser Ile Ile Ser Thr Leu Thr
    370                 375


<210> 732
<211> 379
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 732
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Gly Gly Ser Gly Ile Ser Ser Gly Leu Leu Ser Gly Arg Ser
225                 230                 235                 240
Asp Asn Pro Ser Gly Pro Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr
                245                 250                 255
Gln Leu Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn
            260                 265                 270
Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Ser
        275                 280                 285
Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys
```

```
    290                 295                 300
Leu Glu Glu Ser Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln
305                 310                 315                 320
Ser Lys Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn
                325                 330                 335
Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu
            340                 345                 350
Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile
        355                 360                 365
Thr Phe Ala Gln Ser Ile Ile Ser Thr Leu Thr
    370                 375


<210> 733
<211> 376
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 733
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Gly Ile Ser Ser Gly Leu Leu Ser Gly Arg Ser Asp Gln Pro
225                 230                 235                 240
Ser Gly Pro Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln
                245                 250                 255
```

```
Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn
            260                 265                 270
Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Ser Lys Phe Tyr
        275                 280                 285
Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu
    290                 295                 300
Ser Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn
305                 310                 315                 320
Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val
                325                 330                 335
Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp
            340                 345                 350
Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala
        355                 360                 365
Gln Ser Ile Ile Ser Thr Leu Thr
    370                 375


<210> 734
<211> 379
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Constuct

<400> 734
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
```

```
    210                 215                 220
Pro Gly Gly Gly Ser Gly Ile Ser Ser Gly Leu Leu Ser Gly Arg Ser
225                 230                 235                 240
Asp Gln Pro Ser Gly Pro Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr
                245                 250                 255
Gln Leu Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn
            260                 265                 270
Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Ser
        275                 280                 285
Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys
    290                 295                 300
Leu Glu Glu Ser Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln
305                 310                 315                 320
Ser Lys Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn
                325                 330                 335
Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu
            340                 345                 350
Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile
        355                 360                 365
Thr Phe Ala Gln Ser Ile Ile Ser Thr Leu Thr
    370                 375


<210> 735
<211> 380
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 735
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
```

```
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Gly Lys Gln Leu Arg Val Val Asn Glu Tyr Ser Ser Met Asp
225                 230                 235                 240
Asn Met Leu Leu Gly Gly Pro Ala Pro Thr Ser Ser Ser Thr Lys Lys
                245                 250                 255
Thr Gln Leu Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu
            260                 265                 270
Asn Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr
        275                 280                 285
Ser Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln
    290                 295                 300
Cys Leu Glu Glu Ser Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala
305                 310                 315                 320
Gln Ser Lys Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile
                325                 330                 335
Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys
            340                 345                 350
Glu Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp
        355                 360                 365
Ile Thr Phe Ala Gln Ser Ile Ile Ser Thr Leu Thr
    370                 375                 380
```

<210> 736
<211> 380
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 736

```
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
```

```
    130                 135                 140
Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Gly Lys Gln Leu Arg Val Val Asn Glu Tyr Ser Ser Glu Asp
225                 230                 235                 240
Asn Met Leu Leu Gly Gly Pro Ala Pro Thr Ser Ser Ser Thr Lys Lys
                245                 250                 255
Thr Gln Leu Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu
            260                 265                 270
Asn Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr
        275                 280                 285
Ser Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln
    290                 295                 300
Cys Leu Glu Glu Ser Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala
305                 310                 315                 320
Gln Ser Lys Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile
                325                 330                 335
Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys
            340                 345                 350
Glu Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp
        355                 360                 365
Ile Thr Phe Ala Gln Ser Ile Ile Ser Thr Leu Thr
    370                 375                 380


<210> 737
<211> 380
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 737
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
```

```
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Gly Lys Gln Leu Arg Val Val Asn Gly Tyr Ser Ser Glu Asp
225                 230                 235                 240
Asn Met Leu Leu Gly Gly Pro Ala Pro Thr Ser Ser Ser Thr Lys Lys
                245                 250                 255
Thr Gln Leu Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu
            260                 265                 270
Asn Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr
        275                 280                 285
Ser Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln
    290                 295                 300
Cys Leu Glu Glu Ser Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala
305                 310                 315                 320
Gln Ser Lys Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile
                325                 330                 335
Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys
            340                 345                 350
Glu Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp
        355                 360                 365
Ile Thr Phe Ala Gln Ser Ile Ile Ser Thr Leu Thr
    370                 375                 380
```

<210> 738
<211> 380
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 738

```
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
```

```
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Gly Lys Gln Leu Arg Val Val Gly Gly Leu Val His Leu Lys
225                 230                 235                 240
Asn Thr Met Glu Thr Gly Pro Ala Pro Thr Ser Ser Ser Thr Lys Lys
                245                 250                 255
Thr Gln Leu Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu
            260                 265                 270
Asn Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr
        275                 280                 285
Ser Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln
    290                 295                 300
Cys Leu Glu Glu Ser Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala
305                 310                 315                 320
Gln Ser Lys Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile
                325                 330                 335
Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys
            340                 345                 350
Glu Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp
        355                 360                 365
Ile Thr Phe Ala Gln Ser Ile Ile Ser Thr Leu Thr
    370                 375                 380


<210> 739
<211> 380
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 739
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
```

```
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Gly Thr Arg Asp Arg Leu Asp Glu Val Asn Phe Lys Gln Leu
225                 230                 235                 240
Arg Val Val Asn Gly Gly Pro Ala Pro Thr Ser Ser Ser Thr Lys Lys
                245                 250                 255
Thr Gln Leu Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu
            260                 265                 270
Asn Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr
        275                 280                 285
Ser Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln
    290                 295                 300
Cys Leu Glu Glu Ser Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala
305                 310                 315                 320
Gln Ser Lys Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile
                325                 330                 335
Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys
            340                 345                 350
Glu Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp
        355                 360                 365
Ile Thr Phe Ala Gln Ser Ile Ile Ser Thr Leu Thr
    370                 375                 380
```

<210> 740
<211> 380
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 740
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1   5   10   15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20   25   30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35   40   45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50   55   60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65   70   75   80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85   90   95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100   105   110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115   120   125
Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130   135   140
Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145   150   155   160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165   170   175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180   185   190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195   200   205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210   215   220
Pro Gly Gly Thr Arg Asp Arg Leu Asp Glu Val Asn Phe Lys Leu Leu
225   230   235   240
Arg Val Val Asn Gly Gly Pro Ala Pro Thr Ser Ser Ser Thr Lys Lys
                245   250   255
Thr Gln Leu Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu
            260   265   270
Asn Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr
        275   280   285
Ser Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln
    290   295   300
Cys Leu Glu Glu Ser Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala
305   310   315   320
Gln Ser Lys Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile
                325   330   335
Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys
            340   345   350
Glu Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp
        355   360   365
Ile Thr Phe Ala Gln Ser Ile Ile Ser Thr Leu Thr
    370   375   380

<210> 741

<211> 380
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 741
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1   5   10   15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20   25   30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35   40   45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50   55   60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65   70   75   80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85   90   95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100   105   110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115   120   125
Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130   135   140
Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145   150   155   160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165   170   175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180   185   190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195   200   205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210   215   220
Pro Gly Gly Thr Arg Asp Arg Leu Asp Pro Val Asn Phe Lys Gln Leu
225   230   235   240
Arg Val Val Asn Gly Gly Pro Ala Pro Thr Ser Ser Ser Thr Lys Lys
                245   250   255
Thr Gln Leu Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu
            260   265   270
Asn Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr
        275   280   285
Ser Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln
    290   295   300
Cys Leu Glu Glu Ser Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala
305   310   315   320
Gln Ser Lys Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile
                325   330   335
Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys
            340   345   350
Glu Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp
        355   360   365

```
Ile Thr Phe Ala Gln Ser Ile Ile Ser Thr Leu Thr
    370                 375                 380


<210> 742
<211> 380
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 742
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Gly Thr Arg Asp Arg Leu Asp Pro Val Asn Phe Lys Leu Leu
225                 230                 235                 240
Arg Val Val Asn Gly Gly Pro Ala Pro Thr Ser Ser Ser Thr Lys Lys
                245                 250                 255
Thr Gln Leu Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu
            260                 265                 270
Asn Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr
        275                 280                 285
Ser Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln
    290                 295                 300
Cys Leu Glu Glu Ser Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala
305                 310                 315                 320
Gln Ser Lys Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile
```

```
                325                 330                 335
Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys
            340                 345                 350
Glu Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp
        355                 360                 365
Ile Thr Phe Ala Gln Ser Ile Ile Ser Thr Leu Thr
    370                 375                 380


<210> 743
<211> 380
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 743
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Gly Asn Pro Met Gly Ser Glu Pro Val Asn Phe Lys Gln Leu
225                 230                 235                 240
Arg Val Val Asn Gly Gly Pro Ala Pro Thr Ser Ser Ser Thr Lys Lys
                245                 250                 255
Thr Gln Leu Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu
            260                 265                 270
Asn Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr
        275                 280                 285
```

```
Ser Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln
    290                 295                 300
Cys Leu Glu Glu Ser Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala
305                 310                 315                 320
Gln Ser Lys Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile
                325                 330                 335
Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys
            340                 345                 350
Glu Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp
        355                 360                 365
Ile Thr Phe Ala Gln Ser Ile Ile Ser Thr Leu Thr
    370                 375                 380


<210> 744
<211> 380
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 744
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Gly Asn Pro Met Gly Ser Glu Pro Val Asn Phe Lys Leu Leu
225                 230                 235                 240
Arg Val Val Asn Gly Gly Pro Ala Pro Thr Ser Ser Ser Thr Lys Lys
```

```
                245                 250                 255
Thr Gln Leu Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu
            260                 265                 270
Asn Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr
        275                 280                 285
Ser Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln
    290                 295                 300
Cys Leu Glu Glu Ser Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala
305                 310                 315                 320
Gln Ser Lys Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile
                325                 330                 335
Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys
            340                 345                 350
Glu Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp
        355                 360                 365
Ile Thr Phe Ala Gln Ser Ile Ile Ser Thr Leu Thr
    370                 375                 380


