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(54) **Title**: TGF-B ANTAGONIST MULTI-TARGET BINDING PROTEINS

(57) **Abstract**: This disclosure provides a multi-target fusion protein composed of a TGF? antagonist domain and another binding domain antagonistic for a heterologous target (such as IL6, IL10, VEGF, TNF, HGF, TWEAK, IGF) or agonistic for a heterologous target (such as GITR). The multi-specific fusion protein may also include an intervening domain that separates the binding domains and allows for dimerization. This disclosure also provides polynucleotides encoding the multi-specific fusion proteins, compositions of the fusion proteins, and methods of using the multi-specific fusion proteins and compositions.

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TGF-β ANTAGONIST MULTI-TARGET BINDING PROTEINS

TECHNICAL FIELD

[001] This disclosure relates generally to the field of multi-target binding molecules and therapeutic applications thereof and more specifically to a fusion protein composed of either a transforming growth factor-beta (TGFβ) antagonist domain and another binding domain antagonistic for a heterologous target, such as IL6, IL10, VEGF, TNF, HGF, TWEAK, IGF1 or IGF2, or a TGFβ antagonist domain and another binding domain agonistic for a heterologous target, such as GITR, as well as compositions and therapeutic uses thereof.

BACKGROUND

[002] Transforming growth factor-beta (TGFβ) is a potent cytokine that has significant effects on the immune system. The main function of TGFβ in the immune system is to maintain tolerance and initial immune responses against foreign pathogens. Three isoforms of TGFβ have been identified in mammals, TGFβ1, TGFβ2 and TGFβ3, with TGFβ1 being the predominant isoform. TGFβ is secreted in a latent form and only a small percentage of total secreted TGFβ is activated under physiological conditions. The biological effects of TGFβ occur mostly through binding of TGFβ to the receptors ALK5 and TGFβ receptor II (TGFβR2). Specifically, active TGFβ dimer binds to a tetrameric ALK5 and TGFβR2 complex to initiate cell signaling. ALK5 is not required for the initial binding of TGFβ, but is required for signaling.

[003] TGFβ has been shown to influence many cellular functions such as cell proliferation, differentiation, cell-cell and cell-matrix adhesion, cell motility and activation of lymphocytes. (For a review of the role of TGFβ in regulating immune responses, see Li *et al.* (2006) Annu. Rev. Immunol. 24:99-146.) Furthermore, TGFβ is believed to induce or mediate the progression of many diseases such as osteoporosis, hypertension, atherosclerosis, hepatic cirrhosis and fibrotic diseases of the kidney, liver and lungs, and tumor progression. TGFβ can augment end-organ damage caused by chronic inflammation and TGFβ antagonists have been shown to be effective in attenuating this damage in animal models of diseases such as diabetic kidney disease, glomerulonephritis, cyclosporine-mediated renal injury and systemic lupus erythematosus (SLE) (Border *et al.* (1990) Nature 346:371-374; Border *et al.* (1992) Nature 360:361-364; Isaka *et al.* (1999) Kidney Int. 55:465-475; Sharma *et al.* (1996)

Diabetes 45:522; Xin *et al*. (2004) Transplantation 15:1433; Benigni *et al*. (2003) J. Am. Soc. Nephrol. 14:1816). With respect to cancer, TGFβ can have a direct inhibitory activity on malignant cells and can augment the production or activity of a range of tumor growth factors and angiogenic factors.

[004] While TGFβ knock-out mice have severe pathology related to unrestrained inflammation and autoimmunity, administration of TGFβ antagonists is well tolerated in mice and humans (Rusek *et al*. (2003) Immunopharmacol. Immunotoxicol. 25:235-57; Denton *et al*. (2007) Arthritis Rheum. 56:323-33). Methods of treatment using TGF antagonists known in the art include use of antibodies against TGFβ, use of TGFβR2 ectodomain Ig fusion proteins, and use of small molecule inhibitors of TGFβRI kinase activity. All of these methods have modest beneficial impact in rodent models of disease or in clinical trials in humans (Denton *et al*. (2007) Arthritis Rheum. 56:323). Indeed, chronic use of a TGFβ antagonist in mice shows no evidence of activation of the immune system as might be expected from the phenotype of TGFβ-/- knock-out mice. This is likely to reflect, in part, the complex nature of the biology of cytokines, interleukins, chemokines and growth factors in human diseases and the requirement to inhibit more than one pathway simultaneously to maximize the benefit to patients.

BRIEF DESCRIPTION OF THE FIGURES

[005] Figures 1A-1C show that multi-specific (Xceptor) fusion proteins containing one of various different Hyper-IL6 binding domains fused to a TNFR ectodomain bind to Hyper-IL6 specifically as measured by ELISA, and that these multi-specific fusion proteins preferentially bind Hyper-IL6 over IL6 and IL6R alone. Only two fusion proteins tested bound IL6 and none bound sIL6R.

[006] Figure 2 shows that multi-specific fusion proteins containing a TNFR ectodomain fused to one of various different Hyper-IL6 binding domains bind to TNF-α as measured by ELISA.

[007] Figure 3 shows that multi-specific fusion proteins containing one of various different Hyper-IL6 binding domains fused to a TNFR ectodomain can simultaneously bind to Hyper-IL6 and TNF-α as measured by ELISA.

[008] Figure 4 shows that multi-specific fusion proteins containing one of various different Hyper-IL6 binding domains fused to a TNFR ectodomain block gp130 from binding to Hyper-IL6 as measured by ELISA.

[009] Figures 5A and 5B show that multi-specific fusion proteins containing one of various different Hyper-IL6 binding domains fused to a TNFR ectodomain block (A) IL6 or (B) Hyper-IL6 induced proliferation of TF-1 cells.

[0010] Figure 6 shows that multi-specific fusion proteins containing one of various different Hyper-IL6 binding domains fused to a TNFR ectodomain block TNF-α from binding to TNFR as measured by ELISA.

[0011] Figure 7 shows that multi-specific fusion proteins containing a TNFR ectodomain fused to one of various different Hyper-IL6 binding domains block TNF-α induced killing of L929 cells.

[0012] Figure 8 shows that multi-specific fusion proteins containing a TGFβR2 ectodomain fused to one of various different Hyper-IL6 binding domains bind to TGFβ1 as measured by ELISA.

[0013] Figure 9 shows that multi-specific fusion proteins containing a TNFR ectodomain fused to a TGFβRII ectodomain block TGFβ-1 induced inhibition of IL-4 proliferation of HT2 cells.

[0014] Figure 10 shows that multi-specific fusion proteins containing a TNFR ectodomain fused to an IL6 binding domain did not bind to HepG2 (liver) cells.

[0015] Figure 11 shows that multi-specific fusion proteins containing a TNFR ectodomain fused to an IL6 binding domain blocked the HIL6-induced SAA response in mice.

[0016] Figure 12 shows that multi-specific fusion proteins containing a TNFR ectodomain fused to an IL6 binding domain blocked the HIL6-induced sgp130 response in mice.

[0017] Figures 13A and B show the results of studies on the ability of multi-specific fusion proteins containing a TNFR ectodomain fused to an IL6 binding domain to block the TNFα-induced SAA response in mice, at 2 hours and 24 hours post-administration, respectively.

DETAILED DESCRIPTION

[0018] The present disclosure provides multi-specific fusion proteins, referred to herein as Xceptor molecules. Exemplary structures of such multi-specific fusion proteins, include N-BD-ID-ED-C, N-ED-ID-BD-C, and N-ED1-ID-ED2-C, wherein N- and –C represent the amino- and carboxy-terminus, respectively, BD is an immunoglobulin-like or

immunoglobulin variable region binding domain, ID is an intervening domain, and ED is an ectodomain (*e.g.* an extracellular domain), such as a receptor ligand binding domain, cysteine rich domain (A domain; *see* WO 02/088171 and WO 04/044011), semaphorin or semaphorin-like domain, or the like. In some constructs, the ID can comprise an immunoglobulin constant region or sub-region disposed between the first and second binding domains. In still further constructs, the BD and ED are each linked to the ID via the same or different linker (*e.g.*, a linker comprising one to 50 amino acids), such as an immunoglobulin hinge region (made up of, for example, the upper and core regions) or functional variant thereof, or a lectin interdomain region or functional variant thereof, or a cluster of differentiation (CD) molecule stalk region or functional variant thereof.

[0019] Prior to setting forth this disclosure in more detail, it may be helpful to an understanding thereof to provide definitions of certain terms to be used herein. Additional definitions are set forth throughout this disclosure.

[0020] In the present description, any concentration range, percentage range, ratio range, or integer range is to be understood to include the value of any integer within the recited range and, when appropriate, fractions thereof (such as one tenth and one hundredth of an integer), unless otherwise indicated. Also, any number range recited herein relating to any physical feature, such as polymer subunits, size or thickness, are to be understood to include any integer within the recited range, unless otherwise indicated. As used herein, "about" or "consisting essentially of" mean ± 20% of the indicated range, value, or structure, unless otherwise indicated. It should be understood that the terms "a" and "an" as used herein refer to "one or more" of the enumerated components. The use of the alternative (e.g., "or") should be understood to mean either one, both, or any combination thereof of the alternatives. As used herein, the terms "include" and "comprise" are used synonymously. In addition, it should be understood that the individual compounds, or groups of compounds, derived from the various combinations of the structures and substituents described herein, are disclosed by the present application to the same extent as if each compound or group of compounds was set forth individually. Thus, selection of particular structures or particular substituents is within the scope of the present disclosure.

[0021] A “binding domain” or “binding region” according to the present disclosure may be, for example, any protein, polypeptide, oligopeptide, or peptide that possesses the ability to specifically recognize and bind to a biological molecule (*e.g.*, TGFβ or IL6) or complex of more than one of the same or different molecule or assembly or aggregate,

whether stable or transient (*e.g.*, IL6/IL6R complex). Such biological molecules include proteins, polypeptides, oligopeptides, peptides, amino acids, or derivatives thereof, lipids, fatty acids, or derivatives thereof; carbohydrates, saccharides, or derivatives thereof; nucleotides, nucleosides, peptide nucleic acids, nucleic acid molecules, or derivatives thereof; glycoproteins, glycopeptides, glycolipids, lipoproteins, proteolipids, or derivatives thereof; other biological molecules that may be present in, for example, a biological sample; or any combination thereof. A binding region includes any naturally occurring, synthetic, semi-synthetic, or recombinantly produced binding partner for a biological molecule or other target of interest. A variety of assays are known for identifying binding domains of the present disclosure that specifically bind with a particular target, including Western blot, ELISA, or Biacore analysis.

[0022] Binding domains and fusion proteins thereof of this disclosure can be capable of binding to a desired degree, including "specifically or selectively binding" a target while not significantly binding other components present in a test sample, if they bind a target molecule with an affinity or K_a (*i.e.*, an equilibrium association constant of a particular binding interaction with units of 1/M) of, for example, greater than or equal to about 10^5 M^{-1}, 10^6 M^{-1}, 10^7 M^{-1}, 10^8 M^{-1}, 10^9 M^{-1}, 10^{10} M^{-1}, 10^{11} M^{-1}, 10^{12} M^{-1}, or 10^{13} M^{-1}. "High affinity" binding domains refers to those binding domains with a K_a of at least 10^7 M^{-1}, at least 10^8 M^{-1}, at least 10^9 M^{-1}, at least 10^{10} M^{-1}, at least 10^{11} M^{-1}, at least 10^{12} M^{-1}, at least 10^{13} M^{-1}, or greater. Alternatively, affinity may be defined as an equilibrium dissociation constant (K_d) of a particular binding interaction with units of M (*e.g.*, 10^{-5} M to 10^{-13} M). Affinities of binding domain polypeptides and fusion proteins according to the present disclosure can be readily determined using conventional techniques (*see*, *e.g.*, Scatchard *et al.* (1949) Ann. N.Y. Acad. Sci. 51:660; and U.S. Patent Nos. 5,283,173; 5,468,614; Biacore® analysis; or the equivalent).

[0023] Binding domains of this disclosure can be generated as described herein or by a variety of methods known in the art (*see*, *e.g.*, US Patent Nos. 6,291,161; 6,291,158). Sources include antibody gene sequences from various species (which can be formatted as antibodies, sFvs, scFvs or Fabs, such as in a phage library), including human, camelid (from camels, dromedaries, or llamas; Hamers-Casterman *et al.* (1993) Nature, 363:446 and Nguyen *et al.* (1998) J. Mol. Biol., 275:413), shark (Roux *et al.* (1998) Proc. Nat'l. Acad. Sci. (USA) 95:11804), fish (Nguyen *et al.* (2002) Immunogenetics, 54:39), rodent, avian, ovine, sequences that encode random peptide libraries or sequences that encode an engineered diversity of amino acids in loop regions of alternative non-antibody scaffolds, such as

fibrinogen domains (*see, e.g.*, Weisel *et al*. (1985) Science 230:1388), Kunitz domains (*see, e.g.*, US Patent No. 6,423,498), lipocalin domains (*see, e.g.*, WO 2006/095164), V-like domains (*see, e.g.*, US Patent Application Publication No. 2007/0065431), C-type lectin domains (Zelensky and Gready (2005) FEBS J. 272:6179), mAb^2 or Fcab™ (*see*, *e.g.*, PCT Patent Application Publication Nos. WO 2007/098934; WO 2006/072620), or the like. Additionally, traditional strategies for hybridoma development using a synthetic single chain IL6/IL6R complex, such as a human IL6/IL6R complex or Hyper-IL6 (IL6 joined by a peptide linker to IL6R), as an immunogen in convenient systems (*e.g.*, mice, HuMAb mouse®, TC mouse™, KM-mouse®, llamas, chicken, rats, hamsters, rabbits, *etc*.) can be used to develop binding domains of this disclosure.

[0024] Terms understood by those in the art as referring to antibody technology are each given the meaning acquired in the art, unless expressly defined herein. For example, the terms "V_L" and "V_H" refer to the variable binding region derived from an antibody light and heavy chain, respectively. The variable binding regions are made up of discrete, well-defined sub-regions known as "complementarity determining regions" (CDRs) and "framework regions" (FRs). The terms "C_L" and "C_H" refer to an "immunoglobulin constant region," *i.e.*, a constant region derived from an antibody light or heavy chain, respectively, with the latter region understood to be further divisible into C_{H1}, C_{H2}, C_{H3} and C_{H4} constant region domains, depending on the antibody isotype (IgA, IgD, IgE, IgG, IgM) from which the region was derived. A portion of the constant region domains makes up the Fc region (the "fragment crystallizable" region), which contains domains responsible for the effector functions of an immunoglobulin, such as ADCC (antibody-dependent cell-mediated cytotoxicity), ADCP (antibody-dependent cell-mediated phagocytosis), CDC (complement-dependent cytotoxicity) and complement fixation, binding to Fc receptors, greater half-life in vivo relative to a polypeptide lacking an Fc region, protein A binding, and perhaps even placental transfer (*see* Capon *et al*. (1989) Nature, 337:525). Further, a polypeptide containing an Fc region allows for dimerization or multimerization of the polypeptide. A "hinge region," also referred to herein as a "linker," is an amino acid sequence interposed between and connecting the variable binding and constant regions of a single chain of an antibody, which is known in the art as providing flexibility in the form of a hinge to antibodies or antibody-like molecules.

[0025] The domain structure of immunoglobulins is amenable to engineering, in that the antigen binding domains and the domains conferring effector functions may be exchanged between immunoglobulin classes and subclasses. Immunoglobulin structure and function are reviewed, for example, in Harlow *et al*., Eds., *Antibodies: A Laboratory Manual*, Chapter 14

(Cold Spring Harbor Laboratory, Cold Spring Harbor, 1988). An extensive introduction as well as detailed information about all aspects of recombinant antibody technology can be found in the textbook *Recombinant Antibodies* (John Wiley & Sons, NY, 1999). A comprehensive collection of detailed antibody engineering lab Protocols can be found in R. Kontermann and S. Dübel, Eds., *The Antibody Engineering Lab Manual* (Springer Verlag, Heidelberg/New York, 2000).

[0026] "Derivative" as used herein refers to a chemically or biologically modified version of a compound that is structurally similar to a parent compound and (actually or theoretically) derivable from that parent compound. Generally, a "derivative" differs from an "analogue" in that a parent compound may be the starting material to generate a "derivative," whereas the parent compound may not necessarily be used as the starting material to generate an "analogue." An analogue may have different chemical or physical properties of the parent compound. For example, a derivative may be more hydrophilic or it may have altered reactivity (*e.g.*, a CDR having an amino acid change that alters its affinity for a target) as compared to the parent compound.

[0027] The term "biological sample" includes a blood sample, biopsy specimen, tissue explant, organ culture, biological fluid or any other tissue or cell or other preparation from a subject or a biological source. A subject or biological source may, for example, be a human or non-human animal, a primary cell culture or culture adapted cell line including genetically engineered cell lines that may contain chromosomally integrated or episomal recombinant nucleic acid sequences, somatic cell hybrid cell lines, immortalized or immortalizable cell lines, differentiated or differentiatable cell lines, transformed cell lines, or the like. In further embodiments of this disclosure, a subject or biological source may be suspected of having or being at risk for having a disease, disorder or condition, including a malignant disease, disorder or condition or a B cell disorder. In certain embodiments, a subject or biological source may be suspected of having or being at risk for having a hyperproliferative, inflammatory, or autoimmune disease, and in certain other embodiments of this disclosure the subject or biological source may be known to be free of a risk or presence of such disease, disorder, or condition.

[0028] In certain embodiments, the present disclosure makes possible the depletion or modulation of cells associated with aberrant TGFβ activity by providing multi-specific fusion proteins that bind both a TGFβ and a second target other than TGFβ, such as IL6, IL6R, an IL6/IL6R complex, IL10, GITR, VEGF, TNF, HGF, Tumor necrosis factor-like

weak inducer of apoptosis (TWEAK; also known as tumor necrosis factor (ligand) superfamily, member 12, TNFSF12), IGF1 or IGF2. In certain embodiments, a multi-specific fusion protein comprises a first and second binding domain, a first and second linker, and an intervening domain, wherein one end of the intervening domain is fused via a linker to a first binding domain that is a TGFβR2 ectodomain (*e.g.* an extracellular domain) and at the other end fused via a linker to a second binding domain. In some embodiments, less than an entire TGFβR2 ectodomain is employed. Specifically, domains within the ectodomain that function as a TGFβ antagonist or confer ligand binding are employed.