<210> 745
<211> 380
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 745
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
```

```
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Gly Asn Pro Met Gly Ser Asp Pro Val Asn Phe Lys Gln Leu
225                 230                 235                 240
Arg Val Val Asn Gly Gly Pro Ala Pro Thr Ser Ser Ser Thr Lys Lys
                245                 250                 255
Thr Gln Leu Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu
            260                 265                 270
Asn Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr
        275                 280                 285
Ser Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln
    290                 295                 300
Cys Leu Glu Glu Ser Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala
305                 310                 315                 320
Gln Ser Lys Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile
                325                 330                 335
Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys
            340                 345                 350
Glu Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp
        355                 360                 365
Ile Thr Phe Ala Gln Ser Ile Ile Ser Thr Leu Thr
    370                 375                 380
```

<210> 746
<211> 380
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 746

```
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
```

```
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Gly Asn Pro Met Gly Ser Asp Pro Val Asn Phe Lys Leu Leu
225                 230                 235                 240
Arg Val Val Asn Gly Gly Pro Ala Pro Thr Ser Ser Ser Thr Lys Lys
                245                 250                 255
Thr Gln Leu Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu
            260                 265                 270
Asn Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr
        275                 280                 285
Ser Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln
    290                 295                 300
Cys Leu Glu Glu Ser Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala
305                 310                 315                 320
Gln Ser Lys Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile
                325                 330                 335
Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys
            340                 345                 350
Glu Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp
        355                 360                 365
Ile Thr Phe Ala Gln Ser Ile Ile Ser Thr Leu Thr
    370                 375                 380


<210> 747
<211> 362
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 747
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
```

```
Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Gly Gly Ser Ser Pro Pro Met Pro Tyr Asp Leu Tyr His Pro
225                 230                 235                 240
Ser Gly Pro Ser Gly Ser Pro Gly Asn Trp Val Asn Val Ile Ser Asp
                245                 250                 255
Leu Lys Lys Ile Glu Asp Leu Ile Gln Ser Met His Ile Asp Ala Thr
            260                 265                 270
Leu Tyr Thr Glu Ser Asp Val His Pro Ser Cys Lys Val Thr Ala Met
        275                 280                 285
Lys Cys Phe Leu Leu Glu Leu Gln Val Ile Ser Leu Glu Ser Gly Asp
    290                 295                 300
Ala Ser Ile His Asp Thr Val Glu Asn Leu Ile Ile Leu Ala Asn Asn
305                 310                 315                 320
Ser Leu Ser Ser Asn Gly Asn Val Thr Glu Ser Gly Cys Lys Glu Cys
                325                 330                 335
Glu Glu Leu Glu Glu Lys Asn Ile Lys Glu Phe Leu Gln Ser Phe Val
            340                 345                 350
His Ile Val Gln Met Phe Ile Asn Thr Ser
        355                 360
```

<210> 748
<211> 362
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 748

```
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
```

```
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Gly Gly Ser Ser Pro Pro Gly Gly Gly Ser Ser Gly Gly Gly
225                 230                 235                 240
Ser Gly Pro Ser Gly Ser Pro Gly Asn Trp Val Asn Val Ile Ser Asp
                245                 250                 255
Leu Lys Lys Ile Glu Asp Leu Ile Gln Ser Met His Ile Asp Ala Thr
            260                 265                 270
Leu Tyr Thr Glu Ser Asp Val His Pro Ser Cys Lys Val Thr Ala Met
        275                 280                 285
Lys Cys Phe Leu Leu Glu Leu Gln Val Ile Ser Leu Glu Ser Gly Asp
    290                 295                 300
Ala Ser Ile His Asp Thr Val Glu Asn Leu Ile Ile Leu Ala Asn Asn
305                 310                 315                 320
Ser Leu Ser Ser Asn Gly Asn Val Thr Glu Ser Gly Cys Lys Glu Cys
                325                 330                 335
Glu Glu Leu Glu Glu Lys Asn Ile Lys Glu Phe Leu Gln Ser Phe Val
            340                 345                 350
His Ile Val Gln Met Phe Ile Asn Thr Ser
        355                 360


<210> 749
<211> 557
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 749
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
```

```
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Gly Gly Ser Ser Pro Pro Met Pro Tyr Asp Leu Tyr His Pro
225                 230                 235                 240
Ser Gly Pro Ser Gly Ser Pro Gly Asn Trp Val Asn Val Ile Ser Asp
                245                 250                 255
Leu Lys Lys Ile Glu Asp Leu Ile Gln Ser Met His Ile Asp Ala Thr
            260                 265                 270
Leu Tyr Thr Glu Ser Asp Val His Pro Ser Cys Lys Val Thr Ala Met
        275                 280                 285
Lys Cys Phe Leu Leu Glu Leu Gln Val Ile Ser Leu Glu Ser Gly Asp
    290                 295                 300
Ala Ser Ile His Asp Thr Val Glu Asn Leu Ile Ile Leu Ala Asn Asn
305                 310                 315                 320
Ser Leu Ser Ser Asn Gly Asn Val Thr Glu Ser Gly Cys Lys Glu Cys
                325                 330                 335
Glu Glu Leu Glu Glu Lys Asn Ile Lys Glu Phe Leu Gln Ser Phe Val
            340                 345                 350
His Ile Val Gln Met Phe Ile Asn Thr Ser Gly Gly Gly Gly Ser Gly
        355                 360                 365
Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ile Thr
    370                 375                 380
Cys Pro Pro Pro Met Ser Val Glu His Ala Asp Ile Trp Val Lys Ser
385                 390                 395                 400
Tyr Ser Leu Tyr Ser Arg Glu Arg Tyr Ile Cys Asn Ser Gly Phe Lys
                405                 410                 415
Arg Lys Ala Gly Thr Ser Ser Leu Thr Glu Cys Val Leu Asn Lys Ala
            420                 425                 430
Thr Asn Val Ala His Trp Thr Thr Pro Ser Leu Lys Cys Ile Arg Asp
        435                 440                 445
Pro Ala Leu Val His Gln Arg Pro Ala Pro Pro Ser Thr Val Thr Thr
    450                 455                 460
Ala Gly Val Thr Pro Gln Pro Glu Ser Leu Ser Pro Ser Gly Lys Glu
465                 470                 475                 480
Pro Ala Ala Ser Ser Pro Ser Ser Asn Asn Thr Ala Ala Thr Thr Ala
                485                 490                 495
Ala Ile Val Pro Gly Ser Gln Leu Met Pro Ser Lys Ser Pro Ser Thr
            500                 505                 510
```

Gly Thr Thr Glu Ile Ser Ser His Glu Ser Ser His Gly Thr Pro Ser
515 520 525
Gln Thr Thr Ala Lys Asn Trp Glu Leu Thr Ala Ser Ala Ser His Gln
530 535 540
Pro Pro Gly Val Tyr Pro Gln Gly His Ser Asp Thr Thr
545 550 555

<210> 750
<211> 484
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 750
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
1 5 10 15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
20 25 30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
35 40 45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
50 55 60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65 70 75 80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
85 90 95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
100 105 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
115 120 125
Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
130 135 140
Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145 150 155 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
165 170 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
180 185 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
195 200 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
210 215 220
Pro Gly Gly Gly Ser Ser Pro Pro Met Pro Tyr Asp Leu Tyr His Pro
225 230 235 240
Ser Gly Pro Ser Gly Ser Pro Gly Asn Trp Val Asn Val Ile Ser Asp
245 250 255
Leu Lys Lys Ile Glu Asp Leu Ile Gln Ser Met His Ile Asp Ala Thr
260 265 270
Leu Tyr Thr Glu Ser Asp Val His Pro Ser Cys Lys Val Thr Ala Met
275 280 285
Lys Cys Phe Leu Leu Glu Leu Gln Val Ile Ser Leu Glu Ser Gly Asp

```
    290                 295                 300
Ala Ser Ile His Asp Thr Val Glu Asn Leu Ile Ile Leu Ala Asn Asn
305                 310                 315                 320
Ser Leu Ser Ser Asn Gly Asn Val Thr Glu Ser Gly Cys Lys Glu Cys
                325                 330                 335
Glu Glu Leu Glu Glu Lys Asn Ile Lys Glu Phe Leu Gln Ser Phe Val
            340                 345                 350
His Ile Val Gln Met Phe Ile Asn Thr Ser Gly Gly Gly Gly Ser Gly
        355                 360                 365
Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ile Thr
    370                 375                 380
Cys Pro Pro Pro Met Ser Val Glu His Ala Asp Ile Trp Val Lys Ser
385                 390                 395                 400
Tyr Ser Leu Tyr Ser Arg Glu Arg Tyr Ile Cys Asn Ser Gly Phe Lys
                405                 410                 415
Arg Lys Ala Gly Thr Ser Ser Leu Thr Glu Cys Val Leu Asn Lys Ala
            420                 425                 430
Thr Asn Val Ala His Trp Thr Thr Pro Ser Leu Lys Cys Ile Arg Asp
        435                 440                 445
Pro Ala Leu Val His Gln Arg Pro Ala Pro Pro Ser Thr Val Thr Thr
    450                 455                 460
Ala Gly Val Thr Pro Gln Pro Glu Ser Leu Ser Pro Ser Gly Lys Glu
465                 470                 475                 480
Pro Ala Ala Ser
```

<210> 751
<211> 361
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Constuct

<400> 751

```
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
```

```
Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Gly Gly Ser Ser Pro Pro Gly Gly Gly Ser Ser Gly Gly Gly
225                 230                 235                 240
Ser Gly Pro Gly Ser Gly Ser Asn Trp Val Asn Val Ile Ser Asp Leu
                245                 250                 255
Lys Lys Ile Glu Asp Leu Ile Gln Ser Met His Ile Asp Ala Thr Leu
            260                 265                 270
Tyr Thr Glu Ser Asp Val His Pro Ser Cys Lys Val Thr Ala Met Lys
        275                 280                 285
Cys Phe Leu Leu Glu Leu Gln Val Ile Ser Leu Glu Ser Gly Asp Ala
    290                 295                 300
Ser Ile His Asp Thr Val Glu Asn Leu Ile Ile Leu Ala Asn Asn Ser
305                 310                 315                 320
Leu Ser Ser Asn Gly Asn Val Thr Glu Ser Gly Cys Lys Glu Cys Glu
                325                 330                 335
Glu Leu Glu Glu Lys Asn Ile Lys Glu Phe Leu Gln Ser Phe Val His
            340                 345                 350
Ile Val Gln Met Phe Ile Asn Thr Ser
        355                 360
```

<210> 752
<211> 556
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 752

```
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
```

```
        115                 120                 125
Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Gly Gly Ser Ser Pro Pro Met Pro Tyr Asp Leu Tyr His Pro
225                 230                 235                 240
Ser Gly Pro Gly Ser Gly Ser Asn Trp Val Asn Val Ile Ser Asp Leu
                245                 250                 255
Lys Lys Ile Glu Asp Leu Ile Gln Ser Met His Ile Asp Ala Thr Leu
            260                 265                 270
Tyr Thr Glu Ser Asp Val His Pro Ser Cys Lys Val Thr Ala Met Lys
        275                 280                 285
Cys Phe Leu Leu Glu Leu Gln Val Ile Ser Leu Glu Ser Gly Asp Ala
    290                 295                 300
Ser Ile His Asp Thr Val Glu Asn Leu Ile Ile Leu Ala Asn Asn Ser
305                 310                 315                 320
Leu Ser Ser Asn Gly Asn Val Thr Glu Ser Gly Cys Lys Glu Cys Glu
                325                 330                 335
Glu Leu Glu Glu Lys Asn Ile Lys Glu Phe Leu Gln Ser Phe Val His
            340                 345                 350
Ile Val Gln Met Phe Ile Asn Thr Ser Gly Gly Gly Gly Ser Gly Gly
        355                 360                 365
Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ile Thr Cys
    370                 375                 380
Pro Pro Pro Met Ser Val Glu His Ala Asp Ile Trp Val Lys Ser Tyr
385                 390                 395                 400
Ser Leu Tyr Ser Arg Glu Arg Tyr Ile Cys Asn Ser Gly Phe Lys Arg
                405                 410                 415
Lys Ala Gly Thr Ser Ser Leu Thr Glu Cys Val Leu Asn Lys Ala Thr
            420                 425                 430
Asn Val Ala His Trp Thr Thr Pro Ser Leu Lys Cys Ile Arg Asp Pro
        435                 440                 445
Ala Leu Val His Gln Arg Pro Ala Pro Pro Ser Thr Val Thr Thr Ala
    450                 455                 460
Gly Val Thr Pro Gln Pro Glu Ser Leu Ser Pro Ser Gly Lys Glu Pro
465                 470                 475                 480
Ala Ala Ser Ser Pro Ser Ser Asn Asn Thr Ala Ala Thr Thr Ala Ala
                485                 490                 495
Ile Val Pro Gly Ser Gln Leu Met Pro Ser Lys Ser Pro Ser Thr Gly
            500                 505                 510
Thr Thr Glu Ile Ser Ser His Glu Ser Ser His Gly Thr Pro Ser Gln
        515                 520                 525
Thr Thr Ala Lys Asn Trp Glu Leu Thr Ala Ser Ala Ser His Gln Pro
    530                 535                 540
Pro Gly Val Tyr Pro Gln Gly His Ser Asp Thr Thr
```

545 550 555

<210> 753
<211> 483
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 753
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
1 5 10 15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
20 25 30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
35 40 45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
50 55 60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65 70 75 80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
85 90 95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
100 105 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
115 120 125
Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
130 135 140
Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145 150 155 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
165 170 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
180 185 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
195 200 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
210 215 220
Pro Gly Gly Gly Ser Ser Pro Pro Met Pro Tyr Asp Leu Tyr His Pro
225 230 235 240
Ser Gly Pro Gly Ser Gly Ser Asn Trp Val Asn Val Ile Ser Asp Leu
245 250 255
Lys Lys Ile Glu Asp Leu Ile Gln Ser Met His Ile Asp Ala Thr Leu
260 265 270
Tyr Thr Glu Ser Asp Val His Pro Ser Cys Lys Val Thr Ala Met Lys
275 280 285
Cys Phe Leu Leu Glu Leu Gln Val Ile Ser Leu Glu Ser Gly Asp Ala
290 295 300
Ser Ile His Asp Thr Val Glu Asn Leu Ile Ile Leu Ala Asn Asn Ser
305 310 315 320
Leu Ser Ser Asn Gly Asn Val Thr Glu Ser Gly Cys Lys Glu Cys Glu
325 330 335

```
Glu Leu Glu Glu Lys Asn Ile Lys Glu Phe Leu Gln Ser Phe Val His
            340                 345                 350
Ile Val Gln Met Phe Ile Asn Thr Ser Gly Gly Gly Gly Ser Gly Gly
        355                 360                 365
Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ile Thr Cys
    370                 375                 380
Pro Pro Pro Met Ser Val Glu His Ala Asp Ile Trp Val Lys Ser Tyr
385                 390                 395                 400
Ser Leu Tyr Ser Arg Glu Arg Tyr Ile Cys Asn Ser Gly Phe Lys Arg
                405                 410                 415
Lys Ala Gly Thr Ser Ser Leu Thr Glu Cys Val Leu Asn Lys Ala Thr
            420                 425                 430
Asn Val Ala His Trp Thr Thr Pro Ser Leu Lys Cys Ile Arg Asp Pro
        435                 440                 445
Ala Leu Val His Gln Arg Pro Ala Pro Pro Ser Thr Val Thr Thr Ala
    450                 455                 460
Gly Val Thr Pro Gln Pro Glu Ser Leu Ser Pro Ser Gly Lys Glu Pro
465                 470                 475                 480
Ala Ala Ser
```

<210> 754
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 754

```
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
```

```
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Gly Gly Ser Ser Pro Pro Val Pro Leu Ser Leu Tyr Ser Gly
225                 230                 235                 240
Pro Gly Ser Gly Ser Asn Trp Val Asn Val Ile Ser Asp Leu Lys Lys
                245                 250                 255
Ile Glu Asp Leu Ile Gln Ser Met His Ile Asp Ala Thr Leu Tyr Thr
            260                 265                 270
Glu Ser Asp Val His Pro Ser Cys Lys Val Thr Ala Met Lys Cys Phe
        275                 280                 285
Leu Leu Glu Leu Gln Val Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile
    290                 295                 300
His Asp Thr Val Glu Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser
305                 310                 315                 320
Ser Asn Gly Asn Val Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu
                325                 330                 335
Glu Glu Lys Asn Ile Lys Glu Phe Leu Gln Ser Phe Val His Ile Val
            340                 345                 350
Gln Met Phe Ile Asn Thr Ser
        355


<210> 755
<211> 672
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 755
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
```

```
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Pro Gly Ser Gly Ser Ala Val Asn Gly Thr Ser Gln Phe Thr
225                 230                 235                 240
Cys Phe Tyr Asn Ser Arg Ala Asn Ile Ser Cys Val Trp Ser Gln Asp
                245                 250                 255
Gly Ala Leu Gln Asp Thr Ser Cys Gln Val His Ala Trp Pro Asp Arg
            260                 265                 270
Arg Arg Trp Asn Gln Thr Cys Glu Leu Leu Pro Val Ser Gln Ala Ser
        275                 280                 285
Trp Ala Cys Asn Leu Ile Leu Gly Ala Pro Asp Ser Gln Lys Leu Thr
    290                 295                 300
Thr Val Asp Ile Val Thr Leu Arg Val Leu Cys Arg Glu Gly Val Arg
305                 310                 315                 320
Trp Arg Val Met Ala Ile Gln Asp Phe Lys Pro Phe Glu Asn Leu Arg
                325                 330                 335
Leu Met Ala Pro Ile Ser Leu Gln Val Val His Val Glu Thr His Arg
            340                 345                 350
Cys Asn Ile Ser Trp Glu Ile Ser Gln Ala Ser His Tyr Phe Glu Arg
        355                 360                 365
His Leu Glu Phe Glu Ala Arg Thr Leu Ser Pro Gly His Thr Trp Glu
    370                 375                 380
Glu Ala Pro Leu Leu Thr Leu Lys Gln Lys Gln Glu Trp Ile Cys Leu
385                 390                 395                 400
Glu Thr Leu Thr Pro Asp Thr Gln Tyr Glu Phe Gln Val Arg Val Lys
                405                 410                 415
Pro Leu Gln Gly Glu Phe Thr Thr Trp Ser Pro Trp Ser Gln Pro Leu
            420                 425                 430
Ala Phe Arg Thr Lys Pro Ala Ala Leu Gly Lys Asp Pro Gly Gly Pro
        435                 440                 445
Ser Pro Val Pro Leu Ser Leu Tyr Ser Gly Gly Pro Ile Thr Cys Pro
    450                 455                 460
Pro Pro Met Ser Val Glu His Ala Asp Ile Trp Val Lys Ser Tyr Ser
465                 470                 475                 480
Leu Tyr Ser Arg Glu Arg Tyr Ile Cys Asn Ser Gly Phe Lys Arg Lys
                485                 490                 495
Ala Gly Thr Ser Ser Leu Thr Glu Cys Val Leu Asn Lys Ala Thr Asn
            500                 505                 510
Val Ala His Trp Thr Thr Pro Ser Leu Lys Cys Ile Arg Asp Pro Ala
        515                 520                 525
Leu Val His Gln Arg Pro Ala Pro Pro Ser Gly Gly Gly Gly Ser Gly
    530                 535                 540
Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asn Trp
545                 550                 555                 560
Val Asn Val Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile Gln Ser
                565                 570                 575
Met His Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His Pro Ser
            580                 585                 590
```