[0029] In certain embodiments, the second binding domain is an IL6 antagonist (such as an immunoglobulin variable region that is specific for an IL6, IL6R, or IL6/IL6Ra complex), an IL10 antagonist (such as an immunoglobulin variable region that is specific for IL10, an IL10R1 ectodomain (e.g. SEQ ID NO:745) or a sub-domain of an IL10R1 ectodomain), a GITR agonist (such as an immunoglobulin variable region that is specific for GITR, a GITRL ectodomain (for example, amino acids 74-181 of Genbank Accession NP_005083.2, SEQ ID NO:746) or a sub-domain of a GITRL ectodomain), a VEGF antagonist (such as an immunoglobulin variable region that is specific for VEGF, a VEGFR2 ectodomain (see, Genbank Accession NP_002244.1, SEQ ID NO:747) or a sub-domain of a VEGFR2 ectodomain), a TNF antagonist (such as an immunoglobulin variable region that is specific for TNF, a TNFR1 ectodomain (see, Genbank Accession NP_001056.1; SEQ ID NO:749), a sub-domain of a TNFR1 ectodomain, a TNFR2 ectodomain (see, Genbank Accession NP_001057.1; SEQ ID NO:748), or a sub-domain of a TNFR2 ectodomain), a HGF antagonist (such as an immunoglobulin variable region that is specific for HGF, a c-Met ectodomain or a sub-domain of a c-Met ectodomain (e.g. SEQ ID NO:750-752)), a TWEAK antagonist (such as an immunoglobulin binding domain specific for TWEAK or TWEAKR, or a TWEAKR ectodomain (*e.g.* SEQ ID NO:761) or TWEAK binding fragment thereof), or an IGF1 or IGF2 antagonist (such as an immunoglobulin variable region that is specific for IGF1 or IGF2, an IGF1R ectodomain (for example, an IGF1R ectodomain of Genbank Accession no. NP_000866.1 (SEQ ID NO:753) or a sub-domain thereof), or an IGFBP (for example, an IGFBP ectodomain of Genbank Accession no. NP_000587.1 (IGFBP1; SEQ ID NO:754), NP_000588.2 (IGFBP2; SEQ ID NO:755), NP_001013416.1 (IGFBP3 isoform a; SEQ ID NO:756), NP_000589.2 (IGFBP3 isoform b; SEQ ID NO:757), NP_001543.2 (IGFBP4; SEQ ID NO:758), NP_000590.1 (IGFBP5; SEQ ID NO:759) or NP_002169.1 (IGFBP6; SEQ ID NO:760)), or a sub-domain thereof).

[0030] The complex of IL6 with membrane or soluble IL6 receptor (IL6Rα) is referred to herein as IL6xR when referring to IL6 with either membrane IL6Rα or soluble IL6Rα (sIL6Rα), and as sIL6xR when referring only to the complex of IL6 with sIL6Rα. In some embodiments, multi-specific fusion proteins containing a binding domain specific for IL6xR have one or more of the following properties: (1) greater or equal affinity for an IL6xR complex than for IL6 or IL6Rα alone or has greater affinity for IL6Rα alone or an IL6xR complex than for IL6 alone; (2) compete with membrane gp130 for binding with a sIL6xR complex or enhance soluble gp130 binding with a sIL6xR complex; (3) preferentially inhibit IL6 trans-signaling over IL6 cis-signaling and (4) do not inhibit signaling of gp130 family cytokines other than IL6.

TGFβ Antagonists

[0031] As outlined above, TGFβ has been linked to several diseases such as fibrosis, auto-immunity and cancer. In the early stages of tumor development, TGFβ acts as a growth inhibitory factor. However, as tumors evolve they develop mechanisms to evade the growth-inhibition properties of TGFβ, resulting in increased tumor invasiveness, increased metastatic potential and inhibition of surrounding immune responses (Luwor et al. (2008) J. Clin. Neurosci. June 10 (epub)). A TGFβ antagonist of this disclosure inhibits the tumor-promoting activity of TGF. The antagonist domains may block TGFβ dimerization and TGFβ binding, or the domains may bind to components of the receptor system and block activity either by preventing ligand activity or by preventing the assembly of the receptor complex.

[0032] In some embodiments, a TGFβ antagonist may be an extracellular domain ("ectodomain") of TGFβR2. In certain embodiments, a TGFβ antagonist comprises a TGFβR2 ectodomain as set forth in SEQ ID NO:743, 744 or any combination thereof.

[0033] In one aspect, a TGFβ antagonist or fusion protein thereof of this disclosure is specific for TGFβ wherein it has an affinity with a dissociation constant (K_d) of about 10^{-5} M to 10^{-13} M, or less. In certain embodiments, the TGFβ antagonist or fusion protein thereof binds TGFβ with an affinity that is less than about 300 pM. Another measure, the kinetic dissociation (k_d), also referred to herein as k_{OFF}, is a measure of the rate of complex dissociation and, thus, the 'dwell time' of the target molecule bound by a polypeptide binding domain of this disclosure. The k_d (k_{OFF}) has units of 1/sec. Exemplary TGFβ antagonists of this disclosure can have a k_{OFF} of about 10^{-4}/sec (*e.g.*, about a day) to about 10^{-8}/sec or less. In certain embodiments, the k_{OFF} can range from about 10^{-1}/sec, about 10^{-2}/sec, about 10^{-}

^{3}/sec, about 10^{-4}/sec, about 10^{-5}/sec, about 10^{-6}/sec, about 10^{-7}/sec, about 10^{-8}/sec, about 10^{-9}/sec, about 10^{-10}/sec, or less (*see* Graff *et al.* (2004) Protein Eng. Des. Sel. 17:293). In some embodiments, a TGFβ antagonist or fusion protein thereof of this disclosure will bind TGFβ with higher affinity and have a lower k_{OFF} rate as compared to the cognate TGFβ receptor binding to TGFβ. In further embodiments, a TGFβ antagonist or fusion protein thereof of this disclosure that blocks or alters TGFβ dimerization or other cell surface activity may have a more moderate affinity (*i.e.*, a K_d of about 10^{-8} M to about 10^{-9} M) and a more moderate off rate (*i.e.*, a k_{OFF} closer to about 10^{-4}/sec) as compared to the affinity and dimerization rate of cognate TGFβ receptor.

[0034] Exemplary binding domains that function as TGFβ antagonists of this disclosure can be generated as described herein or by a variety of methods known in the art (*see*, *e.g.*, US Patent Nos. 6,291,161; 6,291,158). Sources include antibody gene sequences from various species (which can be formatted as scFvs or Fabs, such as in a phage library), including human, camelid (from camels, dromedaries, or llamas; Hamers-Casterman *et al.* (1993) Nature, 363:446 and Nguyen *et al.* (1998) J. Mol. Biol., 275:413), shark (Roux *et al.* (1998) Proc. Nat'l. Acad. Sci. (USA) 95:11804), fish (Nguyen *et al.* (2002) Immunogenetics, 54:39), rodent, avian, ovine, sequences that encode random peptide libraries or sequences that encode an engineered diversity of amino acids in loop regions of alternative non-antibody scaffolds, such as fibrinogen domains (*see, e.g.*, Weisel *et al.* (1985) Science 230:1388), Kunitz domains (*see, e.g.*, US Patent No. 6,423,498), lipocalin domains (*see, e.g.*, WO 2006/095164), V-like domains (*see, e.g.*, US Patent Application Publication No. 2007/0065431), C-type lectin domains (Zelensky and Gready (2005) FEBS J. 272:6179), or the like. Additionally, traditional strategies for hybridoma development using a synthetic TGFβ or single chain TGFβR2 ectodomain as an immunogen in convenient systems (*e.g.*, mice, HuMAb mouse®, TC mouse™, KM-mouse®, llamas, chicken, rats, hamsters, rabbits, *etc.*) can be used to develop binding domains of this disclosure.

[0035] In an illustrative example, TGFβ antagonists of this disclosure specific for a TGFβ can be identified using a Fab phage library of fragments (*see*, *e.g.*, Hoet *et al.* (2005) Nature Biotechnol. 23:344) by screening for binding to a synthetic or recombinant TGFβ (using an amino acid sequence or fragment thereof as set forth in GenBank Accession No. NP_000651.3). A TGFβ, as described herein or known in the art, can be used for such a screening. In certain embodiments, a TGFβ used to generate a TGFβ antagonist can further comprise an intervening domain or a dimerization domain, as described herein, such as an immunoglobulin Fc domain or fragment thereof.

[0036] In some embodiments, TGFβ antagonist domains of this disclosure comprise V_H and V_L domains as described herein. In certain embodiments, the V_H and V_L domains are rodent (*e.g.*, mouse, rat), humanized, or human. In further embodiments, there are provided TGFβ antagonist domains of this disclosure that have a sequence that is 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%, at least 99.5% , or at least 100% identical to the amino acid sequence of one or more light chain variable regions (V_L) or to one or more heavy chain variable regions (V_H), or both, wherein each CDr has up to three amino acid changes (*i.e.*, many of the changes are in the framework region(s)), as set forth herein.

[0037] In further embodiments, TGFβ antagonist domains of this disclosure comprise V_H and V_L domains as set forth herein, which are at least 80%, at least 81%, at least 82%, at least 83%, at least 84%, at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, 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 at least 99.5% identical to the amino acid sequence of such V_H domain, V_L domain, or both wherein each CDr has at most up to three amino acid changes (*i.e.*, many of the changes are in the framework region(s)).

[0038] The terms "identical" or “percent identity," in the context of two or more polypeptide or nucleic acid molecule sequences, means two or more sequences or subsequences that are the same or have a specified percentage of amino acid residues or nucleotides that are the same over a specified region (*e.g.*, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity), when compared and aligned for maximum correspondence over a comparison window, or designated region, as measured using methods known in the art, such as a sequence comparison algorithm, by manual alignment, or by visual inspection. For example, preferred algorithms suitable for determining percent sequence identity and sequence similarity are the BLAST and BLAST 2.0 algorithms, which are described in Altschul *et al.* (1977) Nucleic Acids Res. 25:3389 and Altschul *et al.* (1990) J. Mol. Biol. 215:403, respectively.

[0039] In any of these or other embodiments described herein, the V_L and V_H domains may be arranged in either orientation and may be separated by about a five to about a thirty amino acid linker as disclosed herein or any other amino acid sequence capable of providing a spacer function compatible with interaction of the two sub-binding domains. In certain embodiments, a linker joining the V_H and V_L domains comprises an amino acid sequence as set forth in SEQ ID NO:497-604 and 1223-1228, such as Linker 47 (SEQ ID NO:543) or Linker 80 (SEQ ID NO:576). Multi-specific binding domains will have at least

two specific sub-binding domains, by analogy to camelid antibody organization, or at least four specific sub-binding domains, by analogy to the more conventional mammalian antibody organization of paired V_H and V_L chains.

[0040] In further embodiments, TGFβ antagonist domains and fusion proteins thereof of this disclosure may comprise a binding domain including one or more complementarity determining region ("CDR"), or multiple copies of one or more such CDRs, which have been obtained, derived, or designed from variable regions of an anti-TGFβ or anti-TGFβR2 scFv or Fab fragment or from heavy or light chain variable regions thereof.

[0041] CDRs are defined in various ways in the art, including the Kabat, Chothia, AbM, and contact definitions. The Kabat definition is based on sequence variability and is the most commonly used definition to predict CDR regions (Johnson *et al.* (2000) Nucleic Acids Res. 28:214). The Chothia definition is based on the location of the structural loop regions (Chothia et al. (1986) J. Mol. Biol. 196:901; Chothia et al. (1989) Nature 342:877). The AbM definition, a compromise between the Kabat and Chothia definitions, is an integral suite of programs for antibody structure modeling produced by the Oxford Molecular Group (Martin *et al.* (1989) Proc. Nat'l. Acad. Sci. (USA) 86:9268; Rees *et al.*, ABMTM, a computer program for modeling variable regions of antibodies, Oxford, UK; Oxford Molecular, Ltd.). An additional definition, known as the contact definition, has been recently introduced (*see* MacCallum *et al.* (1996) J. Mol. Biol. 5:732), which is based on an analysis of available complex crystal structures.

[0042] By convention, the CDR domains in the heavy chain are referred to as H1, H2, and H3, which are numbered sequentially in order moving from the amino terminus to the carboxy terminus. The CDR-H1 is about ten to 12 residues in length and starts four residues after a Cys according to the Chothia and AbM definitions, or five residues later according to the Kabat definition. The H1 can be followed by a Trp, Trp-Val, Trp-Ile, or Trp-Ala. The length of H1 is approximately ten to 12 residues according to the AbM definition, while the Chothia definition excludes the last four residues. The CDR-H2 starts 15 residues after the end of H1 according to the Kabat and AbM definitions, which is generally preceded by sequence Leu-Glu-Trp-Ile-Gly (but a number of variations are known) and is generally followed by sequence Lys/Arg-Leu/Ile/Val/Phe/Thr/Ala-Thr/Ser/Ile/Ala. According to the Kabat definition, the length of H2 is about 16 to 19 residues, while the AbM definition predicts the length to be nine to 12 residues. The CDR-H3 usually starts 33 residues after the end of H2, is generally preceded by the amino acid sequence Cys-Ala-Arg

and followed by the amino acid Gly, and has a length that ranges from three to about 25 residues.

[0043] By convention, the CDR regions in the light chain are referred to as L1, L2, and L3, which are numbered sequentially in order moving from the amino terminus to the carboxy terminus. The CDR-L1 generally starts at about residue 24 and generally follows a Cys. The residue after the CDR-L1 is always Trp, which begins one of the following sequences: Trp-Tyr-Gln, Trp-Leu-Gln, Trp-Phe-Gln, or Trp-Tyr-Leu. The length of CDR-L1 is approximately ten to 17 residues. The CDR-L2 starts about 16 residues after the end of L1 and will generally follow residues Ile-Tyr, Val-Tyr, Ile-Lys, or Ile-Phe. The CDR-L2 is about seven residues in length. The CDR-L3 usually starts 33 residues after the end of L2 and generally follows a Cys, which is generally followed by the sequence Phe-Gly-XXX-Gly and has a length of about seven to 11 residues. A binding domain of this disclosure can comprise a single CDR from a variable region of an anti-TGFβ or anti-TGFβR2, or it can comprise multiple CDRs that can be the same or different.

[0044] Thus, a binding domain of this disclosure can comprise a single CDR from a variable region of an anti-TGFβ or anti-TGFβR2, or it can comprise multiple CDRs that can be the same or different. In certain embodiments, binding domains of this disclosure comprise V_H and V_L domains specific for a TGFβ or TGFβR2 comprising framework regions and CDR1, CDR2 and CDR3 regions, wherein (a) the V_H domain comprises an amino acid sequence of a heavy chain CDR3; or (b) the V_L domain comprises an amino acid sequence of a light chain CDR3; or (c) the binding domain comprises a V_H amino acid sequence of (a) and a V_L amino acid sequence of (b); or the binding domain comprises a V_H amino acid sequence of (a) and a V_L amino acid sequence of (b) and wherein the V_H and V_L are found in the same reference sequence. In further embodiments, binding domains of this disclosure comprise V_H and V_L domains specific for a TGFβ or TGFβR2 comprising framework regions and CDR1, CDR2 and CDR3 regions, wherein (a) the V_H domain comprises an amino acid sequence of a heavy chain CDR1, CDR2, and CDR3; or (b) the V_L domain comprises an amino acid sequence of a light chain CDR1, CDR2, and CDR3; or (c) the binding domain comprises a V_H amino acid sequence of (a) and a V_L amino acid sequence of (b); or the binding domain comprises a V_H amino acid sequence of (a) and a V_L amino acid sequence of (b), wherein the V_H and V_L amino acid sequences are from the same reference sequence.

[0045] In any of the embodiments described herein comprising specific CDRs, a binding domain can comprise (i) a V_H domain having an amino acid sequence that is at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to the amino

acid sequence of a V_H domain, wherein each CDR has at most three amino acid changes (*i.e.*, many of the changes will be in the framework regions); or (ii) a V_L domain having an amino acid sequence that is at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to the amino acid sequence of a V_L domain, wherein each CDR has at most three amino acid changes (*i.e.*, many of the changes will be in the framework regions); or (iii) both a V_H domain of (i) and a V_L domain of (ii); or both a V_H domain of (i) and a V_L domain of (ii) wherein the V_H and V_L are from the same reference sequence.

[0046] A TGFβ antagonist domain of fusion proteins of this disclosure may be an immunoglobulin-like domain such as an immunoglobulin scaffold. Immunoglobulin scaffolds contemplated by this disclosure include a scFv, a domain antibody or a heavy chain-only antibody. In a scFv, this disclosure contemplates the heavy and light chain variable regions are joined by any linker peptide known in the art to be compatible with domain or region joinder in a binding molecule. Exemplary linkers are linkers based on the Gly_4Ser linker motif, such as $(Gly_4Ser)_n$, wherein n=1-5. If a binding domain of a fusion protein of this disclosure is based on a non-human immunoglobulin or includes non-human CDRs, the binding domain may be "humanized" according to methods known in the art.

[0047] Alternatively, a TGFβ antagonist domain of fusion proteins of this disclosure may be a scaffold other than an immunoglobulin scaffold. Other scaffolds contemplated by this disclosure present the TGFβ-specific CDR(s) in a functional conformation. Other scaffolds contemplated include, but are not limited to, an A domain molecule, a fibronectin III domain, an anticalin, an ankyrin-repeat engineered binding molecule, an adnectin, a Kunitz domain or a protein AZ domain affibody.

IL6 Antagonists

[0048] As noted above, in certain embodiments the present disclosure provides polypeptides containing a binding region or domain that is an IL6 antagonist (*e.g.*, preferentially inhibits IL6 trans-signaling or inhibits both IL6 cis- and trans-signaling). In certain embodiments, the present disclosure provides multi-specific fusion proteins containing a binding region or domain specific for an IL6/IL6R complex that has one or more of the following properties: (1) greater or equal affinity for an IL6/IL6R complex than for IL6 or IL6Rα alone or has greater affinity for IL6Rα alone or an IL6/IL6R complex than for IL6 alone, (2) competes with membrane gp130 for binding with a sIL6/IL6R complex or augments soluble gp130 binding to sIL6/IL6R complex, (3) preferentially inhibits IL6 trans-signaling over IL6 cis-signaling, or (4) does not inhibit signaling of gp130 family cytokines

other than IL6. In certain preferred embodiments, a binding domain specific for an IL6/IL6R complex according to this disclosure has the following properties: (1) greater affinity for IL6Rα alone or an IL6xR complex than for IL6 alone, (2) augments soluble gp130 binding to sIL6/IL6R complex, (3) preferentially inhibits IL6 trans-signaling over IL6 cis-signaling, and (4) does not inhibit signaling of gp130 family cytokines other than IL6. For example, a binding region or domain specific for an IL6/IL6R complex may be an immunoglobulin variable binding domain or derivative thereof, such as an antibody, Fab, scFv, or the like. In the context of this disclosure, it should be understood that a binding region or domain specific for an IL6/IL6R complex is not gp130 as described herein.