```
Cys Lys Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln Val Ile
        595                 600                 605
Ser Leu Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu Asn Leu
    610                 615                 620
Ile Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val Thr Glu
625                 630                 635                 640
Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile Lys Glu
                645                 650                 655
Phe Leu Gln Ser Phe Val His Ile Val Gln Met Phe Ile Asn Thr Ser
            660                 665                 670
```

<210> 756
<211> 673
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 756

```
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Pro Gly Ser Gly Ser Ala Val Asn Gly Thr Ser Gln Phe Thr
225                 230                 235                 240
Cys Phe Tyr Asn Ser Arg Ala Asn Ile Ser Cys Val Trp Ser Gln Asp
                245                 250                 255
Gly Ala Leu Gln Asp Thr Ser Cys Gln Val His Ala Trp Pro Asp Arg
```

```
            260                 265                 270
Arg Arg Trp Asn Gln Thr Cys Glu Leu Leu Pro Val Ser Gln Ala Ser
        275                 280                 285
Trp Ala Cys Asn Leu Ile Leu Gly Ala Pro Asp Ser Gln Lys Leu Thr
    290                 295                 300
Thr Val Asp Ile Val Thr Leu Arg Val Leu Cys Arg Glu Gly Val Arg
305                 310                 315                 320
Trp Arg Val Met Ala Ile Gln Asp Phe Lys Pro Phe Glu Asn Leu Arg
                325                 330                 335
Leu Met Ala Pro Ile Ser Leu Gln Val Val His Val Glu Thr His Arg
            340                 345                 350
Cys Asn Ile Ser Trp Glu Ile Ser Gln Ala Ser His Tyr Phe Glu Arg
        355                 360                 365
His Leu Glu Phe Glu Ala Arg Thr Leu Ser Pro Gly His Thr Trp Glu
    370                 375                 380
Glu Ala Pro Leu Leu Thr Leu Lys Gln Lys Gln Glu Trp Ile Cys Leu
385                 390                 395                 400
Glu Thr Leu Thr Pro Asp Thr Gln Tyr Glu Phe Gln Val Arg Val Lys
                405                 410                 415
Pro Leu Gln Gly Glu Phe Thr Thr Trp Ser Pro Trp Ser Gln Pro Leu
            420                 425                 430
Ala Phe Arg Thr Lys Pro Ala Ala Leu Gly Lys Asp Ser Gly Ser Gly
        435                 440                 445
Gly Ser Pro Val Pro Leu Ser Leu Tyr Ser Gly Gly Pro Ile Thr Cys
    450                 455                 460
Pro Pro Pro Met Ser Val Glu His Ala Asp Ile Trp Val Lys Ser Tyr
465                 470                 475                 480
Ser Leu Tyr Ser Arg Glu Arg Tyr Ile Cys Asn Ser Gly Phe Lys Arg
                485                 490                 495
Lys Ala Gly Thr Ser Ser Leu Thr Glu Cys Val Leu Asn Lys Ala Thr
            500                 505                 510
Asn Val Ala His Trp Thr Thr Pro Ser Leu Lys Cys Ile Arg Asp Pro
        515                 520                 525
Ala Leu Val His Gln Arg Pro Ala Pro Pro Ser Gly Gly Gly Gly Ser
    530                 535                 540
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asn
545                 550                 555                 560
Trp Val Asn Val Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile Gln
                565                 570                 575
Ser Met His Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His Pro
            580                 585                 590
Ser Cys Lys Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln Val
        595                 600                 605
Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu Asn
    610                 615                 620
Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val Thr
625                 630                 635                 640
Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile Lys
                645                 650                 655
Glu Phe Leu Gln Ser Phe Val His Ile Val Gln Met Phe Ile Asn Thr
            660                 665                 670
Ser
```

<210> 757
<211> 672
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 757
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1   5   10   15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20   25   30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35   40   45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50   55   60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65   70   75   80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85   90   95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100   105   110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115   120   125
Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130   135   140
Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145   150   155   160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165   170   175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val
            180   185   190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195   200   205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210   215   220
Pro Gly Pro Gly Ser Gly Ser Ala Val Asn Gly Thr Ser Gln Phe Thr
225   230   235   240
Cys Phe Tyr Asn Ser Arg Ala Asn Ile Ser Cys Val Trp Ser Gln Asp
                245   250   255
Gly Ala Leu Gln Asp Thr Ser Cys Gln Val His Ala Trp Pro Asp Arg
            260   265   270
Arg Arg Trp Asn Gln Thr Cys Glu Leu Leu Pro Val Ser Gln Ala Ser
        275   280   285
Trp Ala Cys Asn Leu Ile Leu Gly Ala Pro Asp Ser Gln Lys Leu Thr
    290   295   300
Thr Val Asp Ile Val Thr Leu Arg Val Leu Cys Arg Glu Gly Val Arg
305   310   315   320
Trp Arg Val Met Ala Ile Gln Asp Phe Lys Pro Phe Glu Asn Leu Arg
                325   330   335
Leu Met Ala Pro Ile Ser Leu Gln Val Val His Val Glu Thr His Arg
            340   345   350

```
Cys Asn Ile Ser Trp Glu Ile Ser Gln Ala Ser His Tyr Phe Glu Arg
        355                 360                 365
His Leu Glu Phe Glu Ala Arg Thr Leu Ser Pro Gly His Thr Trp Glu
    370                 375                 380
Glu Ala Pro Leu Leu Thr Leu Lys Gln Lys Gln Glu Trp Ile Cys Leu
385                 390                 395                 400
Glu Thr Leu Thr Pro Asp Thr Gln Tyr Glu Phe Gln Val Arg Val Lys
                405                 410                 415
Pro Leu Gln Gly Glu Phe Thr Thr Trp Ser Pro Trp Ser Gln Pro Leu
            420                 425                 430
Ala Phe Arg Thr Lys Pro Ala Ala Leu Gly Lys Asp Gly Gly Gly Ser
        435                 440                 445
Ser Pro Val Pro Leu Ser Leu Tyr Ser Gly Gly Pro Ile Thr Cys Pro
    450                 455                 460
Pro Pro Met Ser Val Glu His Ala Asp Ile Trp Val Lys Ser Tyr Ser
465                 470                 475                 480
Leu Tyr Ser Arg Glu Arg Tyr Ile Cys Asn Ser Gly Phe Lys Arg Lys
                485                 490                 495
Ala Gly Thr Ser Ser Leu Thr Glu Cys Val Leu Asn Lys Ala Thr Asn
            500                 505                 510
Val Ala His Trp Thr Thr Pro Ser Leu Lys Cys Ile Arg Asp Pro Ala
        515                 520                 525
Leu Val His Gln Arg Pro Ala Pro Pro Ser Gly Gly Gly Gly Ser Gly
    530                 535                 540
Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asn Trp
545                 550                 555                 560
Val Asn Val Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile Gln Ser
                565                 570                 575
Met His Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His Pro Ser
            580                 585                 590
Cys Lys Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln Val Ile
        595                 600                 605
Ser Leu Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu Asn Leu
    610                 615                 620
Ile Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val Thr Glu
625                 630                 635                 640
Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile Lys Glu
                645                 650                 655
Phe Leu Gln Ser Phe Val His Ile Val Gln Met Phe Ile Asn Thr Ser
            660                 665                 670


<210> 758
<211> 555
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 758
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
```

```
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Gly Gly Ser Ser Pro Pro Val Pro Leu Ser Leu Tyr Ser Gly
225                 230                 235                 240
Pro Ser Gly Ser Pro Gly Asn Trp Val Asn Val Ile Ser Asp Leu Lys
                245                 250                 255
Lys Ile Glu Asp Leu Ile Gln Ser Met His Ile Asp Ala Thr Leu Tyr
            260                 265                 270
Thr Glu Ser Asp Val His Pro Ser Cys Lys Val Thr Ala Met Lys Cys
        275                 280                 285
Phe Leu Leu Glu Leu Gln Val Ile Ser Leu Glu Ser Gly Asp Ala Ser
    290                 295                 300
Ile His Asp Thr Val Glu Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu
305                 310                 315                 320
Ser Ser Asn Gly Asn Val Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu
                325                 330                 335
Leu Glu Glu Lys Asn Ile Lys Glu Phe Leu Gln Ser Phe Val His Ile
            340                 345                 350
Val Gln Met Phe Ile Asn Thr Ser Gly Gly Ser Gly Gly Gly Ser Gly
        355                 360                 365
Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Ile Thr Cys Pro
    370                 375                 380
Pro Pro Met Ser Val Glu His Ala Asp Ile Trp Val Lys Ser Tyr Ser
385                 390                 395                 400
Leu Tyr Ser Arg Glu Arg Tyr Ile Cys Asn Ser Gly Phe Lys Arg Lys
                405                 410                 415
Ala Gly Thr Ser Ser Leu Thr Glu Cys Val Leu Asn Lys Ala Thr Asn
            420                 425                 430
Val Ala His Trp Thr Thr Pro Ser Leu Lys Cys Ile Arg Asp Pro Ala
        435                 440                 445
Leu Val His Gln Arg Pro Ala Pro Pro Ser Thr Val Thr Thr Ala Gly
```

```
    450                 455                 460
Val Thr Pro Gln Pro Glu Ser Leu Ser Pro Ser Gly Lys Glu Pro Ala
465                 470                 475                 480
Ala Ser Ser Pro Ser Ser Asn Asn Thr Ala Ala Thr Thr Ala Ala Ile
                485                 490                 495
Val Pro Gly Ser Gln Leu Met Pro Ser Lys Ser Pro Ser Thr Gly Thr
            500                 505                 510
Thr Glu Ile Ser Ser His Glu Ser Ser His Gly Thr Pro Ser Gln Thr
        515                 520                 525
Thr Ala Lys Asn Trp Glu Leu Thr Ala Ser Ala Ser His Gln Pro Pro
    530                 535                 540
Gly Val Tyr Pro Gln Gly His Ser Asp Thr Thr
545                 550                 555


<210> 759
<211> 559
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 759
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Gly Gly Ser Ser Pro Pro Val Pro Leu Ser Leu Tyr Ser Gly
225                 230                 235                 240
```

```
Pro Ser Gly Ser Pro Gly Asn Trp Val Asn Val Ile Ser Asp Leu Lys
                245                 250                 255
Lys Ile Glu Asp Leu Ile Gln Ser Met His Ile Asp Ala Thr Leu Tyr
            260                 265                 270
Thr Glu Ser Asp Val His Pro Ser Cys Lys Val Thr Ala Met Lys Cys
        275                 280                 285
Phe Leu Leu Glu Leu Gln Val Ile Ser Leu Glu Ser Gly Asp Ala Ser
    290                 295                 300
Ile His Asp Thr Val Glu Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu
305                 310                 315                 320
Ser Ser Asn Gly Asn Val Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu
                325                 330                 335
Leu Glu Glu Lys Asn Ile Lys Glu Phe Leu Gln Ser Phe Val His Ile
            340                 345                 350
Val Gln Met Phe Ile Asn Thr Ser Gly Gly Ser Gly Gly Gly Ser Gly
        355                 360                 365
Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    370                 375                 380
Ile Thr Cys Pro Pro Pro Met Ser Val Glu His Ala Asp Ile Trp Val
385                 390                 395                 400
Lys Ser Tyr Ser Leu Tyr Ser Arg Glu Arg Tyr Ile Cys Asn Ser Gly
                405                 410                 415
Phe Lys Arg Lys Ala Gly Thr Ser Ser Leu Thr Glu Cys Val Leu Asn
            420                 425                 430
Lys Ala Thr Asn Val Ala His Trp Thr Thr Pro Ser Leu Lys Cys Ile
        435                 440                 445
Arg Asp Pro Ala Leu Val His Gln Arg Pro Ala Pro Pro Ser Thr Val
    450                 455                 460
Thr Thr Ala Gly Val Thr Pro Gln Pro Glu Ser Leu Ser Pro Ser Gly
465                 470                 475                 480
Lys Glu Pro Ala Ala Ser Ser Pro Ser Ser Asn Asn Thr Ala Ala Thr
                485                 490                 495
Thr Ala Ala Ile Val Pro Gly Ser Gln Leu Met Pro Ser Lys Ser Pro
            500                 505                 510
Ser Thr Gly Thr Thr Glu Ile Ser Ser His Glu Ser Ser His Gly Thr
        515                 520                 525
Pro Ser Gln Thr Thr Ala Lys Asn Trp Glu Leu Thr Ala Ser Ala Ser
    530                 535                 540
His Gln Pro Pro Gly Val Tyr Pro Gln Gly His Ser Asp Thr Thr
545                 550                 555


<210> 760
<211> 486
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 760
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
```

```
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Gly Gly Ser Ser Pro Pro Val Pro Leu Ser Leu Tyr Ser Gly
225                 230                 235                 240
Pro Gly Ser Gly Ser Asn Trp Val Asn Val Ile Ser Asp Leu Lys Lys
                245                 250                 255
Ile Glu Asp Leu Ile Gln Ser Met His Ile Asp Ala Thr Leu Tyr Thr
            260                 265                 270
Glu Ser Asp Val His Pro Ser Cys Lys Val Thr Ala Met Lys Cys Phe
        275                 280                 285
Leu Leu Glu Leu Gln Val Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile
    290                 295                 300
His Asp Thr Val Glu Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser
305                 310                 315                 320
Ser Asn Gly Asn Val Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu
                325                 330                 335
Glu Glu Lys Asn Ile Lys Glu Phe Leu Gln Ser Phe Val His Ile Val
            340                 345                 350
Gln Met Phe Ile Asn Thr Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
        355                 360                 365
Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
    370                 375                 380
Ile Thr Cys Pro Pro Pro Met Ser Val Glu His Ala Asp Ile Trp Val
385                 390                 395                 400
Lys Ser Tyr Ser Leu Tyr Ser Arg Glu Arg Tyr Ile Cys Asn Ser Gly
                405                 410                 415
Phe Lys Arg Lys Ala Gly Thr Ser Ser Leu Thr Glu Cys Val Leu Asn
            420                 425                 430
Lys Ala Thr Asn Val Ala His Trp Thr Thr Pro Ser Leu Lys Cys Ile
        435                 440                 445
Arg Asp Pro Ala Leu Val His Gln Arg Pro Ala Pro Pro Ser Thr Val
```

```
    450                 455                 460
Thr Thr Ala Gly Val Thr Pro Gln Pro Glu Ser Leu Ser Pro Ser Gly
465                 470                 475                 480
Lys Glu Pro Ala Ala Ser
                485
```

<210> 761
<211> 559
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 761

```
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Gly Gly Ser Ser Pro Pro Val Pro Leu Ser Leu Tyr Ser Gly
225                 230                 235                 240
Pro Gly Ser Gly Ser Asn Trp Val Asn Val Ile Ser Asp Leu Lys Lys
                245                 250                 255
Ile Glu Asp Leu Ile Gln Ser Met His Ile Asp Ala Thr Leu Tyr Thr
            260                 265                 270
Glu Ser Asp Val His Pro Ser Cys Lys Val Thr Ala Met Lys Cys Phe
        275                 280                 285
Leu Leu Glu Leu Gln Val Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile
    290                 295                 300
```

```
His Asp Thr Val Glu Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser
305                 310                 315                 320
Ser Asn Gly Asn Val Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu
                325                 330                 335
Glu Glu Lys Asn Ile Lys Glu Phe Leu Gln Ser Phe Val His Ile Val
            340                 345                 350
Gln Met Phe Ile Asn Thr Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
        355                 360                 365
Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
    370                 375                 380
Ile Thr Cys Pro Pro Pro Met Ser Val Glu His Ala Asp Ile Trp Val
385                 390                 395                 400
Lys Ser Tyr Ser Leu Tyr Ser Arg Glu Arg Tyr Ile Cys Asn Ser Gly
                405                 410                 415
Phe Lys Arg Lys Ala Gly Thr Ser Ser Leu Thr Glu Cys Val Leu Asn
            420                 425                 430
Lys Ala Thr Asn Val Ala His Trp Thr Thr Pro Ser Leu Lys Cys Ile
        435                 440                 445
Arg Asp Pro Ala Leu Val His Gln Arg Pro Ala Pro Pro Ser Thr Val
    450                 455                 460
Thr Thr Ala Gly Val Thr Pro Gln Pro Glu Ser Leu Ser Pro Ser Gly
465                 470                 475                 480
Lys Glu Pro Ala Ala Ser Ser Pro Ser Ser Asn Asn Thr Ala Ala Thr
                485                 490                 495
Thr Ala Ala Ile Val Pro Gly Ser Gln Leu Met Pro Ser Lys Ser Pro
            500                 505                 510
Ser Thr Gly Thr Thr Glu Ile Ser Ser His Glu Ser Ser His Gly Thr
        515                 520                 525
Pro Ser Gln Thr Thr Ala Lys Asn Trp Glu Leu Thr Ala Ser Ala Ser
    530                 535                 540
His Gln Pro Pro Gly Val Tyr Pro Gln Gly His Ser Asp Thr Thr
545                 550                 555


<210> 762
<211> 28
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 762
Pro Gly Pro Gly Pro Met Pro Tyr Asp Leu Tyr His Pro Ser Gly Gly
 1               5                  10                  15
Cys Gly Gly His Gln Tyr Glu Arg Arg Gly Gly Cys
            20                  25


<210> 763
<211> 28
<212> PRT
<213> Artificial Sequence
```

<220>
<223> Synthetic Construct

<400> 763
Pro Gly Pro Gly Pro Met Pro Tyr Asp Leu Tyr His Pro Ser Gly Gly
 1   5   10   15
Cys Ser Gly His Gln Tyr Glu Arg Arg Glu Gly Cys
            20   25

<210> 764
<211> 28
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 764
Pro Gly Pro Gly Pro Met Pro Tyr Asp Leu Tyr His Pro Ser Gly Gly
 1   5   10   15
Cys Gly Gly His Tyr Phe Glu Arg His Gly Gly Cys
            20   25

<210> 765
<211> 28
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 765
Pro Gly Pro Gly Pro Met Pro Tyr Asp Leu Tyr His Pro Ser Gly Gly
 1   5   10   15
Cys Ser Gly His Tyr Phe Glu Arg His Glu Gly Cys
            20   25

<210> 766
<211> 28
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 766
Pro Gly Pro Gly Pro Met Pro Tyr Asp Leu Tyr His Pro Ser Gly Gly
 1   5   10   15
Cys Ser Phe His Gln Tyr Glu Arg His Glu Gly Cys
            20   25

<210> 767
<211> 28
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 767
Pro Ser Gly Ser Ser Met Pro Tyr Asp Leu Tyr His Pro Ser Gly Gly
 1   5   10   15
Cys Gly Gly His Gln Tyr Glu Arg Arg Gly Gly Cys
            20   25

<210> 768
<211> 28
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 768
Pro Ser Gly Ser Ser Met Pro Tyr Asp Leu Tyr His Pro Ser Gly Gly
 1   5   10   15
Cys Ser Gly His Gln Tyr Glu Arg Arg Glu Gly Cys
            20   25

<210> 769
<211> 28
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 769
Pro Ser Gly Ser Ser Met Pro Tyr Asp Leu Tyr His Pro Ser Gly Gly
 1   5   10   15
Cys Gly Gly His Tyr Phe Glu Arg His Gly Gly Cys
            20   25

<210> 770
<211> 28
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 770
Pro Ser Gly Ser Ser Met Pro Tyr Asp Leu Tyr His Pro Ser Gly Gly
 1   5   10   15
Cys Ser Gly His Tyr Phe Glu Arg His Glu Gly Cys
            20   25

<210> 771
<211> 28
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 771
Pro Ser Gly Ser Ser Met Pro Tyr Asp Leu Tyr His Pro Ser Gly Gly
 1   5   10   15
Cys Ser Phe His Gln Tyr Glu Arg His Glu Gly Cys
            20   25

<210> 772
<211> 226
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 772
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1   5   10   15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20   25   30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35   40   45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50   55   60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65   70   75   80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85   90   95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100   105   110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115   120   125
Tyr Thr Leu Pro Pro Cys Arg Lys Lys Leu Thr Lys Asn Gln Val Ser
    130   135   140
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145   150   155   160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165   170   175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val