[0049] As used herein, "IL6xR complex" or "IL6xR" refers to a complex of an IL6 with an IL6 receptor, wherein the IL6 receptor (also known as, for example, *IL6Rα*, IL6RA, IL6R1, and CD126) is either a membrane protein (referred to herein as mIL6R or mIL6Rα) or a soluble form (referred to herein as sIL6R or sIL6Rα). The term "IL6R" encompasses both mIL6Rα and sIL6Rα. In one embodiment, IL6xR comprises a complex of IL6 and mIL6Rα. In certain embodiments, the IL6xR complex is held together via one or more covalent bonds. For example, the carboxy terminus of an IL6R can be fused to the amino-terminus of an IL6 via a peptide linker, which is known in the art as a Hyper-IL6 (*see, e.g.*, Fischer *et al.* (1997) Nat. Biotechnol. 15:142). A Hyper-IL6 linker can be comprised of a cross-linking compound, a one to 50 amino acid sequence, or a combination thereof. A Hyper-IL6 may further include a dimerization domain, such as an immunoglobulin Fc domain or an immunoglobulin constant domain sub-region. In certain embodiments, the IL6xR complex is held together via non-covalent interactions, such as by hydrogen bonding, electrostatic interactions, Van der Waal's forces, salt bridges, hydrophobic interactions, or the like, or any combination thereof. For example, an IL6 and IL6R can naturally associate non-covalently (*e.g.*, as found in nature, or as synthetic or recombinant proteins) or each can be fused to a domain that promotes multimerization, such as an immunoglobulin Fc domain, to further enhance complex stability.

[0050] As used herein, "gp130" refers to a signal transduction protein that binds to an IL6xR complex. The gp130 protein can be in a membrane (mgp130), soluble (sgp130), or any other functional form thereof. Exemplary gp130 proteins have a sequence as set forth in GenBank Accession No. NP_002175.2 or any soluble or derivative form thereof (*see, e.g.*, Narazaki *et al.* (1993) Blood 82:1120 or Diamant *et al.* (1997) FEBS Lett. 412:379). By way of illustration and not wishing to be bound by theory, an mgp130 protein can bind to either an IL6/mILR or an IL6/sILR complex, whereas a sgp130 primarily binds with an IL6/sILR

complex (*see* Scheller *et al.* (2006) Scand. J. Immunol. 63:321). Thus, certain embodiments of binding domains, or fusion proteins thereof, of the instant disclosure can inhibit IL6xR complex trans-signaling by binding with higher affinity to IL6xR than to either IL6 or IL6Rα alone and preferably by competing with sIL6xR complex binding to mgp130. A binding domain of the instant disclosure "competes" with gp130 binding to a sIL6xR when (1) a binding domain or fusion protein thereof prevents gp130 from binding a sIL6xR and the binding domain binds sIL6xR with equal or higher affinity as compared to the binding of gp130 with sIL6xR, or (2) a binding domain or fusion protein thereof enhances or promotes sgp130 binding to sIL6xR.

[0051] In one aspect, an IL6 antagonist of this disclosure has an affinity for IL6 or IL6xR complex that is at least 2-fold to 1000-fold greater than for IL6Rα alone or has an affinity for IL6Rα or IL6xR complex that is at least 2-fold to 1000-fold greater than for IL6 alone. By binding to IL6, IL6R, or IL6xR complex, an IL6 antagonist of this disclosure preferentially inhibits IL6 cis- and trans-signaling. In certain embodiments, the affinity of a binding domain for IL6 or sIL6xR complex is about the same as the affinity of gp130 for IL6xR complex – with "about the same" meaning equal or up to about 2-fold higher affinity. In certain embodiments, the affinity of the binding domain for IL6, IL6R, or IL6xR complex is higher than the affinity of gp130 for IL6xR complex by at least 2-fold, at least 3-fold, at least 4-fold, at least 5-fold, at least 6-fold, at least 7-fold, at least 8-fold, at least 9-fold, at least 10-fold, at least 15-fold, at least 20-fold, at least 25-fold, at least 50-fold, at least 100-fold, 1000-fold, or greater. For example, if the affinity of gp130 for a IL6xR complex is about 2 nM (*see, e.g.*, Gaillard *et al.* (1999) Eur. Cytokine Netw. 10:337), then a binding domain having at least a 10-fold higher affinity for the IL6xR complex would have a dissociation constant (K_d) of about 0.2 nM or less.

[0052] In further embodiments, an IL6 antagonist binding domain of this disclosure comprises a polypeptide sequence that (a) binds to a sIL6xR complex with an affinity at least 2-fold, 10-fold, 25-fold, 50-fold, 75-fold to 100-fold, 100-fold to 1000-fold higher than for either IL6 or IL6Rα alone and (b) competes with membrane gp130 for binding to sIL6xR complex or augments soluble gp130 binding to sIL6xR complex. In further embodiments, a polypeptide binding domain of this disclosure that binds to a sIL6xR complex with an affinity at least 2-fold, 10-fold, 25-fold, 50-fold, 75-fold to 100-fold, 100-fold to 1000-fold higher than for either IL6 or IL6Rα alone may also (i) more significantly or preferentially inhibit IL6 trans-signaling over IL6 cis-signaling, (ii) not inhibit signaling of gp130 cytokine family members other than IL6, (iii) preferentially inhibit IL6 trans-signaling over IL6 cis-signaling

and not detectably inhibit signaling of gp130 family cytokines other than IL6, (iv) may have two or more of these properties, or (v) may have all of these properties.

[0053] In certain embodiments, a polypeptide IL6 antagonist binding domain of this disclosure binds to a sIL6xR complex with an affinity at least 2-fold to 1000-fold higher than for either IL6 or IL6Rα alone and more significantly or preferentially inhibits IL6 trans-signaling over IL6 cis-signaling. To "preferentially inhibit IL6 trans-signaling over IL6 cis-signaling" refers to altering trans-signaling to an extent that sIL6xR activity is measurably decreased while the decrease in IL6 cis-signaling is not substantially altered (*i.e.*, meaning inhibition is minimal, non-existent, or not measurable). For example, a biomarker for sIL6xR activity (*e.g.*, acute phase expression of antichymotrypsin (ACT) in HepG2 cells) can be measured to detect trans-signaling inhibition. A representative assay is described by Jostock *et al*. (Eur. J. Biochem., 2001) – briefly, HepG2 cells can be stimulated to overexpress ACT in the presence of sIL6xR (trans-signaling) or IL6 (cis-signaling), but adding spg130 will inhibit the overexpression of ACT induced by sIL6xR while not substantially affecting IL6 induced expression. Similarly, a polypeptide binding domain of this disclosure that preferentially inhibits IL6 trans-signaling over IL6 cis-signaling will inhibit the overexpression of ACT induced by sIL6xR (*i.e.*, inhibit trans-signaling) while not substantially affecting IL6 induced expression (*i.e.*, not measurably decrease cis-signaling). This and other assays known in the art can be used to measure preferential inhibition of IL6 trans-signaling over IL6 cis-signaling (*see*, *e.g.*, other biomarkers described in Sporri *et al*. (1999) Int. Immunol. 11:1053; Mihara *et al*. (1995) Br. J. Rheum. 34:321; Chen et al. (2004) Immun. 20:59).

[0054] In further embodiments, signaling by gp130 family cytokines other than IL6 is not substantially inhibited by binding domain polypeptides or multi-specific fusion proteins thereof of this disclosure. For example, cis- and trans-signaling by an IL6xR complex via gp130 will be inhibited, but signaling by one or more other gp130 family cytokines will be minimally affected or unaffected, such as signaling via leukemia inhibitory factor (LIF), ciliary neurotropic factor (CNTF), neuropoietin (NPN), cardiotropin like cytokine (CLC), oncostatin M (OSM), IL-11, IL-27, IL-31, cardiotrophin-1 (CT-1), or any combination thereof.

[0055] It will be appreciated by those skilled in the art that the preferred *in vivo* half-life of a binding domain of this disclosure is on the order of days or weeks, but while the binding domain concentration may be low, the target may be plentiful as both IL6 and sIL6 production can be quite elevated in disease states (*see*, *e.g.*, Lu *et al*. (1993) Cytokine 5:578).

Thus, in certain embodiments, a binding domain of this disclosure has a k_{OFF} of about 10^{-5}/sec (*e.g.*, about a day) or less. In certain embodiments, the k_{OFF} can range from about 10^{-1}/sec, about 10^{-2}/sec, about 10^{-3}/sec, about 10^{-4}/sec, about 10^{-5}/sec, about 10^{-6}/sec, about 10^{-7}/sec, about 10^{-8}/sec, about 10^{-9}/sec, about 10^{-10}/sec, or less.

[0056] In an illustrative example, binding domains of this disclosure specific for an IL6 or IL6xR complex were identified in a Fab phage library of fragments (*see* Hoet *et al.* (2005) Nature Biotechnol. 23:344) by screening for binding to a synthetic IL6xR complex. The synthetic IL6xR complex used for this screening comprises a structure of N-IL6Rα(frag)-L1-IL6(frag)-L2-ID-C, wherein N is the amino-terminus and C is the carboxy-terminus, IL6Rα(frag) is a fragment of full length IL6Rα, IL6(frag) is a fragment of IL6, L1 and L2 are linkers, and ID is an intervening or dimerization domain, such as an immunoglobulin Fc domain.

[0057] More specifically, an IL6xR (which is a form of Hyper IL6) used to identify the binding domains specific for IL6xR complex has a structure, from amino-terminus to carboxy-terminus, as follows: (a) a central fragment of 212 amino acids from IL6Rα that is missing the first 110 amino acids of the full length protein and a carboxy-terminal portion that will depend on the isoform used (*see* GenBank Accession No. NP_000556.1, isoform 1 or NP_852004.1, isoform 2) fused to (2) a linker of G_3S that is in turn fused to (3) a 175 amino acid carboxy-terminal fragment of IL6 (*i.e.*, missing the first 27 amino acids of the full length protein; GenBank Accession No. NP_000591.1) that is in turn fused to (4) a linker that is an IgG2A hinge as set forth in SEQ ID NO:589, which is finally fused to a dimerization domain comprised of an immunoglobulin G1 (IgG1) Fc domain. In certain embodiments, the dimerization domain comprised of an IgG1 Fc domain has one or more of the following amino acids mutated (*i.e.*, have a different amino acid at that position): leucine at position 234 (L234), leucine at position 235 (L235), glycine at position 237 (G237), glutamate at position 318 (E318), lysine at position 320 (K320), lysine at position 322 (K322), or any combination thereof (EU numbering). For example, any one of these amino acids can be changed to alanine. In a further embodiment, an IgG1 Fc domain has each of L234, L235, G237, E318, K320, and K322 (according to Kabat numbering) mutated to an alanine (*i.e.*, L234A, L235A, G237A, E318A, K320A, and K322A, respectively).

[0058] In one embodiment, an IL6xR complex used to identify the IL6 antagonist binding domains of this disclosure has an amino acid sequence as set forth in SEQ ID NO:606. In certain embodiments, there are provided polypeptides containing a binding domain specific for an IL6xR complex, wherein the IL6xR is a sIL6xR and has the amino

acid sequence as set forth in SEQ ID NO:606. In further embodiments, polypeptides containing a binding domain specific for an IL6xR complex (1) have greater or equal affinity for an IL6xR complex than for IL6 or IL6Rα alone, or have greater affinity for IL6Rα alone or an IL6xR complex than for IL6 alone, (2) compete with membrane gp130 for binding with a sIL6xR complex or augment soluble gp130 binding to sIL6xR complex, (3) preferentially inhibit IL6 trans-signaling over IL6 cis-signaling, or (4) do not inhibit signaling of gp130 family cytokines other than IL6, (5) have any combination thereof of properties (1) – (4), or (6) have all of the properties of (1) – (4). Other exemplary IL6xR complexes that may be used to identify binding domains of the instant disclosure or used as a reference complex to measure any of the aforementioned binding properties are described, for example, in US Patent Publication Nos. 2007/0172458; 2007/0031376; and US Patent Nos. 7,198,781; 5,919,763.

[0059] In some embodiments, IL6 antagonist binding domains of this disclosure comprise V_H and V_L domains specific for an IL6, IL6R, or IL6xR complex as described herein, and preferably human IL6, human IL6R, or human IL6xR complex. In certain embodiments, the V_H and V_L domains are rodent, (*e.g.*, mouse, rat), humanized, or human. Examples of binding domains containing such V_H and V_L domains specific for IL6, IL6R, or IL6xR are set forth in SEQ ID NOS:435-496 and 373-434, respectively. In further embodiments, there are provided polypeptide binding domains specific for an IL6xR wherein the binding domain comprises a sequence that is 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%, at least 99.5% , or at least 100% identical to the amino acid sequence of one or more light chain variable regions (V_L) or to one or more heavy chain variable regions (V_H), or both, as set forth in SEQ ID NOS:373-434 and 435-496, respectively, wherein each CDR has up to three amino acid changes (*i.e.*, many of the changes are found in one or more of the framework regions).

[0060] In further embodiments, binding domains of this disclosure comprise V_H and V_L domains specific for an IL6xR as set forth in SEQ ID NOS:435-496 and 373-434, respectively, which are at least 80%, at least 81%, at least 82%, at least 83%, at least 84%, at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, 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 at least 99.5% identical to the amino acid sequence of such V_H domain, V_L domain, or both, wherein each CDR has zero, one, two, or three amino acid changes. For example, the amino acid sequence of a V_H domain, V_L domain, or both of this disclosure can

be at least 80%, at least 81%, at least 82%, at least 83%, at least 84%, at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, 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 at least 99.5% identical to the amino acid sequence of V_H domain (*e.g.*, amino acids 512 to 636), V_L domain (*e.g.*, amino acids 652 to 759), or both, respectively, from an exemplary xceptor molecule containing binding domain TRU6-1002 (*see* SEQ ID NO:608), wherein each CDR has zero, one, two, or three amino acid changes.

[0061] In any of these or other embodiments described herein, the V_L and V_H domains may be arranged in either orientation and may be separated by up to about a ten amino acid linker as disclosed herein or any other amino acid sequence capable of providing a spacer function compatible with interaction of the two sub-binding domains. In certain embodiments, a linker joining the V_H and V_L domains comprises an amino acid sequence as set forth in SEQ ID NO:497-604 and SEQ ID NO:1223-1228, such as Linker 47 (SEQ ID NO:543) or Linker 80 (SEQ ID NO:576).

[0062] In further embodiments, IL6 antagonist binding domains of this disclosure may comprise one or more complementarity determining region ("CDR"), or multiple copies of one or more such CDRs, which have been obtained, derived, or designed from variable regions of an anti-IL6, anti-IL6R, or anti-IL6xR complex scFv or Fab fragment or from heavy or light chain variable regions thereof. Thus, a binding domain of this disclosure can comprise a single CDR from a variable region of an IL6 or anti-IL6xR, or it can comprise multiple CDRs that can be the same or different. In certain embodiments, IL6 antagonist binding domains of this disclosure comprise V_H and V_L domains comprising framework regions and CDR1, CDR2 and CDR3 regions, wherein (a) the V_H domain comprises the amino acid sequence of a heavy chain CDR3 found in any one of SEQ ID NOS:435-496; or (b) the V_L domain comprises the amino acid sequence of a light chain CDR3 found in any one of SEQ ID NOS:373-434; or (c) the binding domain comprises a V_H amino acid sequence of (a) and a V_L amino acid sequence of (b); or the binding domain comprises a V_H amino acid sequence of (a) and a V_L amino acid sequence of (b) and wherein the V_H and V_L are found in the same reference sequence. In further embodiments, binding domains of this disclosure comprise V_H and V_L domains specific for an IL6xR complex comprising framework regions and CDR1, CDR2 and CDR3 regions, wherein (a) the V_H domain comprises the amino acid sequence of a heavy chain CDR1, CDR2, and CDR3 found in any one of SEQ ID NOS:435-496; or (b) the V_L domain comprises the amino acid sequence of a light chain CDR1, CDR2, and CDR3 found in any one of SEQ ID NOS:373-434; or (c) the binding domain comprises a

V_H amino acid sequence of (a) and a V_L amino acid sequence of (b); or the binding domain comprises a V_H amino acid sequence of (a) and a V_L amino acid sequence of (b), wherein the V_H and V_L amino acid sequences are from the same reference sequence. Exemplary light and heavy chain variable domain CDRs directed against IL6, IL6R, or IL6xR complex are provided in SEQ ID NO:1-186 and 1187-1192, and 187-372 and 1193-1198, respectively.

[0063] Amino acid sequences of IL6 antagonist light chain variable regions are provided in SEQ ID NO:373-434 and 1199-1204, with the corresponding heavy chain variable regions being provided in SEQ ID NO:435-496 and 1205-1210, respectively.

[0064] In any of the embodiments described herein comprising specific CDRs against IL6, IL6R, or IL6xR, a binding domain can comprise (i) a V_H domain having an amino acid sequence that is at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to the amino acid sequence of a V_H domain found in any one of SEQ ID NOS:435-496; or (ii) a V_L domain having an amino acid sequence that is at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to the amino acid sequence of a V_L domain found in any one of SEQ ID NOS:373-434; or (iii) both a V_H domain of (i) and a V_L domain of (ii); or both a V_H domain of (i) and a V_L domain of (ii) wherein the V_H and V_L are from the same reference sequence.

[0065] In certain embodiments, a binding domain of this disclosure may be an immunoglobulin-like domain, such as an immunoglobulin scaffold. Immunoglobulin scaffolds contemplated in this disclosure include a scFv, Fab, a domain antibody, or a heavy chain-only antibody. In further embodiments, there are provided anti-IL6 or anti-IL6xR antibodies (*e.g.*, non-human such as mouse or rat, chimeric, humanized, human) or Fab fragments or scFv fragments that have an amino acid sequence that is at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of a V_H and V_L domain set in any one of SEQ ID NOS:435-496 and 373-434, respectively, which may also have one or more of the following properties: (1) have greater or equal affinity for an IL6xR complex than for IL6 or IL6Rα alone, or have greater affinity for IL6Rα alone or an IL6xR complex than for IL6 alone, (2) compete with membrane gp130 for binding with a sIL6xR complex or augment soluble gp130 binding to sIL6xR complex, (3) preferentially inhibit IL6 trans-signaling over IL6 cis-signaling, or (4) do not inhibit signaling of gp130 family cytokines other than IL6. Such antibodies, Fabs, or scFvs can be used in any of the methods described herein. In certain embodiments, the present disclosure provides polypeptides containing a binding domain that is an IL6 antagonist (*i.e.*, can inhibit IL6 cis- and trans-signaling). In further embodiments, an IL6 antagonist according to this

disclosure does not inhibit signaling of gp130 family cytokines other than IL6. Exemplary IL6 antagonists include binding domains specific for an IL6 or IL6xR, such as an immunoglobulin variable binding domain or derivative thereof (*e.g.*, an antibody, Fab, scFv, or the like).

[0066] Alternatively, binding domains of this disclosure may be part of a scaffold other than an immunoglobulin. Other scaffolds contemplated include an A domain molecule, a fibronectin III domain, an anticalin, an ankyrin-repeat engineered binding molecule, an adnectin, a Kunitz domain, or a protein AZ domain affibody.

IL10 Antagonists

[0067] In certain embodiments the present disclosure provides polypeptides containing a binding region or domain that is an IL10 antagonist (*i.e.*, can inhibit IL10 signaling). Exemplary IL10 antagonists include binding domains specific for an IL10 or IL10R1, such as an immunoglobulin variable binding domain or derivative thereof (*e.g.*, an antibody, Fab, scFv, or the like), or an IL10R1 ectodomain.

[0068] IL10 is a member of a cytokine superfamily that share an alpha-helical structure. Although no empirical evidence exists, it has been suggested that all possess six alpha-helices (Fickenscher, H. et al., 2002, Trends Immunol. 23: 89). IL10 has four cysteines, only one of which is conserved among family members. Since IL10 demonstrates a V-shaped fold that contributes to its dimerization, it appears that disulfide bonds are not critical to this structure. Amino acid identity of family members to IL10 ranges from 20% (IL-19) to 28% (IL-20) (Dumouter et al., 2002, Eur. Cytokine Netw. 13: 5).

[0069] IL10 was first described as a Th2 cytokine in mice that inhibited IFN-α and GM-CSF cytokine production by Th1 cells (Moore et al., 2001, Annu. Rev. Immunol. 19: 683; Fiorentino et al., 1989, J. Exp. Med. 170:2081).

[0070] Human IL10 is 178 amino acids in length with an 18 amino acid signal sequence and a 160 amino acid mature segment and a molecular weight of approximately 18 kDa (monomer). Human IL10 contains no potential N-linked glycosylation site and is not glycosylated (Dumouter et al., 2002, Eur. Cytokine Netw. 13: 5; Vieira et al., 1991, Proc. Natl. Acad. Sci. USA 88:1172). It contains four cysteine residues that form two intrachain disulfide bonds. The length of α-helices A to F in human IL10 are 21, 8, 19, 20, 12 and 23 amino acids, respectively. Helices A to D of one monomer noncovalently interact with helices E and F of a second monomer, forming a noncovalent V-shaped homodimer. Functional areas have been mapped on the IL10 molecule. In the N-terminus, pre-helix A

residues no. 1-9 are involved in mast cell proliferation, while in the C-terminus, helix F residues no. 152-160 mediate leukocyte secretion and chemotaxis.

[0071] Cells known to express IL10 include CD8+ T cells, microglia, CD14+ (but not CD16+) monocytes, Th2 CD4+ cells (mice), keratinocytes, hepatic stellate cells, Th1 and Th2 CD4+ T cells (human), melanoma cells, activated macrophages, NK cells, dendritic cells, B cells (CD5+ and CD19+) and eosinophils.

[0072] On T cells, the initial observations of IL10 inhibition of IFN-gamma production are now believed to be an indirect effect mediated by accessory cells. Additional effects on T cells, however, include: IL10 induced CD8+ T cell chemotaxis, an inhibition of CD4+ T cell chemotaxis towards IL-8, suppression of IL-2 production following activation, an inhibition of T cell apoptosis via Bcl-2 up-regulation, and an interruption of T cell proliferation following low antigen exposure accompanied by B7/CD28 costimulation (Akdis et al., 2001, Immunology 103: 131).

[0073] On B cells, IL10 has a number of related, yet distinct functions. In conjunction with TNF-β and CD40L, IL10 induces IgA production in naïve (IgD+) B cells. It is believed that TGF-β/CD40L promotes class switching while IL10 initiates differentiation and growth. When TGF-β is not present, IL10 cooperates with CD40L in inducing IgG1 and IgG3 (human), and thus may be a direct switch factor for IgG subtypes. IL10 has divergent effects on IL-4 induced IgE secretion. If IL10 is present at the time of IL-4 induced class switching, it reverses the effect; if it is present after IgE commitment, it augments IgE secretion. CD27/CD70 interaction in the presence of IL10 promotes plasma cell formation from memory B cells (Agematsu et al., 1998, Blood 91: 173).

[0074] Mast cells and NK cells are also impacted by IL10. On mast cells, IL10 induces histamine release while blocking GM-CSF and TNF-α release. This effect may be autocrine as IL10 is known to be released by mast cells in rat. As evidence of its pleiotrophic nature, IL10 has the opposite effects on NK cells. Rather than blocking TNF-α and GM-CSF production, IL10 actually promotes this function on NK cells. In addition, it potentiates IL-2 induced NK cell proliferation and facilitates IFN-γ secretion in NK cells primed by IL-18. In concert with both IL-12 and/or IL-18, IL10 potentiates NK cell cytotoxicity (Cai et al., 1999, Eur. J. Immunol. 29: 2658).

[0075] IL10 has a pronounced anti-inflammatory impact on neutrophils. It inhibits the secretion of the chemokines MIP-1α, MIP-1β and IL-8, and blocks production of the proinflammatory mediators IL-1 β and TNF-α. In addition, it decreases the ability of

neutrophils to produce superoxide, and as a result interferes with PMN-mediated antibody-dependent cellular cytotoxicity. IL10 also blocks IL-8 and fMLP-induced chemotaxis, possibly via CXCR1 (Vicioso et al., 1998 Eur. Cytokine Netw. 9: 247).

[0076] On dendritic cells (DCs), IL10 generally exhibits immunosuppressive effects. It would appear to promote CD14+ macrophage differentiation at the expense of DCs. Macrophages, while phagocytic, are poor antigen-presenting cells. IL10 seems to decrease the ability of DCs to stimulate T cells, particularly for Th1 type cells. How IL10 accomplishes this is unclear, as the data within the literature is conflicting. Relative to MHC-II expression, it can be down-regulated, unchanged, or up-regulated (Sharma et al., 1999, J. Immunol. 163:5020). With respect to B7-1/CD80, IL10 will either up-regulate or down-regulate its expression. B7-2/CD86 plays a key role in T cell activation. For this molecule, IL10 is involved in both up-regulation and down-regulation. Perhaps the most significant modulation, however, occurs with CD40 (IL10 seems to reduce its expression). At the regional level, IL10 may block immunostimulation by inhibiting Langerhans cell migration in response to proinflammatory cytokines. Alternatively, IL10 blocks an inflammation-induced DC maturation step that normally involves CCR1, CCR2 and CCR5 down-regulation and CCR7 up-regulation. This blockage, with retention of CCR1, CCR2 and CCR5, results in a failure of DCs to migrate to regional nodes. The result is an immobile DC that will not stimulate T cells but will bind (and clear) proinflammatory chemokines without responding to them (D-Amico et al., 2000 Nat. Immunol. 1:387).

[0077] On monocytes, IL10 has a number of documented effects. For example, IL10 seems to clearly reduce cell surface MHC-II expression. It also inhibits IL-12 production following stimulation. While it promotes a monocyte to macrophage transition in conjunction with M-CSF, the phenotype of the macrophage is not clear (i.e. CD16+/cytotoxic vs. CD16-). IL10 also reduces monocyte GM-CSF secretion and IL-8 production, while promoting IL-1ra release (Gesser et al., 1997, Proc. Natl. Acad. Sci. USA 94:14620). Hyaluronectin, a connective tissue component, is now known to be secreted by monocytes in response to IL10. This may have some importance in cell migration, particularly tumor cell metastases, where hyaluronectin is known to interrupt cell migration through extracellular space (Gesser et al., 1997).

[0078] Human IL10R1 is a 90-110 kDa, single-pass type I transmembrane glycoprotein that is expressed on a limited number of cell types (Liu et al., 1994, J. Immunol. 152:1821). Weak expression is seen in pancreas, skeletal muscle, brain, heart and kidney. Placenta, lung, and liver showed intermediate levels of expression, while monocytes, B-cells,

large granular lymphocytes and T-cells express high levels (Liu et al., 1994). The expressed protein is a 578 amino acid protein that contains a 21 amino acid signal peptide, a 215 amino acid extracellular region, a 25 amino acid transmembrane segment, and a 317 amino acid cytoplasmic domain. There are two FNIII motifs within the extracellular region and a STAT3 docking site plus a JAK1 association region within the cytoplasmic domain (Kotenko et al., 2000 Oncogene 19:2557; Kotenko et al., 1997, EMBO J. 16:5894). IL10R1 binds human IL10 with a Kd of about 200 pM.

[0079] In some embodiments, binding domains of this disclosure comprise V_H and V_L domains specific for an IL10 or an IL10R1. In certain embodiments, the V_H and V_L domains are rodent (*e.g.*, mouse, rat), humanized, or human. Examples of binding domains containing such V_H and V_L domains specific for IL10 include, but are not limited to, those disclosed in US Patent Application Publication no. US 2007/0178097A1. Binding domains of this disclosure may also, or alternatively, comprise an IL10R1 ectodomain as shown, for example, in SEQ ID NO:745, or a fragment thereof. In further embodiments, there are provided polypeptide binding domains specific for IL10, wherein the binding domain comprises a sequence that is at least 80%, at least 85%, 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%, at least 99.5% , or at least 100% identical to an amino acid sequence of SEQ ID NO:745 or to amino acids 22-401 of SEQ ID NO:745, wherein the polypeptide binding domain binds to IL10 and inhibits the activity thereof.

GITR Agonists

[0080] In certain embodiments the present disclosure provides polypeptides containing a binding region or domain that is a GITR agonist (*i.e.*, can increase GITR signaling). Exemplary GITR agonists include binding domains specific for a GITR or GITRL, such as an immunoglobulin variable binding domain or derivative thereof (*e.g.*, an antibody, Fab, scFv, or the like), or a GITRL ectodomain.

[0081] Glucocorticoid-induced tumor necrosis factor receptor (GITR; also known as AITR) is a type I transmembrane protein and a member of the TNF receptor superfamily (Nocentini et al., (2007) Eur. J. Immunol. 37:1165-9). The cytoplasmic domain has homology to the cytoplasmic domain of 4-1BB and CD27. GITR is expressed in peripheral blood T cells, bone marrow, thymus, spleen, and lymph nodes, and is constitutively expressed in $CD4^+CD25^+$ regulatory T cells (Kwon et al., (2003) Exp. Mol. Med. 35:13). In addition, it is constitutively expressed at low levels in natural killer (NK) cells and is induced upon

stimulation by either Toll-like receptor ligand or IL-15 (Liu et al., (2008) J. Biol. Chem. 283:8202).

[0082] Expression of GITR is increased following T cell activation. Activation of GITR coactivates effector T lymphocytes and modulates regulatory T cell activity. Binding of GITR to its ligand GITRL has been shown to render $CD4^+CD25^-$ effector T cells resistant to the inhibitory effects of $CD4^+CD25^+$ regulatory T cells.

[0083] GITR ligand (GITRL) is a type II membrane protein. It is 173 amino acids long with a predicted molecular weight of 20 kDa. The experimental molecular weight of 25-28 kDa is suggestive of glycosylation. GITRL is expressed in antigen presenting cells (APC) and is constitutively expressed in human umbilical vein endothelial cells (Nocentini et al. *Ibid*). It is not, however, expressed in resting or stimulated T cells, B cell lines, or peripheral blood mononuclear cells.

[0084] The GITR/GITRL system has been shown to increase resistance to tumors and viral infections (Nocentini et al., *ibid*). Specifically, the anti-GITR monoclonal antibody DTA-1 was shown to inhibit regulatory T cell-dependent suppression and enhance T cell responses. Administration of DTA-1 in mice induced B16 melanoma tumor rejection. GITR is also involved in autoimmune/inflammatory processes and regulates leukocyte extravasation. GITR-/- mice exhibit decreased sensitivity to inflammatory disease conditions, indicating a positive role for GITR in inflammation.

[0085] In some embodiments, binding domains of this disclosure comprise V_H and V_L domains specific for a GITR or a GITRL. In certain embodiments, the V_H and V_L domains are rodent (*e.g.*, mouse, rat), humanized, or human. Examples of binding domains containing such V_H and V_L domains specific for GITR include, but are not limited to, those disclosed in US Patent Application Publication no. US 2007/0098719A1. Binding domains of this disclosure may also, or alternatively, comprise a GITRL ectodomain (e.g. amino acids 74-181 of Genbank Accession NP_005083.2 (SEQ ID NO:746) or a fragment thereof. In further embodiments, there are provided polypeptide binding domains specific for GITR, wherein the binding domain comprises a sequence that is at least 80%, at least 85%, 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%, at least 99.5% , or at least 100% identical to amino acids 74-181 of SEQ ID NO:746, wherein the polypeptide binding domain binds to GITR and increases the activity thereof.

VEGF Antagonists

[0086] In certain embodiments the present disclosure provides polypeptides containing a binding region or domain that is a VEGF antagonist (*i.e.*, can inhibit VEGF signaling). Exemplary VEGF antagonists include binding domains specific for a VEGF or VEGFR2, such as an immunoglobulin variable binding domain or derivative thereof (*e.g.*, an antibody, Fab, scFv, or the like), or a VEGFR2 ectodomain.

[0087] Vascular endothelial growth factor (VEGF or VEGF-A) is an evolutionarily conserved homodimeric glycoprotein and a potent endothelial cell–specific mitogen that plays a critical role in angiogenesis and vasculogenesis (Lee et al. (2007) PLOS Medicine 6:1101-1116). VEGF induces various intracellular signaling and physiologic responses that are essential for angiogenesis, such as intracellular Ca^{2+} influx, chemotaxis (migration), expression of plasminogen activators, urokinase receptor and collagenases, and vascular permeability. Its biological effects are elicited through two high-affinity receptor tyrosine kinases, namely VEGF receptors 1 (VEGFR1) and 2 (VEGFR2), which are mainly expressed in endothelial cells.

[0088] VEGFA is a secreted protein that is a homodimer linked by disulfide bonds. It is also found as heterodimer with PlGF. Alternative splicing of VEGF mRNA results in various isoforms, which include VEGF121, VEGF145, VEGF165, VEGF189 and VEGF206, in humans and VEGF120, VEGF164 and VEGF188 in mice. Studies of genetically engineered mice expressing only one VEGF isoform indicate that VEGF isoforms have distinct yet some overlapping roles in vascular development and function as evidenced by tissue-specific vascular defects in these mice. The VEGF isoforms display differences in their biochemical properties, including receptor binding with VEGF165 and VEGF188 but not VEGF120 binding to neuropilins and heparan sulfate. The differential affinity to heparan sulfate is important in their binding to VEGFR1 and VEGF2, as heparan sulfate can mediate the binding and transactivation of these receptors. Furthermore, differential binding to heparan sulfate is reported to lead to different VEGF actions, including endothelial cell survival, adhesion and vascular branch formation. Both VEGF164 and VEGF188 bind heparan sulfate, making them partially or fully cell-bound, respectively, whereas VEGF120 does not bind heparan sulfate, and is freely diffusible.

[0089] The VEGF isoforms display tissue-specific patterns of expression. The VEGF189, VEGF-165 and VEGF-121 isoforms are widely expressed, whereas the VEGF206 and VEGF-145 are uncommon. Its expression is regulated by growth factors, cytokines, gonadotropins, nitric oxide, hypoxia, hypoglycemia and oncogenic mutations.

[0090] The classical role of VEGF in tumor progression is as a positive regulator of angiogenesis, the process of forming new capillaries from preexisting blood vessels. Tumor growth is highly dependent on the ability of tumors to induce their own vascularization. VEGF expression has been reported in a number of cancer cell lines and in several clinical specimens derived from breast, brain, and ovarian cancers. Thus, antagonism of VEGF can effectively prevent tumor growth through incomplete blood vessel formation. VEGF exerts its effects on endothelial cells in a paracrine mode after its release by other cells such as tumor cells, or in an autocrine manner in VEGF-producing endothelial cells. VEGF binds to its cognate receptors VEGFR1 (also known as FLT1), VEGFR2 (also known as KDR or FLK1), and neuropilin 1 (NRP1).

[0091] VEGF expression in the adult is cell-type specific and is controlled at many levels from transcription to translation, and is upregulated in tumors and in various pathologic states. One of the best-characterized stimuli of VEGF transcription is hypoxia, which acts by stabilization of the hypoxia-inducible factor-1 alpha (HIF1α) transcription factor. Hypoxic regulation of VEGF also takes place post-transcriptionally via mRNA stabilization. VEGF expression is induced by other growth factors and cytokines including IGF-1, Il-6, Il-1, PDGF, TNF-α, TGF-β and FGF-4. In addition, VEGF expression is also stimulated by physical forces, including stretch, with one putative transcription factor being the Kruppel like factor-2. Analysis of the VEGF promoter reveals many other potential transcription factor responsive elements, of which several pathways have been elucidated, for example EGF and HGF signaling via the SP1 responsive element.

[0092] Members of the VEGF family promote two very important processes *in vivo*, angiogenesis and lymphangiogenesis, which involve growth of new blood and lymphatic vessels from pre-existing vasculature, respectively. These processes control the normal processes of wound healing, ovarian-follicular development, endometrium growth and pathological processes such as retinopathies, rheumatoid arthritis and solid tumor growth. A newly identified splice variant of VEGF, VEGF165b, is postulated to have an inhibitory effect on angiogenesis. Lymphangiogenesis is correlated with lymph node metastasis and cancer spread via the lymphatic system.