```
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly
225
```

<210> 773
<211> 226
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 773

```
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Tyr Thr Leu Pro Pro Cys Arg Lys Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Lys Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly
225
```

<210> 774
<211> 226
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 774
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1   5   10   15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20   25   30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35   40   45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50   55   60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65   70   75   80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85   90   95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100   105   110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115   120   125
Tyr Thr Leu Pro Pro Cys Arg Lys Lys Leu Thr Lys Asn Gln Val Ser
    130   135   140
Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145   150   155   160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165   170   175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180   185   190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195   200   205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210   215   220
Pro Gly
225

<210> 775
<211> 133
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 775
Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu Ile
 1   5   10   15
Leu Cys Leu Leu Leu Gln Met Ile Leu Asn Gly Ile Leu Asn Tyr Lys
            20   25   30
Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys
        35   40   45
Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys
    50   55   60

```
Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu
65                  70                  75                  80
Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu
                85                  90                  95
Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala
            100                 105                 110
Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Cys Gln Ser Ile
        115                 120                 125
Ile Ser Thr Leu Thr
    130
```

<210> 776
<211> 133
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 776

```
Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu Ile
 1               5                  10                  15
Leu Leu Leu Leu Leu Gln Met Ile Leu Asn Gly Ile Leu Asn Tyr Lys
            20                  25                  30
Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys
        35                  40                  45
Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys
    50                  55                  60
Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu
65                  70                  75                  80
Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu
                85                  90                  95
Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala
            100                 105                 110
Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ile Gln Ser Ile
        115                 120                 125
Ile Ser Thr Leu Thr
    130
```

<210> 777
<211> 133
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 777

```
Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu Ile
 1               5                  10                  15
Leu Cys Leu Phe Leu Gln Met Ile Leu Asn Gly Ile Leu Asn Tyr Lys
            20                  25                  30
```

```
Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys
        35                  40                  45
Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys
    50                  55                  60
Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu
65                  70                  75                  80
Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu
                85                  90                  95
Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala
            100                 105                 110
Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Cys Gln Ser Ile
        115                 120                 125
Ile Ser Thr Leu Thr
    130
```

<210> 778
<211> 133
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 778

```
Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu Ile
 1               5                  10                  15
Leu Leu Leu Phe Leu Gln Met Ile Leu Asn Gly Ile Leu Asn Tyr Lys
            20                  25                  30
Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys
        35                  40                  45
Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys
    50                  55                  60
Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu
65                  70                  75                  80
Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu
                85                  90                  95
Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala
            100                 105                 110
Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ile Gln Ser Ile
        115                 120                 125
Ile Ser Thr Leu Thr
    130
```

<210> 779
<211> 133
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 779

```
Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His
 1               5                  10                  15
Leu Cys Leu Leu Leu Gln Met Ile Leu Asn Gly Ile Leu Asn Tyr Lys
            20                  25                  30
Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys
        35                  40                  45
Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys
    50                  55                  60
Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu
65                  70                  75                  80
Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu
                85                  90                  95
Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala
            100                 105                 110
Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Cys Gln Ser Ile
        115                 120                 125
Ile Ser Thr Leu Thr
    130
```

<210> 780
<211> 133
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 780

```
Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His
 1               5                  10                  15
Leu Leu Leu Leu Leu Gln Met Ile Leu Asn Gly Ile Leu Asn Tyr Lys
            20                  25                  30
Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys
        35                  40                  45
Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys
    50                  55                  60
Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu
65                  70                  75                  80
Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu
                85                  90                  95
Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala
            100                 105                 110
Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ile Gln Ser Ile
        115                 120                 125
Ile Ser Thr Leu Thr
    130
```

<210> 781
<211> 133
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 781
Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu Ile
 1   5   10   15
Leu Leu Leu Leu Leu Gln Met Ile Leu Asn Gly Ile Leu Asn Tyr Lys
            20   25   30
Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys
        35   40   45
Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys
    50   55   60
Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu
65   70   75   80
Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu
                85   90   95
Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala
            100   105   110
Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser Ile
        115   120   125
Ile Ser Thr Leu Thr
    130

<210> 782
<211> 133
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 782
Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu Ile
 1   5   10   15
Leu Leu Leu Phe Leu Gln Met Ile Leu Asn Gly Ile Leu Asn Tyr Lys
            20   25   30
Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys
        35   40   45
Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys
    50   55   60
Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu
65   70   75   80
Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu
                85   90   95
Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala
            100   105   110
Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser Ile
        115   120   125
Ile Ser Thr Leu Thr
    130

<210> 783

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

<220>
<223> Synthetic Construct

<400> 783
Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His
 1   5   10   15
Leu Leu Leu Leu Leu Gln Met Ile Leu Asn Gly Ile Leu Asn Tyr Lys
            20   25   30
Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys
        35   40   45
Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys
    50   55   60
Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu
65   70   75   80
Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu
                85   90   95
Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala
            100   105   110
Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser Ile
        115   120   125
Ile Ser Thr Leu Thr
    130

<210> 784
<211> 133
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 784
Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His
 1   5   10   15
Leu Cys Leu Phe Leu Gln Met Ile Leu Asn Gly Ile Leu Asn Tyr Lys
            20   25   30
Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys
        35   40   45
Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys
    50   55   60
Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu
65   70   75   80
Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu
                85   90   95
Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala
            100   105   110
Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Cys Gln Ser Ile
        115   120   125
Ile Ser Thr Leu Thr

130

<210> 785
<211> 133
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 785
Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His
 1   5   10   15
Leu Leu Leu Phe Leu Gln Met Ile Leu Asn Gly Ile Leu Asn Tyr Lys
            20   25   30
Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys
        35   40   45
Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys
    50   55   60
Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu
65   70   75   80
Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu
                85   90   95
Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala
            100   105   110
Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ile Gln Ser Ile
        115   120   125
Ile Ser Thr Leu Thr
    130

<210> 786
<211> 133
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 786
Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His
 1   5   10   15
Leu Leu Leu Phe Leu Gln Met Ile Leu Asn Gly Ile Leu Asn Tyr Lys
            20   25   30
Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys
        35   40   45
Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys
    50   55   60
Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu
65   70   75   80
Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu
                85   90   95
Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala

```
            100                 105                 110
Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser Ile
        115                 120                 125
Ile Ser Thr Leu Thr
    130
```

<210> 787
<211> 133
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 787

```
Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu Ile
 1               5                  10                  15
Leu Cys Leu Leu Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys
            20                  25                  30
Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys
        35                  40                  45
Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys
    50                  55                  60
Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu
65                  70                  75                  80
Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu
                85                  90                  95
Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala
            100                 105                 110
Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Cys Gln Ser Ile
        115                 120                 125
Ile Ser Thr Leu Thr
    130
```

<210> 788
<211> 133
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 788

```
Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu Ile
 1               5                  10                  15
Leu Leu Leu Leu Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys
            20                  25                  30
Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys
        35                  40                  45
Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys
    50                  55                  60
Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu
```

65 70 75 80
Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu
85 90 95
Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala
100 105 110
Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ile Gln Ser Ile
115 120 125
Ile Ser Thr Leu Thr
130

<210> 789
<211> 133
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 789
Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu Ile
1 5 10 15
Leu Leu Leu Leu Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys
20 25 30
Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys
35 40 45
Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys
50 55 60
Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu
65 70 75 80
Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu
85 90 95
Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala
100 105 110
Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser Ile
115 120 125
Ile Ser Thr Leu Thr
130

<210> 790
<211> 133
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 790
Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu Ile
1 5 10 15
Leu Cys Leu Phe Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys
20 25 30
Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys

```
        35                  40                  45
Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys
    50                  55                  60
Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu
65                  70                  75                  80
Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu
                85                  90                  95
Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala
            100                 105                 110
Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Cys Gln Ser Ile
        115                 120                 125
Ile Ser Thr Leu Thr
    130
```

<210> 791
<211> 133
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 791

```
Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu Ile
 1               5                  10                  15
Leu Leu Leu Phe Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys
            20                  25                  30
Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys
        35                  40                  45
Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys
    50                  55                  60
Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu
65                  70                  75                  80
Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu
                85                  90                  95
Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala
            100                 105                 110
Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ile Gln Ser Ile
        115                 120                 125
Ile Ser Thr Leu Thr
    130
```

<210> 792
<211> 133
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 792

```
Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu Ile
```

```
 1               5                  10                  15
Leu Leu Leu Phe Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys
            20                  25                  30
Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys
        35                  40                  45
Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys
    50                  55                  60
Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu
65                  70                  75                  80
Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu
                85                  90                  95
Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala
            100                 105                 110
Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser Ile
        115                 120                 125
Ile Ser Thr Leu Thr
    130
```

<210> 793
<211> 226
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 793

```
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Asp Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Asp Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
```

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210   215   220
Pro Gly
225

<210> 794
<211> 2
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 794
Ser Gly
 1

<210> 795
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 795
Pro Gly Ser Gly
 1

<210> 796
<211> 226
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 796
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1   5   10   15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20   25   30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35   40   45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50   55   60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65   70   75   80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85   90   95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile

```
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Ser Cys Ala Val Glu Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Glu Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly
225
```

<210> 797
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 797
```
Gly Ile Ser Ser Gly Leu Leu Ser Gly Arg Ser Ser Gly Pro
 1               5                  10
```

<210> 798
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 798
```
Gly Gly Ser Gly Ile Ser Ser Gly Leu Leu Ser Gly Arg Ser Ser Gly
 1               5                  10                  15
Pro
```

<210> 799
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 799
Gly Ser Gly
 1

<210> 800
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 800
Gly Ile Ser Ser Gly Leu Leu Ser Gly Arg Ser Asp Asn His Ser Gly
 1   5   10   15
Pro

<210> 801
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 801
Gly Gly Ala Val Gly Leu Leu Ala Pro Pro Gly Gly Leu Ser Gly Arg
 1   5   10   15
Ser Asp Asn His Ser Gly Pro
            20

<210> 802
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 802
Gly Ser Pro Gly Val Pro Leu Ser Leu Tyr Ser Gly Pro
 1   5   10

<210> 803
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 803
Gly Gly Ser Ser Pro Pro Val Pro Leu Ser Leu Tyr Ser Gly Pro
 1   5   10   15

<210> 804
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 804
Gly Gly Ser Pro Gly Gly Val Pro Leu Ser Leu Tyr Ser Gly Pro
 1   5   10   15

<210> 805
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 805
Gly Gly Ser Ser Pro Pro Arg Ala Ala Ala Val Lys Ser Pro Ser Gly
 1   5   10   15
Pro

<210> 806
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 806
Gly Gly Pro Gly Gly Pro Arg Ala Ala Ala Val Lys Ser Pro Ser Gly
 1   5   10   15
Pro

<210> 807
<211> 15
<212> PRT

<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 807
Gly Gly Ser Gly Arg Ala Ala Ala Val Lys Ser Pro Ser Gly Pro
 1   5   10   15

<210> 808
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 808
Gly Gly Ser Gly His Glu Gln Leu Thr Val Ser Gly Pro
 1   5   10

<210> 809
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 809
Gly Gly Ser Ser Pro Pro His Glu Gln Leu Thr Val Ser Gly Pro
 1   5   10   15

<210> 810
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 810
Gly Ser Pro Pro Gly Gly His Glu Gln Leu Thr Val Ser Gly Pro
 1   5   10   15

<210> 811
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 811
Gly Ser Gly Pro Asp Ser Gly Gly Phe Met Leu Thr Ser Gly Pro
 1   5   10   15

<210> 812
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 812
Gly Pro Gly Ser Pro Gly Asp Ser Gly Gly Phe Met Leu Thr Ser Gly
 1   5   10   15
Pro

<210> 813
<211> 133
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 813
Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His
 1   5   10   15
Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys
            20   25   30
Asn Pro Lys Leu Thr Arg Met Leu Thr Ser Lys Phe Tyr Met Pro Lys
        35   40   45
Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Ser Leu Lys
    50   55   60
Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu
65   70   75   80
Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu
                85   90   95
Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala
            100   105   110
Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser Ile
        115   120   125
Ile Ser Thr Leu Thr
    130

<210> 814
<211> 133

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 814
Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His
 1   5   10   15
Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys
            20   25   30
Asn Pro Lys Leu Thr Gly Met Leu Thr Phe Lys Phe Ala Met Pro Lys
        35   40   45
Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Ser Leu Lys
    50   55   60
Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu
65   70   75   80
Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu
                85   90   95
Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala
            100   105   110
Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser Ile
        115   120   125
Ile Ser Thr Leu Thr
    130

<210> 815
<211> 133
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 815
Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His
 1   5   10   15
Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys
            20   25   30
Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys
        35   40   45
Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Arg Leu Lys
    50   55   60
Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu
65   70   75   80
Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu
                85   90   95
Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala
            100   105   110
Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser Ile
        115   120   125
Ile Ser Thr Leu Thr
    130

<210> 816
<211> 133
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 816
Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His
 1   5   10   15
Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys
            20   25   30
Asn Pro Lys Leu Thr Arg Met Leu Thr Glu Lys Phe Tyr Met Pro Lys
        35   40   45
Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys
    50   55   60
Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu
65   70   75   80
Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu
                85   90   95
Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala
            100   105   110
Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser Ile
        115   120   125
Ile Ser Thr Leu Thr
    130

<210> 817
<211> 133
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 817
Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His
 1   5   10   15
Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys
            20   25   30
Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Asn Met Pro Lys
        35   40   45
Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys
    50   55   60
Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu
65   70   75   80
Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu
                85   90   95
Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala
            100   105   110

Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser Ile
        115   120   125
Ile Ser Thr Leu Thr
    130

<210> 818
<211> 133
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 818
Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His
 1   5   10   15
Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys
            20   25   30
Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys
        35   40   45
Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Ser Leu Lys
    50   55   60
Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu
65   70   75   80
Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu
                85   90   95
Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala
            100   105   110
Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser Ile
        115   120   125
Ile Ser Thr Leu Thr
    130

<210> 819
<211> 133
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 819
Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His
 1   5   10   15
Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys
            20   25   30
Asn Pro Lys Leu Thr Arg Met Leu Thr Ala Lys Phe Tyr Met Pro Lys
        35   40   45
Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys
    50   55   60
Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu
65   70   75   80

```
Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu
                85                  90                  95
Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala
            100                 105                 110
Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser Ile
        115                 120                 125
Ile Ser Thr Leu Thr
    130
```

<210> 820
<211> 133
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 820

```
Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His
 1               5                  10                  15
Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys
            20                  25                  30
Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Arg Met Pro Lys
        35                  40                  45
Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys
    50                  55                  60
Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu
65                  70                  75                  80
Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu
                85                  90                  95
Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala
            100                 105                 110
Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser Ile
        115                 120                 125
Ile Ser Thr Leu Thr
    130
```

<210> 821
<211> 133
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 821

```
Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His
 1               5                  10                  15
Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys
            20                  25                  30
Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Ala Phe Tyr Met Pro Lys
        35                  40                  45
```

```
Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys
    50                  55                  60
Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu
65                  70                  75                  80
Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu
                85                  90                  95
Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala
            100                 105                 110
Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser Ile
        115                 120                 125
Ile Ser Thr Leu Thr
    130
```

<210> 822
<211> 133
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 822

```
Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His
 1               5                  10                  15
Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys
            20                  25                  30
Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Ala Met Pro Lys
        35                  40                  45
Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Ser Leu Lys
    50                  55                  60
Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu
65                  70                  75                  80
Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu
                85                  90                  95
Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala
            100                 105                 110
Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser Ile
        115                 120                 125
Ile Ser Thr Leu Thr
    130
```

<210> 823
<211> 175
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 823

```
Ile Thr Cys Pro Pro Pro Met Ser Val Glu His Ala Asp Ile Trp Val
 1               5                  10                  15
```

```
Lys Ser Tyr Ser Leu Tyr Ser Arg Glu Arg Tyr Ile Cys Asn Ser Gly
            20                  25                  30
Phe Lys Arg Lys Ala Gly Thr Ser Ser Leu Thr Glu Cys Val Leu Asn
        35                  40                  45
Lys Ala Thr Asn Val Ala His Trp Thr Thr Pro Ser Leu Lys Cys Ile
    50                  55                  60
Arg Asp Pro Ala Leu Val His Gln Arg Pro Ala Pro Pro Ser Thr Val
65                  70                  75                  80
Thr Thr Ala Gly Val Thr Pro Gln Pro Glu Ser Leu Ser Pro Ser Gly
                85                  90                  95
Lys Glu Pro Ala Ala Ser Ser Pro Ser Ser Asn Asn Thr Ala Ala Thr
            100                 105                 110
Thr Ala Ala Ile Val Pro Gly Ser Gln Leu Met Pro Ser Lys Ser Pro
        115                 120                 125
Ser Thr Gly Thr Thr Glu Ile Ser Ser His Glu Ser Ser His Gly Thr
    130                 135                 140
Pro Ser Gln Thr Thr Ala Lys Asn Trp Glu Leu Thr Ala Ser Ala Ser
145                 150                 155                 160
His Gln Pro Pro Gly Val Tyr Pro Gln Gly His Ser Asp Thr Thr
                165                 170                 175
```

<210> 824
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 824