[0093] VEGF activities are mediated by high-affinity receptor tyrosine kinases expressed primarily in endothelial cells. These are: VEGFR-1 (Flt-1) and VEGFR-2 (Flk-1/KDR), which are mainly expressed by blood vessel endothelial cells and VEGFR-3 (Flt-4) expressed in lymphatic endothelial cells. These receptors are characterized by seven extracellular immunoglobulin-like domains, which bind the growth factor, followed by a

single membrane-spanning region and a conserved intracellular tyrosine kinase domain interrupted by a kinase insert sequence. These receptors are themselves enzymes and once activated by ligand binding, they dimerize and undergo autophosphorylation. This step enhances the capacity of the receptor to directly activate other target proteins by phosphorylating them on specific tyrosine residues.

[0094] The VEGF-kinase ligand/receptor signaling system plays a key role in vascular development and regulation of vascular permeability. In case of HIV-1 infection, the interaction with extracellular viral Tat protein seems to enhance angiogenesis in Kaposi's sarcoma lesions.

[0095] Although VEGF binds to VEGFR1, VEGFR2, Nrp-1 and Nrp-2, its main signaling receptor in the endothelium is VEGFR2. VEGFR2 belongs to the family of receptor tyrosine kinases, and upon VEGF binding, there is dimerization and activation of the tyrosine kinase, resulting in phosphorylation of specific tyrosine residues on the cytoplasmic tail, which in turn promotes docking of signal transducing molecules. VEGFR2 is responsible for initiating signal transduction pathways within endothelial cells. Following the binding of VEGF to VEGFR2, VEGF mediates its effects on proliferation, survival, adhesion, migration, capillary morphogenesis, and gene expression in endothelial cells. VEGFR1 has a relatively minor role in VEGF-mediated signal transduction as compared to VEGFR2, since its kinase activity is 10-fold less than that of VEGFR2. Breast cancer cell lines express both VEGF and the VEGF receptors VEGFR1, VEGFR2, and NRP1. Recent studies have shown that VEGF acts as an autocrine growth and survival factor for VEGF receptor-expressing tumor cells. However, the mechanism by which VEGF mediates the survival of tumor cells needs to be investigated in depth (Lee *et al.*, 2007, PLOS Medicine 6: 1101-1116).

[0096] Although VEGFR1 is also expressed by endothelial cells (EC), it is believed to act primarily to modulate VEGFR2 signaling. Mitogenesis, chemotaxis, cell survival and changes in the morphology of endothelial cells are mainly mediated by VEGFR-2. The mitogenic signal is induced by activation of the Raf-Mek-Erk pathway, while the antiapoptotic effects and chemotaxis are mediated by PI3K/Akt activation. VEGF binding to VEGFR-2 also results in activation of several integrins, which are adhesion molecules involved in angiogenesis, in a PI3K/Akt dependent manner. Apart from being expressed in endothelial cells, VEGFR-2 is also found in haematopoietic stem cells, where it increases their survival, and in retinal progenitor cells, where it plays a critical role in neurogenesis and vasculogenesis.

[0097] In some embodiments, binding domains of this disclosure comprise V_H and V_L domains specific for a VEGF or a VEGFR2. In certain embodiments, the V_H and V_L domains are rodent (*e.g.*, mouse, rat), humanized, or human. Examples of binding domains containing such V_H and V_L domains specific for VEGF include, but are not limited to, those disclosed in US Patent Application Publication no. US 2007/0141065A1. Binding domains of this disclosure may also, or alternatively, comprise a VEGFR2 ectodomain (see, Genbank Accession NP_002244.1, SEQ ID NO:747) or a fragment thereof. In further embodiments, there are provided polypeptide binding domains specific for VEGF, wherein the binding domain comprises a sequence that is at least 80%, at least 85%, 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%, at least 99.5% , or at least 100% identical to an amino acid sequence of SEQ ID NO:747, wherein the polypeptide binding domain binds to VEGF and inhibits the activity thereof.

TNFα Antagonists

[0098] In certain embodiments the present disclosure provides polypeptides containing a binding region or domain that is a TNFα antagonist (*i.e.*, can inhibit TNFα signaling). Exemplary TNFα antagonists include binding domains specific for a TNFα, such as an immunoglobulin variable binding domain or derivative thereof (*e.g.*, an antibody, Fab, scFv, or the like), or a TNFR1 or TNFR2 ectodomain.

[0099] Tumor Necrosis Factor Receptor (TNFR) is a member of the tumor necrosis factor receptor superfamily and is the receptor for Tumor Necrosis Factor-α (TNFα), also known as CD120 or cachectin. There are two variants of this cytokine receptor, TNFR1 and TNFR2, (CD120a receptor and CD120b receptor). TNFR1 (Genbank accession no. NP_001056.1) has a molecular weight of about 55 KD and is therefore sometimes referred to as p55. A TNFR domain that may be used as a TNFα binding domain in the disclosed fusion proteins is located at amino acids 44-149 of the TNFR1 sequence. TNFR2 (Genbank accession no. NP_001057.1) has a molecular weight of about 75 KD and is therefore sometimes referred to as p75. A TNFR domain that may be used as a TNFα binding domain in the disclosed fusion proteins is located at amino acids 40-141 of the TNFR2 sequence.

[00100] A majority of cell types and tissues appear to express both TNF receptors. Both exist in cell surface as well as soluble forms and both are active in signal transduction, although they are able to mediate distinct cellular responses. TNFR1 appears to be responsible for signaling most TNF responses. Among other activities, TNFR2 stimulates

thymocyte proliferation, activates NF-κβ, and is an accessory to TNFR1 in the signaling of responses primarily mediated by TNF-R1, like cytotoxicity.

[00101] TNF antagonists, such as anti-TNF antibodies, can positively affect various inflammatory conditions. For example, infliximab is indicated in the United States for the treatment of rheumatoid arthritis, Crohn's disease, ankylosing spondylitis, psoriatic arthritis, plaque psoriasis, and ulcerative colitis. Recently, perispinal delivery of the TNFα inhibitor etanercept has been shown to reduce symptoms in patients with Alzheimer's disease (Tobinick and Gross (2008) BMC Neurol. 8:27-36; Griffin (2008) J. Neuroinflammation, 5:3-6).

[00102] According to REMICADE® (infliximab) prescribing information, biological activities attributed to TNF include: induction of pro-inflammatory cytokines such as interleukins (IL) 1 and 6, enhancement of leukocyte migration by increasing endothelial layer permeability and expression of adhesion molecules by endothelial cells and leukocytes, activation of neutrophil and eosinophil functional activity, induction of acute phase reactants and other liver proteins, as well as tissue degrading enzymes produced by synoviocytes and/or chondrocytes.

[00103] In some embodiments, binding domains of this disclosure comprise V_H and V_L domains specific for a TNFα. In certain embodiments, the V_H and V_L domains are human. Examples of binding domains containing such V_H and V_L domains specific for TNFα include, but are not limited to, those disclosed in US Patent Application Publication no. US 2007/0249813. Binding domains of this disclosure may also, or alternatively, comprise a TNFR1 ectodomain (see, Genbank Accession NP_001056.1, SEQ ID NO:749) or a fragment thereof, or a TNFR2 ectodomain (see, Genbank Accession NP_001057.1, SEQ ID NO:748) or a fragment thereof. TNFR1 and TNFR2 ectodomains are described in US Patent Application Publication no. US 2007/ 0128177. In further embodiments, there are provided polypeptide binding domains specific for TNFα, wherein the binding domain comprises a sequence that is at least 80%, at least 85%, 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%, at least 99.5% , or at least 100% identical to an amino acid sequence of SEQ ID NO:748 or 749, wherein the polypeptide binding domain binds to TNFα and inhibits the activity thereof.

HGF Antagonists

[00104] As noted above, in certain embodiments the present disclosure provides polypeptides containing a binding region or domain that is a HGF antagonist (*i.e.*, can inhibit

HGF signaling). Exemplary HGF antagonists include binding domains specific for a HGF, such as an immunoglobulin variable binding domain or derivative thereof (*e.g.*, an antibody, Fab, scFv, or the like), or a c-Met ectodomain or sub-domain thereof (*e.g.*, a Sema domain, a PSI domain, or both domains of c-Met).

[00105] The tyrosine kinase receptor c-Met (also known as the hepatocyte growth factor receptor, HGFR, because hepatocyte growth factor (HGF) is one of its ligands) is active during the normal processes of embryogenesis and tissue repair. In both of these processes, cells dissociate from neighboring cells and enter the bloodstream. In the bloodstream, c-Met-induced protection from apoptosis and ability to grow in an anchorage-independent manner allow the cells to survive until they extravasate, proliferate and eventually differentiate. In tissue repair, c-Met is involved in the process of epithelial-mesenchymal transition when epithelial cells adjacent to the injury detach, change shape and migrate toward the injured area where they proliferate and reconstitute the epithelial layer.

[00106] However, when c-Met is constitutively activated, the cells expressing it become tumorigenic and metastatic. Constitutive c-Met activation has been demonstrated to occur by multiple mechanisms. The most common is over-expression of the receptor, which occurs as a result of *c-Met* gene amplification (*e.g.*, in colectoral tumors), enhanced *c-Met* transcription induced by other oncogenes, or hypoxia-activated transcription. Another mechanism includes *c-Met* gene structural alterations including point mutations (*e.g.*, in hereditary papillary renal carcinomas, childhood hepatocellular carcinomas, sporadic papillary renal carcinomas, gastric carcinomas and head and neck squamous-cell carcinomas) and chromosomal translocations. Yet another mechanism includes c-Met structural alterations such as abnormal posttranslational processing, lack of cleavage of the precursor protein, mutations that prevent receptor downregulation and truncation of the receptor (*e.g.*, in musculoskeletal tumors). Still another mechanism is HGF-dependent autocrine/paracrine activation. Paracrine activation can become pathological in the presence of abnormal HGF production by mesenchymal cells. Autocrine activation occurs when tumor cells aberrantly expression both c-Met and HGF (*e.g.*, in osteosarcomas, rhabdomyosarcomas, gliomas and carcinomas of the thyroid, breast and lung). Finally, constitutive c-Met activation can also be caused by transactivation by other membrane receptors (*e.g.*, RON, EGF-receptor family members, FAS and B plexins). *See* Corso *et al., TRENDS Mol. Med. 11*:284 (2005).

[00107] Anti-cancer strategies targeting the c-Met signaling pathway are also discussed in Corso *et al., supra*. These have included antagonism or neutralization of HGF, inhibition of c-Met kinase activity, prevention of c-Met dimerization, inhibition of c-Met

intracellular activities, and silencing of *c-Met* or *Hgf* expression. Michielli *et al., Cancer Cell, 6*: 61-73 (2004) describe a soluble c-Met receptor, termed "decoy Met," that interferes with both HGF binding to c-Met and c-Met homodimerization. Delivery of the decoy Met by a lentiviral vector in mice was reported to inhibit tumor cell proliferation and survival in human xenografts. Decoy Met was observed to impair tumor angiogenesis, suppress formation of spontaneous metastases, and synergize with radiotherapy in inducing tumor regression.

[00108] In some embodiments, binding domains of this disclosure comprise V_H and V_L domains specific for a HGF. In certain embodiments, the V_H and V_L domains are rodent (*e.g.*, mouse, rat), humanized, or human. Examples of binding domains containing such V_H and V_L domains specific for HGF include, but are not limited to, those disclosed in US Patent Application Publication no. US 2005/0118643. Binding domains of this disclosure may also, or alternatively, comprise a cMet ectodomain of SEQ ID NO:750, 751 or 752, or a fragment thereof. In further embodiments, there are provided polypeptide binding domains specific for HGF, wherein the binding domain comprises a sequence that is at least 80%, at least 85%, 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%, at least 99.5% , or at least 100% identical to an amino acid sequence of SEQ ID NO:750, 751 or 752, wherein the polypeptide binding domain binds to HGF and inhibits the activity thereof.

[00109] In some embodiments, binding domains of this disclosure are c-Met antagonist domains that comprise V_H and V_L domains as described herein. In certain embodiments, the V_H and V_L domains are human. Examples of binding domains containing such V_H and V_L domains are set forth in SEQ ID NOS:1132-1184 and 1079-1131, respectively. In further embodiments, there are provided c-Met antagonist domains of this disclosure that have a sequence that is 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%, at least 99.5% , or at least 100% identical to the amino acid sequence of one or more light chain variable regions (V_L) or to one or more heavy chain variable regions (V_H), or both, as set forth in SEQ ID NOS:1079-1131 and 1132-1184, respectively, wherein each CDR has at most up to three amino acid changes.

[00110] In further embodiments, c-Met antagonist domains of this disclosure comprise V_H and V_L domains as set forth in SEQ ID NOS:1132-1184 and 1079-1131, respectively, which are at least 80%, at least 81%, at least 82%, at least 83%, at least 84%, at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, 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 at least 99.5% identical to the amino acid sequence of such V_H domain, V_L domain, or both, wherein each CDR has no more than zero, one, two, or three mutations. For example, the amino acid sequence of a V_H domain, V_L domain, or both of this disclosure can be at least 80%, at least 81%, at least 82%, at least 83%, at least 84%, at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, 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 at least 99.5% identical to the amino acid sequence of V_H domain (SEQ ID NO:1174), V_L domain (SEQ ID NO:1121), or both, respectively, from exemplary binding domain TRU(H)-343.

[00111] A binding domain of this disclosure can comprise a single CDR from a variable region of an anti-HGF or anti-c-Met, or it can comprise multiple CDRs that can be the same or different. In certain embodiments, binding domains of this disclosure comprise V_H and V_L domains specific for an HGF or c-Met comprising framework regions and CDR1, CDR2 and CDR3 regions, wherein (a) the V_H domain comprises an amino acid sequence of a heavy chain CDR3 found in any one of SEQ ID NOS:1132-1184; or (b) the V_L domain comprises an amino acid sequence of a light chain CDR3 found in any one of SEQ ID NOS:1079-1131; or (c) the binding domain comprises a V_H amino acid sequence of (a) and a V_L amino acid sequence of (b); or the binding domain comprises a V_H amino acid sequence of (a) and a V_L amino acid sequence of (b) and wherein the V_H and V_L are found in the same reference sequence. In further embodiments, binding domains of this disclosure comprise V_H and V_L domains specific for an HGF or c-Met comprising framework regions and CDR1, CDR2 and CDR3 regions, wherein (a) the V_H domain comprises an amino acid sequence of a heavy chain CDR1, CDR2, and CDR3 found in any one of SEQ ID NOS:1132-1184; or (b) the V_L domain comprises an amino acid sequence of a light chain CDR1, CDR2, and CDR3 found in any one of SEQ ID NOS:1079-1131; or (c) the binding domain comprises a V_H amino acid sequence of (a) and a V_L amino acid sequence of (b); or the binding domain comprises a V_H amino acid sequence of (a) and a V_L amino acid sequence of (b), wherein the V_H and V_L amino acid sequences are from the same reference sequence.

[00112] In any of the embodiments described herein comprising specific CDRs, a binding domain can comprise (i) a V_H domain having an amino acid sequence that is at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to the amino acid sequence of a V_H domain found in any one of SEQ ID NOS:1132-1184; or (ii) a V_L domain having an amino acid sequence that is at least 80%, 85%, 90%, 91%, 92%, 93%,

94%, 95%, 96%, 97%, 98%, or 99% identical to the amino acid sequence of a V_L domain found in any one of SEQ ID NOS:1079-1131; or (iii) both a V_H domain of (i) and a V_L domain of (ii); or both a V_H domain of (i) and a V_L domain of (ii) wherein the V_H and V_L are from the same reference sequence. Exemplary light and heavy chain variable domain CDRs directed against c-Met are provided in SEQ ID NO:762-920 and 921-1078, respectively.

[00113] Amino acid sequences of c-Met antagonist light chain and heavy chain variable regions are provided in SEQ ID NO:1079-1131 and 1132-1184, respectively.

TWEAK Antagonists

[00114] In certain embodiments the present disclosure provides polypeptides containing a binding region or domain that is a TWEAK antagonist (*i.e.*, can inhibit TWEAKR signaling). Exemplary TWEAK antagonists include binding domains specific for a TWEAK, such as an immunoglobulin variable binding domain or derivative thereof (*e.g.*, an antibody, Fab, scFv, or the like), or a TWEAKR ectodomain or fragment thereof.

[00115] TWEAK is a cytokine that belongs to the tumor necrosis factor (TNF) ligand family and regulates multiple cellular responses including pro-inflammatory activity, angiogenesis and cell proliferation. TWEAK is a type II-transmembrane protein that is cleaved to generate a soluble cytokine with biological activity. The position of various domains within the TWEAK protein is shown, for example, in US Published Patent Application No. 2007/0280940. TWEAK has overlapping signaling functions with TNF, but displays a much wider tissue distribution. TWEAK can induce apoptosis via multiple pathways of cell death in a cell type-specific manner and has also been found to promote proliferation and migration of endothelial cells, and thus acts as a regulator of angiogenesis.

[00116] The cognate TWEAK receptor, TWEAKR or fibroblast growth factor-inducible 14 (Fn14), is a TNF receptor superfamily member expressed by non-lymphoid cell types (Wiley *et al.* (2001) Immunity 15:837). Expression of TWEAK and TWEAKR is relatively low in normal tissues but undergoes dramatic upregulation in settings of tissue injury and diseases. The TWEAK/R pathway facilitates acute tissue repair functions and thus functions physiologically after acute injury but functions pathologically in chronic inflammatory disease settings. In contrast to TNF, TWEAK plays no apparent role in development or homeostasis. A review of the TWEAK/R pathway is provided in Burkly *et al.* (2007) Cytokine 40:1. Persistently activated TWEAK promotes chronic inflammation, pathological hyperplasia and angiogenesis, and potentially impedes tissue repair by inhibiting differentiation of progenitor cells. TWEAK protein has been identified on the surface of

activated monocytes and T cells and on tumor cell lines, and intracellularly in resting and activated monocytes, dendritic cells and NK cells. TWEAK expression is significantly increased locally in target tissues in contexts of acute injury, inflammatory disease and cancer, all of which are associated with infiltration of inflammatory cells and/or activation of resident innate immune cell types. Circulating TWEAK levels have been shown to be significantly increased in patients with chronic inflammatory diseases such as multiple sclerosis and systemic lupus erythematosus.

[00117] TWEAK blocking monoclonal antibodies have been shown to be effective in a mouse collagen-induced arthritis (CIA) model (Kamata *et al*. (2006) J. Immunol. 177:6433; Perper *et al*. (2006) J. Immunol. 177:2610). The arthritogenic activities of TWEAK and TNF on human synoviocytes are often additive or synergistic and appear independent of one another, indicating that TWEAK and TNF may act in parallel in pathology of rheumatoid arthritis. It has been speculated that the heterogeneity of RA patients with respect to their clinical response to TNF inhibitors may reflect a pathological contribution by TWEAK.

[00118] US Patent No. 7,169,387 describes the preparation of a monoclonal antibody specific for TWEAK and its use to block aspects of the development of graft-versus-host disease (GVHD) using a mouse model of chronic GVHD. US Patent Application Publication No. 2007/0280940 describes TWEAKR decoy receptors and antibodies against TWEAKR and TWEAK and their use in the treatment of central nervous system diseases associated with cerebral edema and cell death.

[00119] In some embodiments, binding domains of this disclosure comprise V_H and V_L domains specific for a TWEAK. In certain embodiments, the V_H and V_L domains are rodent (*e.g.*, mouse, rat), humanized, or human. Examples of binding domains containing such V_H and V_L domains specific for TWEAK, include those disclosed, for example, in US Patent No. 7,169,387. Monoclonal antibodies that block TWEAK have been shown to be effective in a mouse collagen-induced arthritis (CIA) model (Kamata *et al*. (2006) J. Immunol. 177:6433; Perper *et al*. (2006) J. Immunol. 177:2610).

[00120] In certain embodiments, a TWEAK antagonist may be an extracellular domain ("ectodomain") of a TWEAKR (also known as FN14). As used herein, a TWEAKR ectodomain refers to an extracellular portion of TWEAKR, a soluble TWEAKR, or any combination thereof. In certain embodiments, a TWEAK antagonist comprises an amino-terminal portion of TWEAKR, such as the first 70 amino acids of TWEAKR as set forth in GenBank Accession No. NP_057723.1 (SEQ ID NO:761), or any fragment thereof that continues to function as a TWEAK antagonist. In other embodiments, a TWEAK antagonist

comprises amino acids 28-70 of SEQ ID NO:761 (*i.e.*, without the native leader sequence). In yet further embodiments, a TWEAK antagonist comprises a sequence that is at least 80%, at least 85%, 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%, at least 99.5% , or at least 100% identical to an amino acid sequence of SEQ ID NO:761, or amino acids 28-70 of SEQ ID NO:761, wherein the antagonist binds to TWEAK and inhibits the activity thereof.

[00121] The ability of binding proteins or fusion proteins described herein to reduce binding of TWEAK to TWEAKR may be determined using assays known to those of skill in the art including those described in US Patent Application Publication No. 2007/0280940.

IGF Antagonists

[00122] As noted above, in certain embodiments the present disclosure provides polypeptides containing a binding region or domain that is an IGF1 or IGF2 antagonist (*i.e.*, can inhibit IGF1 or IGF2 signaling). Exemplary IGF1 or IGF2 antagonists include binding domains specific for IGF1 or IGF2, such as an immunoglobulin variable binding domain or derivative thereof (*e.g.*, an antibody, Fab, scFv, or the like), or an IGF1R or IGFBP ectodomain or sub-domain thereof.

[00123] The insulin-like growth factors (IGFs), comprise a family of peptides that play important roles in mammalian growth and development. Insulin-like growth factor 1 (IGF1) is a secreted protein that has the following features: disulfide bonds (amino acids 54-96,66-109,95-100); D peptide domain (amino acids 111-118); carboxyl-terminal propeptide domain (E peptide) (amino acids 119-153); insulin chain A-like domain (amino acids 90-110); insulin chain B-like domain (amino acids 49-77); insulin connecting C peptide-like domain (amino acids 78-89); propeptide domain (amino acids 22-48); and signal sequence domain (amino acids 1-21).

[00124] IGF1 is synthesized in multiple tissues including liver, skeletal muscle, bone and cartilage. The changes in blood concentrations of IGF1 reflect changes in its synthesis and secretion from the liver, which accounts for 80% of the total serum IGF1 in experimental animals. The remainder of the IGF1 is synthesized in the periphery, usually by connective tissue cell types, such as stromal cells that are present in most tissues. IGF1 that is synthesized in the periphery can function to regulate cell growth by autocrine and paracrine mechanisms. Within these tissues, the newly synthesized and secreted IGF1 can bind to receptors that are present either on the connective tissue cells themselves and stimulate growth (autocrine), or it can bind to receptors on adjacent cell types (often epithelial cell

types) that do not actually synthesize IGF1 but are stimulated to grow by locally secreted IGF1 (paracrine) (Clemmons, 2007, Nat Rev Drug Discov. 6(10): 821-33). IGF1 synthesis is controlled by several factors, including the human pituitary growth hormone (GH, also known as somatotropin). IGF2 concentrations are high during fetal growth but are less GH-dependent in adult life compared with IGF1.

[00125] IGF1 enhances growth and/or survival of cells in a variety of tissues including musculoskeletal systems, liver, kidney, intestines, nervous system tissues, heart, and lung. IGF1 also has an important role in promoting cell growth and consequently IGF1 inhibition is being pursued as a potential adjunctive measure for treating atherosclerosis. Inhibiting IGF1 action has been proposed as a specific treatment either for potentiating the effects of other forms of anticancer therapies or for directly inhibiting tumor cell growth.

[00126] Like IGF1, IGF2 acts through IGF1R. IGF2 is an important autocrine growth factor in tumors due to its mitogenic and antiapoptotic functions (Kaneda et al., 2005, Cancer Res 65(24): 11236-11240). Increased expression of IGF2 is found frequently in a wide variety of malignancies, including colorectal, liver, esophageal and adrenocortical cancer, as well as sarcomas. Paracrine signaling by IGF2 also plays a role in tumors including breast cancers, as abundant expression of IGF2 is found in stromal fibroblasts surrounding malignant breast epithelial cells.

[00127] Insulin-like growth factor 1 receptor (IGF1R) is a tetramer of two alpha and two beta chains linked by disulfide bonds. Cleavage of a precursor generates the alpha and beta subunits. IGF1R is related to the protein kinase superfamily, the tyrosine protein kinase family, and the insulin receptor subfamily. It contains three fibronectin type-III domains, and one protein kinase domain (Lawrence et al., 2007, Current Opinion in Structural Biology 17: 699-705). The alpha chains contribute to the formation of the ligand-binding domain, while the beta chain carries a kinase domain. It is a single-pass type I membrane protein and is expressed in a variety of tissues.

[00128] The kinase domain has tyrosine-protein kinase activity, which is necessary for the activation of the IGF1- or IGF2-stimulated downstream signaling cascade. Auto-phosphorylation activates the kinase activity. IGF1R interacts with PIK3R1 and with the PTB/PID domains of IRS1 and SHC1 *in vitro* when autophosphorylated on tyrosine residues in the cytoplasmic domain of the beta subunit. IGF1R plays a critical role in transformation events. It is highly over-expressed in most malignant tissues where it functions as an anti-apoptotic agent by enhancing cell survival. Cells lacking this receptor cannot be transformed by most oncogenes, with the exception of v-Src.

[00129] The insulin-like growth factor-binding protein (IGFBP) family comprises six soluble proteins (IGFBP1–6) of approximately 250 residues that bind to IGFs with nanomolar affinities. Because of their sequence homology, IGFBPs are assumed to share a common overall fold and are expected to have closely related IGF-binding determinants. Each IGFBP can be divided into three distinct domains of approximately equal lengths: highly conserved cysteine-rich N and C domains and a central linker domain unique to each IGFBP species. Both the N and C domains participate in the binding to IGFs, although the specific roles of each of these domains in IGF binding have not been decisively determined. The C-terminal domain may be responsible for preferences of IGFBPs for one species of IGF over the other; the C-terminal domain is also involved in regulation of the IGF-binding affinity through interaction with extracellular matrix components and is most probably engaged in mediating IGF1-independent actions. The central linker domain is the least conserved region and has never been cited as part of the IGF-binding site for any IGFBP. This domain is the site of posttranslational modifications, specific proteolysis, and the acid-labile subunit and extracellular matrix associations known for IGFBPs. Proteolytic cleavage in this domain is believed to produce lower-affinity N- and C-terminal fragments that cannot compete with IGF receptors for IGFs, and, thus, the proteolysis is assumed to be the predominant mechanism for IGF release from IGFBPs. However, recent studies indicate that the resulting N- and C-terminal fragments still can inhibit IGF activity and have functional properties that differ from those of the intact proteins (Sitar et al. (2006) Proc. Natl. Acad. Sci. USA. 103(35):13028-33).

[00130] IGF-binding proteins are secreted proteins that prolong the half-life of the IGFs and have been shown to either inhibit or stimulate the growth promoting effects of the IGFs on cell culture. They alter the interaction of IGFs with their cell surface receptors and also promote cell migration. They bind equally well to IGF1 and IGF2. The C-terminal domains of all IGFBPs show sequence homology with thyroglobulin type-1 domains and share common elements of secondary structure: an α-helix and a 3- to 4-β-stranded β-sheet. The core of the molecule is connected by the consensus three disulfide pairings, has conserved Tyr/Phe amino acids and has the QC, CWCV motifs. These essential features are preserved in CBP1, CBP4, and CBP-6, the structures of C domains solved so far, although there are significant variations in detail. For example, CBP4 has helix α2, whereas the corresponding residues in CBP1 form a short beta-strand seen in other structures of the thyroglobulin type-1 domain superfamily. This particular region of CBPs has high sequence

diversity and is involved in the IGF complex formation and thus may perform the role of an affinity regulator.

[00131] Inhibition of IGF/IGF-receptor binding interferes with cell growth and represents a strategy for the development of IGFBPs and variants as natural IGF antagonists in many common diseases that arise from disregulation of the IGF system, including diabetes, atherosclerosis, and cancer.

[00132] In some embodiments, binding domains of this disclosure comprise V_H and V_L domains specific for IGF1 or IGF2. In certain embodiments, the V_H and V_L domains are rodent (*e.g.*, mouse, rat), humanized, or human. Binding domains of this disclosure may also, or alternatively, comprise an IGF1R ectodomain of Genbank Accession no. NP_000866.1 (SEQ ID NO:753) or a sub-domain thereof, or an IGFBP ectodomain of Genbank Accession no. NP_000587.1 (IGFBP1; SEQ ID NO:754), NP_000588.2 (IGFBP2; SEQ ID NO:755), NP_001013416.1 (IGFBP3 isoform a; SEQ ID NO:756), NP_000589.2 (IGFBP3 isoform b; SEQ ID NO:757), NP_001543.2 (IGFBP4; SEQ ID NO:758), NP_000590.1 (IGFBP5; SEQ ID NO:759) or NP_002169.1 (IGFBP6; SEQ ID NO:760) or a sub-domain thereof. In yet further embodiments, an IGF1 or IGF2 antagonist comprises a sequence that is at least 80%, at least 85%, 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%, at least 99.5% or at least 100% identical to an amino acid sequence of SEQ ID NO:754-760, wherein the antagonist inhibits the activity of at least one or IGF1 and IGF2.

Multi-Specific Fusion Proteins

[00133] The present disclosure provides multi-specific fusion proteins comprising a domain that is an antagonist of TGFβ ("TGFβ antagonist domain") and a domain that is an antagonist or agonist of a ligand other than a TGFβ ligand ("heterologous binding domain"), such as an IL6 antagonist, IL10 antagonist, GITR agonist, VEGF antagonist, TNF antagonist, HGF antagonist, TWEAK antagonist, or IGF antagonist. It is contemplated that the TGFβ antagonist domain may be at the amino-terminus and the heterologous binding domain at the carboxy-terminus of a fusion protein, or the heterologous binding domain may be at the amino-terminus and the TGFβ antagonist may be at the carboxy-terminus. As set forth herein, the binding domains of this disclosure may be fused to each end of an intervening domain (*e.g.*, an immunoglobulin constant region or sub-region thereof). Furthermore, the two or more binding domains may be each joined to an intervening domain via a linker known in the art or as described herein.

[00134] As used herein, an "intervening domain" refers to an amino acid sequence that simply functions as a scaffold for one or more binding domains so that the fusion protein will exist primarily (*e.g.*, 50% or more of a population of fusion proteins) or substantially (*e.g.*, 90% or more of a population of fusion proteins) as a single chain polypeptide in a composition. For example, certain intervening domains can have a structural function (*e.g.*, spacing, flexibility, rigidity) or biological function (*e.g.*, an increased half-life in plasma, such as in human blood). Exemplary intervening domains that can increase half-life of the fusion proteins of this disclosure in plasma include albumin, transferrin, a scaffold domain that binds a serum protein, or the like, or fragments thereof.

[00135] In certain preferred embodiments, the intervening domain contained in a multi-specific fusion protein of this disclosure is a "dimerization domain," which refers to an amino acid sequence that is capable of promoting the association of at least two single chain polypeptides or proteins via non-covalent or covalent interactions, such as by hydrogen bonding, electrostatic interactions, Van der Waal's forces, disulfide bonds, hydrophobic interactions, or the like, or any combination thereof. Exemplary dimerization domains include immunoglobulin heavy chain constant regions or sub-regions. It should be understood that a dimerization domain can promote the formation of dimers or higher order multimer complexes (such as trimers, tetramers, pentamers, hexamers, septamers, octamers, *etc*.).

[00136] A "constant sub-region" is a term defined herein to refer to a peptide, polypeptide, or protein sequence that corresponds to or is derived from part or all of one or more immunoglobulin constant region domains, but does not contain all constant region domains found in a source antibody. In preferred embodiments, the constant region domains of a fusion protein of this disclosure contains a CH2 domain and a CH3 domain of IgG, IgA, or IgD, more preferably IgG1 CH2 and CH3, and even more preferably human IgG1 CH2 and CH3. In some embodiments, the constant region domains of a fusion protein of this disclosure lack or have minimal effector functions of antibody-dependent cell-mediated cytotoxicity (ADCC), antibody-dependent cell-mediated phagocytosis (ADCP), and complement activation and complement-dependent cytotoxicity (CDC), while retaining the ability to bind some F_C receptors (such as F_CRn binding) and retaining a relatively long half life *in vivo*. In certain embodiments, a binding domain of this disclosure is fused to a human IgG1 constant region or sub-region, wherein the IgG1 constant region or sub-region has one or more of the following amino acids mutated: leucine at position 234 (L234), leucine at position 235 (L235), glycine at position 237 (G237), glutamate at position 318 (E318), lysine

at position 320 (K320), lysine at position 322 (K322), or any combination thereof (EU numbering).

[00137] Methods are known in the art for making mutations inside or outside an Fc domain that can alter Fc interactions with Fc receptors (CD16, CD32, CD64, CD89, FcεR1, FcRn) or with the complement component C1q (*see*, *e.g.*, US Patent No. 5,624,821; Presta (2002) Curr. Pharma. Biotechnol. 3:237). Particular embodiments of this disclosure include compositions comprising immunoglobulin or fusion proteins that have a constant region or sub-region from human IgG wherein binding to FcRn and protein A are preserved and wherein the Fc domain no longer interacts or minimally interacts with other Fc receptors or C1q. For example, a binding domain of this disclosure can be fused to a human IgG1 constant region or sub-region wherein the asparagine at position 297 (N297 under EU numbering) has been mutated to another amino acid to reduce or eliminate glycosylation at this site and, therefore, abrogate efficient Fc binding to FcγR and C1q. Another exemplary mutation is a P331S, which knocks out C1q binding but does not affect Fc binding.

[00138] In further embodiments, an immunoglobulin Fc region may have an altered glycosylation pattern relative to an immunoglobulin referent sequence. For example, any of a variety of genetic techniques may be employed to alter one or more particular amino acid residues that form a glycosylation site (*see* Co *et al*. (1993) Mol. Immunol. 30:1361; Jacquemon *et al*. (2006) J. Thromb. Haemost. 4:1047; Schuster *et al*. (2005) Cancer Res. 65:7934; Warnock *et al*. (2005) Biotechnol. Bioeng. 92:831). Alternatively, the host cells in which fusion proteins of this disclosure are produced may be engineered to produce an altered glycosylation pattern. One method known in the art, for example, provides altered glycosylation in the form of bisected, non-fucosylated variants that increase ADCC. The variants result from expression in a host cell containing an oligosaccharide-modifying enzyme. Alternatively, the Potelligent technology of BioWa/Kyowa Hakko is contemplated to reduce the fucose content of glycosylated molecules according to this disclosure. In one known method, a CHO host cell for recombinant immunoglobulin production is provided that modifies the glycosylation pattern of the immunoglobulin Fc region, through production of GDP-fucose.

[00139] Alternatively, chemical techniques are used to alter the glycosylation pattern of fusion proteins of this disclosure. For example, a variety of glycosidase and/or mannosidase inhibitors provide one or more of desired effects of increasing ADCC activity, increasing Fc receptor binding, and altering glycosylation pattern. In certain embodiment, cells expressing a multispecific fusion protein of the instant disclosure (containing a TGFβ

antagonist domain linked to a IL6, IL6R, IL6xR, IL10, VEGF, TNF, HGF, TWEAK, IGF antagonist or to a GITR agonist) are grown in a culture medium comprising a carbohydrate modifier at a concentration that increases the ADCC of immunoglycoprotein molecules produced by said host cell, wherein said carbohydrate modifier is at a concentration of less than 800 μM. In a preferred embodiment, the cells expressing these multispecific fusion proteins are grown in a culture medium comprising castanospermine or kifunensine, more preferably castanospermine at a concentration of 100-800 μM, such as 100 μM, 200 μM, 300 μM, 400 μM, 500 μM, 600 μM, 700 μM, or 800 μM. Methods for altering glycosylation with a carbohydrate modifier such as castanospermine are provided in US Patent Application Publication No. 2009/0041756 or PCT Publication No. WO 2008/052030.

[00140] In another embodiment, the immunoglobulin Fc region may have amino acid modifications that affect binding to effector cell Fc receptors. These modifications can be made using any technique known in the art, such as the approach disclosed in Presta *et al.* (2001) *Biochem. Soc. Trans. 30*:487. In another approach, the Xencor XmAb technology is available to engineer constant sub-regions corresponding to Fc domains to enhance cell killing effector function (*see* Lazar *et al.* (2006) *Proc. Nat'l. Acad. Sci. (USA) 103*:4005). Using this approach, for example, one can generate constant sub-regions with improved specificity and binding for FCγR, thereby enhancing cell killing effector function.