```
Ile Thr Cys Pro Pro Pro Met Ser Val Glu His Ala Asp Ile Trp Val
 1               5                  10                  15
Lys Ser Tyr Ser Leu Tyr Ser Arg Glu Arg Tyr Ile Cys Asn Ser Gly
            20                  25                  30
Phe Lys Arg Lys Ala Gly Thr Ser Ser Leu Thr Glu Cys Val Leu Asn
        35                  40                  45
Lys Ala Thr Asn Val Ala His Trp Thr Thr Pro Ser Leu Lys Cys Ile
    50                  55                  60
Arg Asp Pro Ala Leu Val His Gln Arg Pro Ala Pro Pro Ser Thr Val
65                  70                  75                  80
Thr Thr Ala Gly Val Thr Pro Gln Pro Glu Ser Leu Ser Pro Ser Gly
                85                  90                  95
Lys Glu Pro Ala Ala Ser
            100
```

<210> 825
<211> 78
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 825
Ile Thr Cys Pro Pro Pro Met Ser Val Glu His Ala Asp Ile Trp Val
 1   5   10   15
Lys Ser Tyr Ser Leu Tyr Ser Arg Glu Arg Tyr Ile Cys Asn Ser Gly
            20   25   30
Phe Lys Arg Lys Ala Gly Thr Ser Ser Leu Thr Glu Cys Val Leu Asn
        35   40   45
Lys Ala Thr Asn Val Ala His Trp Thr Thr Pro Ser Leu Lys Cys Ile
    50   55   60
Arg Asp Pro Ala Leu Val His Gln Arg Pro Ala Pro Pro Ser
65   70   75

<210> 826
<211> 213
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 826
Ala Val Asn Gly Thr Ser Gln Phe Thr Cys Phe Tyr Asn Ser Arg Ala
 1   5   10   15
Asn Ile Ser Cys Val Trp Ser Gln Asp Gly Ala Leu Gln Asp Thr Ser
            20   25   30
Cys Gln Val His Ala Trp Pro Asp Arg Arg Arg Trp Asn Gln Thr Cys
        35   40   45
Glu Leu Leu Pro Val Ser Gln Ala Ser Trp Ala Cys Asn Leu Ile Leu
    50   55   60
Gly Ala Pro Asp Ser Gln Lys Leu Thr Thr Val Asp Ile Val Thr Leu
65   70   75   80
Arg Val Leu Cys Arg Glu Gly Val Arg Trp Arg Val Met Ala Ile Gln
                85   90   95
Asp Phe Lys Pro Phe Glu Asn Leu Arg Leu Met Ala Pro Ile Ser Leu
            100   105   110
Gln Val Val His Val Glu Thr His Arg Ser Asn Ile Ser Trp Glu Ile
        115   120   125
Ser Gln Ala Ser His Tyr Phe Glu Arg His Leu Glu Phe Glu Ala Arg
    130   135   140
Thr Leu Ser Pro Gly His Thr Trp Glu Glu Ala Pro Leu Leu Thr Leu
145   150   155   160
Lys Gln Lys Gln Glu Trp Ile Ser Leu Glu Thr Leu Thr Pro Asp Thr
                165   170   175
Gln Tyr Glu Phe Gln Val Arg Val Lys Pro Leu Gln Gly Glu Phe Thr
            180   185   190
Thr Trp Ser Pro Trp Ser Gln Pro Leu Ala Phe Arg Thr Lys Pro Ala
        195   200   205
Ala Leu Gly Lys Asp
    210

<210> 827

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

<220>
<223> Synthetic Construct

<400> 827
Ala Val Asn Gly Thr Ser Gln Phe Thr Cys Phe Tyr Asn Ser Arg Ala
 1   5   10   15
Asn Ile Ser Cys Val Trp Ser Gln Asp Gly Ala Leu Gln Asp Thr Ser
            20   25   30
Cys Gln Val His Ala Trp Pro Asp Arg Arg Arg Trp Asn Gln Thr Cys
        35   40   45
Glu Leu Leu Pro Val Ser Gln Ala Ser Trp Ala Cys Asn Leu Ile Leu
    50   55   60
Gly Ala Pro Asp Ser Gln Lys Leu Thr Thr Val Asp Ile Val Thr Leu
65   70   75   80
Arg Val Leu Cys Arg Glu Gly Val Arg Trp Arg Val Met Ala Ile Gln
                85   90   95
Asp Phe Lys Pro Phe Glu Asn Leu Arg Leu Met Ala Pro Ile Ser Leu
            100   105   110
Gln Val Val His Val Glu Thr His Arg Ser Asn Ile Ser Trp Glu Ile
        115   120   125
Ser Gln Ala Ser His Tyr Phe Glu Asp His Leu Glu Phe Glu Ala Arg
    130   135   140
Thr Leu Ser Pro Gly His Thr Trp Glu Glu Ala Pro Leu Leu Thr Leu
145   150   155   160
Lys Trp Lys Gln Glu Trp Ile Ser Leu Ala Thr Leu Thr Pro Asp Thr
                165   170   175
Gln Tyr Glu Phe Gln Val Arg Val Lys Pro Leu Gln Gly Glu Phe Thr
            180   185   190
Thr Trp Ser Pro Trp Ser Gln Pro Leu Ala Phe Arg Thr Lys Pro Ala
        195   200   205
Ala Leu Gly Lys Asp
    210

<210> 828
<211> 444
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 828
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1   5   10   15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20   25   30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35   40   45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val

```
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Pro Gly Ser Gly Ser Ala Val Asn Gly Thr Ser Gln Phe Thr
225                 230                 235                 240
Cys Phe Tyr Asn Ser Arg Ala Asn Ile Ser Cys Val Trp Ser Gln Asp
                245                 250                 255
Gly Ala Leu Gln Asp Thr Ser Cys Gln Val His Ala Trp Pro Asp Arg
            260                 265                 270
Arg Arg Trp Asn Gln Thr Cys Glu Leu Leu Pro Val Ser Gln Ala Ser
        275                 280                 285
Trp Ala Cys Asn Leu Ile Leu Gly Ala Pro Asp Ser Gln Lys Leu Thr
    290                 295                 300
Thr Val Asp Ile Val Thr Leu Arg Val Leu Cys Arg Glu Gly Val Arg
305                 310                 315                 320
Trp Arg Val Met Ala Ile Gln Asp Phe Lys Pro Phe Glu Asn Leu Arg
                325                 330                 335
Leu Met Ala Pro Ile Ser Leu Gln Val Val His Val Glu Thr His Arg
            340                 345                 350
Ser Asn Ile Ser Trp Glu Ile Ser Gln Ala Ser His Tyr Phe Glu Arg
        355                 360                 365
His Leu Glu Phe Glu Ala Arg Thr Leu Ser Pro Gly His Thr Trp Glu
    370                 375                 380
Glu Ala Pro Leu Leu Thr Leu Lys Gln Lys Gln Glu Trp Ile Ser Leu
385                 390                 395                 400
Glu Thr Leu Thr Pro Asp Thr Gln Tyr Glu Phe Gln Val Arg Val Lys
                405                 410                 415
Pro Leu Gln Gly Glu Phe Thr Thr Trp Ser Pro Trp Ser Gln Pro Leu
            420                 425                 430
Ala Phe Arg Thr Lys Pro Ala Ala Leu Gly Lys Asp
        435                 440
```

<210> 829
<211> 444
<212> PRT

<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 829
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1   5   10   15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20   25   30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35   40   45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50   55   60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65   70   75   80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85   90   95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100   105   110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115   120   125
Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130   135   140
Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145   150   155   160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165   170   175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val
            180   185   190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195   200   205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210   215   220
Pro Gly Pro Gly Ser Gly Ser Ala Val Asn Gly Thr Ser Gln Phe Thr
225   230   235   240
Cys Phe Tyr Asn Ser Arg Ala Asn Ile Ser Cys Val Trp Ser Gln Asp
                245   250   255
Gly Ala Leu Gln Asp Thr Ser Cys Gln Val His Ala Trp Pro Asp Arg
            260   265   270
Arg Arg Trp Asn Gln Thr Cys Glu Leu Leu Pro Val Ser Gln Ala Ser
        275   280   285
Trp Ala Cys Asn Leu Ile Leu Gly Ala Pro Asp Ser Gln Lys Leu Thr
    290   295   300
Thr Val Asp Ile Val Thr Leu Arg Val Leu Cys Arg Glu Gly Val Arg
305   310   315   320
Trp Arg Val Met Ala Ile Gln Asp Phe Lys Pro Phe Glu Asn Leu Arg
                325   330   335
Leu Met Ala Pro Ile Ser Leu Gln Val Val His Val Glu Thr His Arg
            340   345   350
Ser Asn Ile Ser Trp Glu Ile Ser Gln Ala Ser His Tyr Phe Glu Asp
        355   360   365
His Leu Glu Phe Glu Ala Arg Thr Leu Ser Pro Gly His Thr Trp Glu
    370   375   380

Glu Ala Pro Leu Leu Thr Leu Lys Trp Lys Gln Glu Trp Ile Ser Leu
385 390 395 400
Ala Thr Leu Thr Pro Asp Thr Gln Tyr Glu Phe Gln Val Arg Val Lys
405 410 415
Pro Leu Gln Gly Glu Phe Thr Thr Trp Ser Pro Trp Ser Gln Pro Leu
420 425 430
Ala Phe Arg Thr Lys Pro Ala Ala Leu Gly Lys Asp
435 440

<210> 830
<211> 444
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 830
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
1 5 10 15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
20 25 30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
35 40 45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
50 55 60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
65 70 75 80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
85 90 95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
100 105 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
115 120 125
Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
130 135 140
Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145 150 155 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
165 170 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val
180 185 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
195 200 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
210 215 220
Pro Gly Pro Gly Ser Gly Ser Ala Val Asn Gly Thr Ser Gln Phe Thr
225 230 235 240
Cys Phe Tyr Asn Ser Arg Ala Asn Ile Ser Cys Val Trp Ser Gln Asp
245 250 255
Gly Ala Leu Gln Asp Thr Ser Cys Gln Val His Ala Trp Pro Asp Arg
260 265 270
Arg Arg Trp Asn Gln Thr Cys Glu Leu Leu Pro Val Ser Gln Ala Ser

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        275                 280                 285
Trp Ala Cys Asn Leu Ile Leu Gly Ala Pro Asp Ser Gln Lys Leu Thr
    290                 295                 300
Thr Val Asp Ile Val Thr Leu Arg Val Leu Cys Arg Glu Gly Val Arg
305                 310                 315                 320
Trp Arg Val Met Ala Ile Gln Asp Phe Lys Pro Phe Glu Asn Leu Arg
                325                 330                 335
Leu Met Ala Pro Ile Ser Leu Gln Val Val His Val Glu Thr His Arg
            340                 345                 350
Ser Asn Ile Ser Trp Glu Ile Ser Gln Ala Ser His Tyr Phe Glu Arg
        355                 360                 365
His Leu Glu Phe Glu Ala Arg Thr Leu Ser Pro Gly His Thr Trp Glu
    370                 375                 380
Glu Ala Pro Leu Leu Thr Leu Lys Gln Lys Gln Glu Trp Ile Ser Leu
385                 390                 395                 400
Glu Thr Leu Thr Pro Asp Thr Gln Tyr Glu Phe Gln Val Arg Val Lys
                405                 410                 415
Pro Leu Gln Gly Glu Phe Thr Thr Trp Ser Pro Trp Ser Gln Pro Leu
            420                 425                 430
Ala Phe Arg Thr Lys Pro Ala Ala Leu Gly Lys Asp
        435                 440
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