[00141] In still further embodiments, a constant region or sub-region can optionally increase plasma half-life or placental transfer in comparison to a corresponding fusion protein lacking such an intervening domain. In certain embodiments, the extended plasma half-life of a fusion protein of this disclosure is at least two, at least three, at least four, at least five, at least ten, at least 12, at least 18, at least 20, at least 24, at least 30, at least 36, at least 40, at least 48 hours, at least several days, at least a week, at least two weeks, at least several weeks, at least a month, at least two months, at least several months, or more in a human.

[00142] A constant sub-region may include part or all of any of the following domains: a C_{H2} domain, a C_{H3} domain (IgA, IgD, IgG, IgE, or IgM), and a C_{H4} domain (IgE or IgM). A constant sub-region as defined herein, therefore, can refer to a polypeptide that corresponds to a portion of an immunoglobulin constant region. The constant sub-region may comprise a C_{H2} domain and a C_{H3} domain derived from the same, or different, immunoglobulins, antibody isotypes, or allelic variants. In some embodiments, the C_{H3} domain is truncated and comprises a carboxy-terminal sequence listed in PCT Publication No. WO 2007/146968 as SEQ ID NO:366-371, which sequences are hereby incorporated by

reference. In certain embodiments, a constant sub-region of a polypeptide of this disclosure has a C_{H2} domain and C_{H3} domain, which may optionally have an amino-terminal linker, a carboxy-terminal linker, or a linker at both ends.

[00143] A "linker" is a peptide that joins or links other peptides or polypeptides, such as a linker of about 2 to about 150 amino acids. In fusion proteins of this disclosure, a linker can join an intervening domain (*e.g.*, an immunoglobulin-derived constant sub-region) to a binding domain or a linker can join two variable regions of a binding domain. For example, a linker can be an amino acid sequence obtained, derived, or designed from an antibody hinge region sequence, a sequence linking a binding domain to a receptor, or a sequence linking a binding domain to a cell surface transmembrane region or membrane anchor. In some embodiments, a linker can have at least one cysteine capable of participating in at least one disulfide bond under physiological conditions or other standard peptide conditions (*e.g.*, peptide purification conditions, conditions for peptide storage). In certain embodiments, a linker corresponding or similar to an immunoglobulin hinge peptide retains a cysteine that corresponds to the hinge cysteine disposed toward the amino-terminus of that hinge. In further embodiments, a linker is from an IgG1 or IgG2A hinge and has one cysteine or two cysteines corresponding to hinge cysteines. In certain embodiments, one or more disulfide bonds are formed as inter-chain disulfide bonds between intervening domains. In other embodiments, fusion proteins of this disclosure can have an intervening domain fused directly to a binding domain (*i.e.*, absent a linker or hinge). In some embodiments, the intervening domain is a dimerization domain.

[00144] The intervening or dimerization domain of multi-specific fusion proteins of this disclosure may be connected to one or more terminal binding domains by a peptide linker. In addition to providing a spacing function, a linker can provide flexibility or rigidity suitable for properly orienting the one or more binding domains of a fusion protein, both within the fusion protein and between or among the fusion proteins and their target(s). Further, a linker can support expression of a full-length fusion protein and stability of the purified protein both in vitro and in vivo following administration to a subject in need thereof, such as a human, and is preferably non-immunogenic or poorly immunogenic in those same subjects. In certain embodiments, a linker of an intervening or a dimerization domain of multi-specific fusion proteins of this disclosure may comprise part or all of a human immunoglobulin hinge.

[00145] Additionally, a binding domain may comprise a V_H and a V_L domain, and these variable region domains may be combined by a linker. Exemplary variable region

binding domain linkers include those belonging to the (Gly_nSer) family, such as $(Gly_3Ser)_n(Gly_4Ser)_1$, $(Gly_3Ser)_1(Gly_4Ser)_n$, $(Gly_3Ser)_n(Gly_4Ser)_n$, or $(Gly_4Ser)_n$, wherein n is an integer of 1 to 5 (*see, e.g.*, Linkers 22, 29, 46, 89, 90, and 116 corresponding to SEQ ID NOS:518, 525, 542, 585, 586 and 603, respectively). In preferred embodiments, these (Gly_4Ser)-based linkers are used to link variable domains and are not used to link a binding domain (*e.g.*, scFv) to an intervening domain (*e.g.*, an IgG CH2CH3).

[00146] Exemplary linkers that can be used join an intervening domain (*e.g.*, an immunoglobulin-derived constant sub-region) to a binding domain or to join two variable regions of a binding domain are provided in SEQ ID NO:497-604 and 1223-1228.

[00147] Linkers contemplated in this disclosure include, for example, peptides derived from any inter-domain region of an immunoglobulin superfamily member (*e.g.*, an antibody hinge region) or a stalk region of C-type lectins, a family of type II membrane proteins. These linkers range in length from about two to about 150 amino acids, or about two to about 40 amino acids, or about eight to about 20 amino acids, preferably about ten to about 60 amino acids, more preferably about 10 to about 30 amino acids, and most preferably about 15 to about 25 amino acids. For example, Linker 1 (SEQ ID NO:497) is two amino acids in length and Linker 116 (SEQ ID NO:603) is 36 amino acids in length.

[00148] Beyond general length considerations, a linker suitable for use in the fusion proteins of this disclosure includes an antibody hinge region selected from an IgG hinge, IgA hinge, IgD hinge, IgE hinge, or variants thereof. In certain embodiments, a linker may be an antibody hinge region (upper and core region) selected from human IgG1, human IgG2, human IgG3, human IgG4, or fragments or variants thereof. As used herein, a linker that is an "immunoglobulin hinge region" refers to the amino acids found between the carboxyl end of CH1 and the amino terminal end of CH2 (for IgG, IgA, and IgD) or the amino terminal end of CH3 (for IgE and IgM). A “wild type immunoglobulin hinge region,” as used herein, refers to a naturally occurring amino acid sequence interposed between and connecting the CH1 and CH2 regions (for IgG, IgA, and IgD) or interposed between and connecting the CH2 and CH3 regions (for IgE and IgM) found in the heavy chain of an antibody. In preferred embodiments, the wild type immunoglobulin hinge region sequences are human.

[00149] According to crystallographic studies, an IgG hinge domain can be functionally and structurally subdivided into three regions: the upper hinge region, the core or middle hinge region, and the lower hinge region (Shin *et al.* (1992) *Immunological Reviews* 130:87). Exemplary upper hinge regions include EPKSCDKTHT (SEQ ID NO:1240) as found in IgG1, ERKCCVE (SEQ ID NO:1241) as found in IgG2, ELKTPLGDTT HT (SEQ

ID NO:1242) or EPKSCDTPPP (SEQ ID NO:1243) as found in IgG3, and ESKYGPP (SEQ ID NO:1244) as found in IgG4. Exemplary middle hinge regions include CPPCP (SEQ ID NO:1245) as found in IgG1 and IgG2, CPRCP (SEQ ID NO:1246) as found in IgG3, and CPSCP (SEQ ID NO:1247) as found in IgG4. While IgG1, IgG2, and IgG4 antibodies each appear to have a single upper and middle hinge, IgG3 has four in tandem – one of ELKTPLGDTT HTCPRCP (SEQ ID NO:1248) and three of EPKSCDTPPP CPRCP (SEQ ID NO:1249).

[00150] IgA and IgD antibodies appear to lack an IgG-like core region, and IgD appears to have two upper hinge regions in tandem (*see* SEQ ID NOS:1250 and 1251). Exemplary wild type upper hinge regions found in IgA1 and IgA2 antibodies are set forth in SEQ ID NOS:1252 and 1253.

[00151] IgE and IgM antibodies, in contrast, instead of a typical hinge region have a CH2 region with hinge-like properties. Exemplary wild-type CH2 upper hinge-like sequences of IgE and IgM are set forth in SEQ ID NO:1254 (VCSRDFTPPT VKILQSSSDG GGHFPPTIQL LCLVSGYTPG TINITWLEDG QVMDVDLSTA STTQEGELAS TQSELTLSQK HWLSDRTYTC QVTYQGHTFE DSTKKCA) and SEQ ID NO:1255 (VIAELPPKVS VFVPPRDGFF GNPRKSKLIC QATGFSPRQI QVSWLREGKQ VGSGVTTDQV QAEAKESGPT TYKVTSTLTI KESDWLGQSM FTCRVDHRGL TFQQNASSMC VP), respectively.

[00152] An "altered wild type immunoglobulin hinge region" or "altered immunoglobulin hinge region" refers to (a) a wild type immunoglobulin hinge region with up to 30% amino acid changes (*e.g.*, up to 25%, 20%, 15%, 10%, or 5% amino acid substitutions or deletions), (b) a portion of a wild type immunoglobulin hinge region that is at least 10 amino acids (*e.g.*, at least 12, 13, 14 or 15 amino acids) in length with up to 30% amino acid changes (*e.g.*, up to 25%, 20%, 15%, 10%, or 5% amino acid substitutions or deletions), or (c) a portion of a wild type immunoglobulin hinge region that comprises the core hinge region (which portion may be 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, or 15, or at least 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, or 15 amino acids in length). In certain embodiments, one or more cysteine residues in a wild type immunoglobulin hinge region may be substituted by one or more other amino acid residues (*e.g.*, one or more serine residues). An altered immunoglobulin hinge region may alternatively or additionally have a proline residue of a wild type immunoglobulin hinge region substituted by another amino acid residue (*e.g.*, a serine residue).

[00153] Alternative hinge and linker sequences that can be used as connecting regions may be crafted from portions of cell surface receptors that connect IgV-like or IgC-like domains. Regions between IgV-like domains where the cell surface receptor contains multiple IgV-like domains in tandem and between IgC-like domains where the cell surface receptor contains multiple tandem IgC-like regions could also be used as connecting regions or linker peptides. In certain embodiments, hinge and linker sequences are from five to 60 amino acids long, and may be primarily flexible, but may also provide more rigid characteristics, and may contain primarily an α-helical structure with minimal β-sheet structure. Preferably, sequences are stable in plasma and serum and are resistant to proteolytic cleavage. In some embodiments, sequences may contain a naturally occurring or added motif such as CPPC that confers the capacity to form a disulfide bond or multiple disulfide bonds to stabilize the C-terminus of the molecule. In other embodiments, sequences may contain one or more glycosylation sites. Examples of hinge and linker sequences include interdomain regions between the IgV-like and IgC-like or between the IgC-like or IgV-like domains of CD2, CD4, CD22, CD33, CD48, CD58, CD66, CD80, CD86, CD96, CD150, CD166, and CD244. Alternative hinges may also be crafted from disulfide-containing regions of Type II receptors from non-immunoglobulin superfamily members such as CD69, CD72, and CD161.

[00154] In some embodiments, a hinge linker has a single cysteine residue for formation of an interchain disulfide bond. In other embodiments, a linker has two cysteine residues for formation of interchain disulfide bonds. In further embodiments, a hinge linker is derived from an immunoglobulin interdomain region (*e.g.*, an antibody hinge region comprising an upper and core sequence of, for example, an IgG1 hinge) or a Type II C-type lectin stalk region (derived from a Type II membrane protein; *see, e.g.*, exemplary lectin stalk region sequences set forth in of PCT Application Publication No. WO 2007/146968, such as SEQ ID NOS:111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 287, 289, 297, 305, 307, 309-311, 313-331, 346, 373-377, 380, or 381 from that publication), which sequences are herein incorporated by reference.

[00155] In one aspect, exemplary multi-specific fusion proteins containing a TGFβ antagonist as described herein will also contain at least one additional binding region or domain that is specific for a target other than TGFβ, such as an IL6, IL10, VEGF, TNF,

HGF, TWEAK, IGF antagonist or a GITR agonist. For example, a multi-specific fusion protein of this disclosure has a TGFβ antagonist domain linked to an IL6, IL10, VEGF, TNF, HGF, TWEAK, IGF antagonist or a GITR agonist domain by an intervening domain (such as a human IgG1 CH2CH3 Fc region). In certain embodiments, a multi-specific fusion protein comprises a first and second binding domain, a first and second linker, and an intervening domain, wherein one end of the intervening domain is fused via the first linker to a first binding domain that is a TGFβ antagonist (*e.g.*, a TGFβR2 ectodomain, an anti-TGFβR2 ectodomain, an anti-TGFβ) and at the other end is fused via the second linker to a different binding domain that is an IL6, IL10, VEGF, TNF, HGF, TWEAK, IGF antagonist or a GITR agonist.

[00156] In certain embodiments, the first linker and second linker of a multi-specific fusion protein of this disclosure are each independently selected from, for example, SEQ ID NO:497-604 and 1223-1228. For example, the first or second linker can be Linker 102 (SEQ ID NO:589), 47 (SEQ ID NO:543), 80 (SEQ ID NO:576), or any combination thereof. In further examples, one linker is Linker 102 (SEQ ID NO:589) and the other linker is Linker 47 (SEQ ID NO:543), or one linker is Linker 102 (SEQ ID NO:589) and the other linker is Linker 80 (SEQ ID NO:576). In further examples, binding domains of this disclosure that comprise V_H and V_L domains, such as those specific for IL6, IL6R, IL6xR, IL10, VEGF, TNF, HGF, TWEAK, IGF, GITR, TGFβR2 ectodomain, or TGFβ, can have a further (third) linker between the V_H and V_L domains, such as Linker 46 (SEQ ID NO:542). In any of these embodiments, the linkers may be flanked by one to five additional junction amino acids, which may simply be a result of creating such a recombinant molecule (*e.g.*, use of a particular restriction enzyme site to join nucleic acid molecules may result in the insertion of one to several amino acids), or for purposes of this disclosure may be considered a part of any particular linker core sequence.

[00157] In further embodiments, the intervening domain of a multi-specific fusion protein of this disclosure is comprised of an immunoglobulin constant region or sub-region (preferably CH2CH3 of IgG, IgA, or IgD; or CH3CH4 of IgE or IgM), wherein the intervening domain is disposed between a TGFβ antagonist domain and an IL6, IL10, VEGF, TNF, HGF, TWEAK, IGF antagonist binding domain or a GITR agonist binding domain. In certain embodiments, the intervening domain of a multi-specific fusion protein of this disclosure has a TGFβ antagonist at the amino-terminus and a binding domain specific for an IL6, IL6xR, IL10, VEGF, TNF, HGF, TWEAK, IGF, or GITR at the carboxy-terminus. In other embodiments, the intervening domain of a multi-specific fusion protein of this

disclosure has a binding domain specific for an IL6, IL10, VEGF, TNF, HGF, TWEAK, IGF antagonist binding domain or a GITR agonist binding domain at the amino-terminus and a TGFβ antagonist at the carboxy-terminus. In further embodiments, the immunoglobulin constant region sub-region includes CH2 and CH3 domains of immunoglobulin G1 (IgG1). In related embodiments, the IgG1 CH2 and CH3 domains have one or more of the following amino acids mutated (*i.e.*, have a different amino acid at that position): leucine at position 234 (L234), leucine at position 235 (L235), glycine at position 237 (G237), glutamate at position 318 (E318), lysine at position 320 (K320), lysine at position 322 (K322), or any combination thereof (EU numbering). For example, any one of these amino acids can be changed to alanine. In a further embodiment, according to Kabat numbering, the CH2 domain has each of L234, L235, G237, E318, K320 and K322 mutated to an alanine (*i.e.*, L234A, L235A, G237A, E318A, K320A and K322A, respectively).

[00158] In some embodiments, a multi-specific fusion protein of this disclosure has a TGFβ antagonist that comprises a TGFβR2 ectodomain or a sub-domain of a TGFβR2 ectodomain, or any combination thereof. For example, a TGFβ antagonist can comprise amino acids 73-176 as set forth in GenBank Accession No. NP_001020018.1, amino acids 48-151 as set forth in GenBank Accession No. NP_003233.4, or any combination thereof. In further embodiments, the TGFβ antagonist comprises an amino acid sequence as set forth in SEQ ID NO:743 or 744.

[00159] In further embodiments, a multi-specific fusion protein of this disclosure having a TGFβ antagonist of this disclosure also has an IL6 antagonist binding domain that binds with higher affinity to IL6xR than to either IL6 or IL6Rα alone and competes with sIL6xR complex binding to mgp130 or enhances sgp103 binding to sIL6xR complex. In certain embodiments, a binding domain specific for an IL6xR comprises (i) a V_H domain having an amino acid sequence that is at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identical to the amino acid sequence of a V_H domain found in any one of SEQ ID NOS:435-496; or (ii) a V_L domain having an amino acid sequence that is at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identical to the amino acid sequence of a V_L domain found in any one of SEQ ID NOS:373-434; or (iii) both a V_H domain of (i) and a V_L domain of (ii); or both a V_H domain of (i) and a V_L domain of (ii) wherein the V_H and V_L are from the same reference sequence. In one embodiment, such V_H and V_L domains can form exemplary binding domain TRU6-1019 (*see* SEQ ID NOS:453 and 391, respectively).

[00160] In still further embodiments, an IL6 antagonist binding domain, which binds to the IL6xR with a higher affinity than IL6 or IL6Rα or either IL6 or IL6Rα alone, and competes with gp130 for binding to the sIL6xR complex or enhances sgp130 binding to sIL6xR complex, comprises V_H and V_L domains comprising framework regions and CDR1, CDR2 and CDR3 regions, wherein (a) the V_H domain comprises the amino acid sequence of a heavy chain CDR1, CDR2, and CDR3 found in any one of SEQ ID NOS:435-496; or (b) the V_L domain comprises the amino acid sequence of a light chain CDR1, CDR2, and CDR3 found in any one of SEQ ID NOS:373-434; or (c) the binding domain comprises a V_H amino acid sequence of (a) and a V_L amino acid sequence of (b); or the binding domain comprises a V_H amino acid sequence of (a) and a V_L amino acid sequence of (b), wherein the V_H and V_L amino acid sequences are from the same reference sequence. The V_L and V_H domains of these multi-specific fusion proteins may be arranged in either orientation and may be separated by up to about a 5-30 amino acid linker as disclosed herein. In certain embodiments, a linker joining the V_H and V_L domains comprises an amino acid sequence of Linker 47 (SEQ ID NO:543) or Linker 80 (SEQ ID NO:576). In certain embodiments, a multi-specific fusion protein comprising the IL6 antagonist binding domain measurably inhibits IL6 cis- and trans-signaling, preferably trans-signaling and, optionally, does not inhibit signaling of gp130 family cytokines other than IL6.

[00161] Exemplary structures of such multi-specific fusion proteins, referred to herein as Xceptor molecules, include N-BD-X-ED-C, N-ED-X-BD-C, N-ED1-X-ED2-C, wherein BD is an immunoglobulin-like or immunoglobulin variable region binding domain, X is an intervening domain, and ED is a receptor ectodomain, or the like. In some constructs, X can comprise an immunoglobulin constant region or sub-region disposed between the first and second binding domains. In some embodiments, a multi-specific fusion protein of this disclosure has an intervening domain (X) comprising, from amino-terminus to carboxy-terminus, a structure as follows: -L1-X-L2-, wherein L1 and L2 are each independently a linker comprising from two to about 150 amino acids; and X is an immunoglobulin constant region or sub-region. In further embodiments, the multi-specific fusion protein will have an intervening domain that is albumin, transferrin, or another serum protein binding protein, wherein the fusion protein remains primarily or substantially as a single chain polypeptide in a composition. In still further embodiments, a multi-specific fusion protein of this disclosure has the following structure: N-BD1-X-L2-BD2-C, wherein N and C represent the amino-terminus and carboxy-terminus, respectively; BD1 is a TGFβ antagonist that is at least about

90% identical to an ectodomain of TGFβR2; -X- is -L1-CH2CH3-, wherein L1 is the first IgG1 hinge, optionally mutated by substituting the first cysteine and wherein -CH2CH3- is the CH2CH3 region of an IgG1 Fc domain, optionally mutated to eliminate FcγRI-III interaction while retaining FcRn interaction; L2 is a linker selected from SEQ ID NO:497-604 and 1223-1228; and BD2 is a binding domain specific for an IL6 or IL6/IL6R complex.

[00162] In particular embodiments, a multi-specific Xceptor fusion protein has (a) a TGFβ antagonist comprising an amino acid sequence at least 80% to 100% identical to a sequence as set forth in SEQ ID NO:743 or 744 and (b) an IL6 antagonist comprising a heavy chain variable region with CDRl, CD2, and CDR3 amino acid sequences at least 80% to 100% identical to sequences set forth in SEQ ID NOS:435-496, respectively, and a light chain variable region with CDRl, CDR2, and CDR3 amino acid sequences at least 80% to 100% identical to sequences set forth in SEQ ID NOS:373-434, respectively, wherein, from amino-terminus to carboxy-terminus or from carboxy-terminus to amino-terminus, (i) a TGFβ antagonist of (a) or an IL6 antagonist of (b) is fused to a first linker, (ii) the first linker is fused to an immunoglobulin heavy chain constant region of CH2 and CH3 comprising amino acids 276 to 489 of SEQ ID NO:625, (iii) the CH2CH3 constant region polypeptide is fused to a second linker, and (iv) the second linker is fused to a TGFβ antagonist of (a) or an IL6 antagonist of (b). In certain embodiments, the first linker is Linker 47 (SEQ ID NO:543) or Linker 80 (SEQ ID NO:576), the second linker is Linker 102 (SEQ ID NO:589), and a further (third) linker between the IL6 antagonist V_H and V_L domains is Linker 46 (SEQ ID NO:542).

[00163] In other embodiments, a multi-specific Xceptor fusion protein has (a) a TGFβ antagonist comprising an amino acid sequence at least 80% to 100% identical to a sequence as set forth in SEQ ID NO:743 or 744 and (b) an IL10 antagonist comprising an amino acid sequence at least 80% to 100% identical to an amino acid sequence of SEQ ID NO:745 or to amino acids 22-401 of SEQ ID NO:745, wherein, from amino-terminus to carboxy-terminus or from carboxy-terminus to amino-terminus, (i) a TGFβ antagonist of (a) or an IL10 antagonist of (b) is fused to a first linker, (ii) the first linker is fused to an immunoglobulin heavy chain constant region of CH2 and CH3, (iii) the CH2CH3 constant region polypeptide is fused to a second linker, and (iv) the second linker is fused to a TGFβ antagonist of (a) or an IL10 antagonist of (b). In certain embodiments, the first linker is Linker 47 (SEQ ID NO:543) or Linker 80 (SEQ ID NO:576), and the second linker is Linker 102 (SEQ ID NO:589).

[00164] In further embodiments, a multi-specific Xceptor fusion protein has (a) a TGFβ antagonist comprising an amino acid sequence at least 80% to 100% identical to a sequence as set forth in SEQ ID NO:743 or 744 and (b) a VEGF antagonist comprising an amino acid sequence at least 80% to 100% identical to an amino acid sequence of SEQ ID NO:747, wherein, from amino-terminus to carboxy-terminus or from carboxy-terminus to amino-terminus, (i) a TGFβ antagonist of (a) or a VEGF antagonist of (b) is fused to a first linker, (ii) the first linker is fused to an immunoglobulin heavy chain constant region of CH2 and CH3, (iii) the CH2CH3 constant region polypeptide is fused to a second linker, and (iv) the second linker is fused to a TGFβ antagonist of (a) or a VEGF antagonist of (b). In certain embodiments, the first linker is Linker 47 (SEQ ID NO:543) or Linker 80 (SEQ ID NO:576) and the second linker is Linker 102 (SEQ ID NO:589.

[00165] In further embodiments, a multi-specific Xceptor fusion protein has (a) a TGFβ antagonist comprising an amino acid sequence at least 80% to 100% identical to a sequence as set forth in SEQ ID NO:743 or 744 and (b) a TNFα antagonist comprising an amino acid sequence at least 80% to 100% identical to an amino acid sequence of SEQ ID NO:748 or 749, wherein, from amino-terminus to carboxy-terminus or from carboxy-terminus to amino-terminus, (i) a TGFβ antagonist of (a) or a TNFα antagonist of (b) is fused to a first linker, (ii) the first linker is fused to an immunoglobulin heavy chain constant region of CH2 and CH3, (iii) the CH2CH3 constant region polypeptide is fused to a second linker, and (iv) the second linker is fused to a TGFβ antagonist of (a) or a TNFα antagonist of (b). In certain embodiments, the first linker is Linker 47 (SEQ ID NO:543) or Linker 80 (SEQ ID NO:576), and the second linker is Linker 102 (SEQ ID NO:589). In specific embodiments, the multi-specific Xceptor fusion protein has an amino acid sequence of SEQ ID NO:1236.

[00166] In further embodiments, a multi-specific Xceptor fusion protein has (a) a TGFβ antagonist comprising an amino acid sequence at least 80% to 100% identical to a sequence as set forth in SEQ ID NO:743 or 744 and (b) a HGF antagonist comprising a heavy chain variable region with CDRl, CD2, and CDR3 amino acid sequences at least 80% to 100% identical to sequences set forth in SEQ ID NOS:921-1078, respectively, and a light chain variable region with CDRl, CDR2, and CDR3 amino acid sequences at least 80% to 100% identical to sequences set forth in SEQ ID NOS:762-920, respectively, wherein, from amino-terminus to carboxy-terminus or from carboxy-terminus to amino-terminus, (i) a TGFβ antagonist of (a) or a HGF antagonist of (b) is fused to a first linker, (ii) the first linker is fused to an immunoglobulin heavy chain constant region of CH2 and CH3, (iii) the

CH2CH3 constant region polypeptide is fused to a second linker, and (iv) the second linker is fused to a TGFβ antagonist of (a) or a HGF antagonist of (b). In certain embodiments, the first linker is Linker 47 (SEQ ID NO:543) or Linker 80 (SEQ ID NO:576), the second linker is Linker 102 (SEQ ID NO:589), and a further (third) linker between the HGF antagonist V_H and V_L domains is Linker 46 (SEQ ID NO:542).

[00167] In yet other embodiments, a multi-specific Xceptor fusion protein has (a) a TGFβ antagonist comprising an amino acid sequence at least 80% to 100% identical to a sequence as set forth in SEQ ID NO:743 or 744 and (b) a TWEAK antagonist comprising an amino acid sequence at least 80% to 100% identical to an amino acid sequence of SEQ ID NO:761, wherein, from amino-terminus to carboxy-terminus or from carboxy-terminus to amino-terminus, (i) a TGFβ antagonist of (a) or a TWEAK antagonist of (b) is fused to a first linker, (ii) the first linker is fused to an immunoglobulin heavy chain constant region of CH2 and CH3, (iii) the CH2CH3 constant region polypeptide is fused to a second linker, and (iv) the second linker is fused to a TGFβ antagonist of (a) or a TWEAK antagonist of (b). In certain embodiments, the first linker is Linker 47 (SEQ ID NO:543) or Linker 80 (SEQ ID NO:576), and the second linker is Linker 102 (SEQ ID NO:589). In specific embodiments, the multi-specific Xceptor fusion protein has an amino acid sequence of SEQ ID NO:1237.

[00168] In yet other embodiments, a multi-specific Xceptor fusion protein has (a) a TGFβ antagonist comprising an amino acid sequence at least 80% to 100% identical to a sequence as set forth in SEQ ID NO:743 or 744 and (b) an IGF antagonist comprising an amino acid sequence at least 80% to 100% identical to an amino acid sequence of SEQ ID NO:754-760, wherein, from amino-terminus to carboxy-terminus or from carboxy-terminus to amino-terminus, (i) a TGFβ antagonist of (a) or an IGF antagonist of (b) is fused to a first linker, (ii) the first linker is fused to an immunoglobulin heavy chain constant region of CH2 and CH3, (iii) the CH2CH3 constant region polypeptide is fused to a second linker, and (iv) the second linker is fused to a TGFβ antagonist of (a) or an IGF antagonist of (b). In certain embodiments, the first linker is Linker 47 (SEQ ID NO:543) or Linker 80 (SEQ ID NO:576), and the second linker is Linker 102 (SEQ ID NO:589).

[00169] In other embodiments, a multi-specific Xceptor fusion protein has (a) a TGFβ antagonist comprising an amino acid sequence at least 80% to 100% identical to a sequence as set forth in SEQ ID NO:743 or 744 and (b) a GITR agonist comprising an amino acid sequence at least 80% to 100% identical to amino acids 74-181 of SEQ ID NO:746, wherein, from amino-terminus to carboxy-terminus or from carboxy-terminus to amino-

terminus, (i) a TGFβ antagonist of (a) or a GITR agonist of (b) is fused to a first linker, (ii) the first linker is fused to an immunoglobulin heavy chain constant region of CH2 and CH3, (iii) the CH2CH3 constant region polypeptide is fused to a second linker, and (iv) the second linker is fused to a TGFβ antagonist of (a) or a GITR agonist of (b). In certain embodiments, the first linker is Linker 47 (SEQ ID NO:543) or Linker 80 (SEQ ID NO:576), and the second linker is Linker 102 (SEQ ID NO:589).

Making Multi-Specific Fusion Proteins

[00170] To efficiently produce any of the binding domain polypeptides or fusion proteins described herein, a leader peptide is used to facilitate secretion of expressed polypeptides and fusion proteins. Using any of the conventional leader peptides (signal sequences) is expected to direct nascently expressed polypeptides or fusion proteins into a secretory pathway and to result in cleavage of the leader peptide from the mature polypeptide or fusion protein at or near the junction between the leader peptide and the polypeptide or fusion protein. A particular leader peptide will be chosen based on considerations known in the art, such as using sequences encoded by polynucleotides that allow the easy inclusion of restriction endonuclease cleavage sites at the beginning or end of the coding sequence for the leader peptide to facilitate molecular engineering, provided that such introduced sequences specify amino acids that either do not interfere unacceptably with any desired processing of the leader peptide from the nascently expressed protein or do not interfere unacceptably with any desired function of a polypeptide or fusion protein molecule if the leader peptide is not cleaved during maturation of the polypeptides or fusion proteins. Exemplary leader peptides of this disclosure include natural leader sequences (*i.e.*, those expressed with the native protein) or use of heterologous leader sequences, such as H_3N-MDFQVQIFSFLLISASVIMSRG$(X)_n$-CO_2H, wherein X is any amino acid and n is zero to three (SEQ ID NO:1185) or H_3N-MEAPAQLLFLLLLWLPDTTG-CO_2H (SEQ ID NO:1186).

[00171] As noted herein, variants and derivatives of binding domains, such as ectodomains, light and heavy variable regions, and CDRs described herein, are contemplated. In one example, insertion variants are provided wherein one or more amino acid residues supplement a specific binding agent amino acid sequence. Insertions may be located at either or both termini of the protein, or may be positioned within internal regions of the specific binding agent amino acid sequence. Variant products of this disclosure also include mature specific binding agent products, *i.e.*, specific binding agent products wherein a leader or

signal sequence is removed, and the resulting protein having additional amino terminal residues. The additional amino terminal residues may be derived from another protein, or may include one or more residues that are not identifiable as being derived from a specific protein. Polypeptides with an additional methionine residue at position -1 are contemplated, as are polypeptides of this disclosure with additional methionine and lysine residues at positions -2 and -1. Variants having additional Met, Met-Lys, or Lys residues (or one or more basic residues in general) are particularly useful for enhanced recombinant protein production in bacterial host cells.

[00172] As used herein, "amino acids" refer to a natural (those occurring in nature) amino acid, a substituted natural amino acid, a non-natural amino acid, a substituted non-natural amino acid, or any combination thereof. The designations for natural amino acids are herein set forth as either the standard one- or three-letter code. Natural polar amino acids include asparagine (Asp or N) and glutamine (Gln or Q); as well as basic amino acids such as arginine (Arg or R), lysine (Lys or K), histidine (His or H), and derivatives thereof; and acidic amino acids such as aspartic acid (Asp or D) and glutamic acid (Glu or E), and derivatives thereof. Natural hydrophobic amino acids include tryptophan (Trp or W), phenylalanine (Phe or F), isoleucine (Ile or I), leucine (Leu or L), methionine (Met or M), valine (Val or V), and derivatives thereof; as well as other non-polar amino acids such as glycine (GIy or G), alanine (Ala or A), proline (Pro or P), and derivatives thereof. Natural amino acids of intermediate polarity include serine (Ser or S), threonine (Thr or T), tyrosine (Tyr or Y), cysteine (Cys or C), and derivatives thereof. Unless specified otherwise, any amino acid described herein may be in either the D- or L-configuration.

[00173] Substitution variants include those fusion proteins wherein one or more amino acid residues in an amino acid sequence are removed and replaced with alternative residues. In some embodiments, the substitutions are conservative in nature; however, this disclosure embraces substitutions that are also non-conservative. Amino acids can be classified according to physical properties and contribution to secondary and tertiary protein structure. A conservative substitution is recognized in the art as a substitution of one amino acid for another amino acid that has similar properties. Exemplary conservative substitutions are set out in Table 1 (*see* WO 97/09433, page 10, published March 13, 1997), immediately below.

Table 1. Conservative Substitutions I

Side Chain	Characteristic	Amino Acid
Aliphatic	Non-polar	G, A, P, I, L, V
	Polar – uncharged	S, T, M, N, Q
	Polar – charged	D, E, K, R
Aromatic		H, F, W, Y
Other		N, Q, D, E

[00174] Alternatively, conservative amino acids can be grouped as described in Lehninger (Biochemistry, Second Edition; Worth Publishers, Inc. NY:NY (1975), pp.71-77) as set out in Table 2, immediately below.

Table 2. Conservative Substitutions II

Side Chain	Characteristic	Amino Acid
Non-polar (hydrophobic)	Aliphatic:	A, L, I, V, P
	Aromatic	F, W
	Sulfur-containing	M
	Borderline	G
Uncharged-polar	Hydroxyl	S, T, Y
	Amides	N, Q
	Sulfhydryl	C
	Borderline	G
Positively Charged (Basic)		K, R, H
Negatively Charged (Acidic)		D, E

[00175] Variants or derivatives can also have additional amino acid residues which arise from use of specific expression systems. For example, use of commercially available vectors that express a desired polypeptide as part of a glutathione-S-transferase (GST) fusion product provides the desired polypeptide having an additional glycine residue at position -1 after cleavage of the GST component from the desired polypeptide. Variants which result from expression in other vector systems are also contemplated, including those wherein histidine tags are incorporated into the amino acid sequence, generally at the carboxy and/or amino terminus of the sequence.

[00176] Deletion variants are also contemplated wherein one or more amino acid residues in a binding domain of this disclosure are removed. Deletions can be effected at one

or both termini of the fusion protein, or from removal of one or more residues within the amino acid sequence.

[00177] In certain illustrative embodiments, fusion proteins of this disclosure are glycosylated, the pattern of glycosylation being dependent upon a variety of factors including the host cell in which the protein is expressed (if prepared in recombinant host cells) and the culture conditions.

[00178] This disclosure also provides derivatives of fusion proteins. Derivatives include specific binding domain polypeptides bearing modifications other than insertion, deletion, or substitution of amino acid residues. In certain embodiments, the modifications are covalent in nature, and include for example, chemical bonding with polymers, lipids, other organic, and inorganic moieties. Derivatives of this disclosure may be prepared to increase circulating half-life of a specific binding domain polypeptide, or may be designed to improve targeting capacity for the polypeptide to desired cells, tissues, or organs.

[00179] This disclosure further embraces fusion proteins that are covalently modified or derivatized to include one or more water-soluble polymer attachments such as polyethylene glycol, polyoxyethylene glycol, or polypropylene glycol, as described U.S. Patent NOS: 4,640,835; 4,496,689; 4,301,144; 4,670,417; 4,791,192 and 4,179,337. Still other useful polymers known in the art include monomethoxy-polyethylene glycol, dextran, cellulose, and other carbohydrate-based polymers, poly-(N-vinyl pyrrolidone)-polyethylene glycol, propylene glycol homopolymers, a polypropylene oxide/ethylene oxide co-polymer, polyoxyethylated polyols (e.g., glycerol) and polyvinyl alcohol, as well as mixtures of these polymers. Particularly preferred are polyethylene glycol (PEG)–derivatized proteins. Water-soluble polymers may be bonded at specific positions, for example at the amino terminus of the proteins and polypeptides according to this disclosure, or randomly attached to one or more side chains of the polypeptide. The use of PEG for improving therapeutic capacities is described in US Patent No. 6,133,426.

[00180] A particular embodiment of this disclosure is an immunoglobulin or an Fc fusion protein. Such a fusion protein can have a long half-life, *e.g.*, several hours, a day or more, or even a week or more, especially if the Fc domain is capable of interacting with FcRn, the neonatal Fc receptor. The binding site for FcRn in an Fc domain is also the site at which the bacterial proteins A and G bind. The tight binding between these proteins can be used as a means to purify antibodies or fusion proteins of this disclosure by, for example, employing protein A or protein G affinity chromatography during protein purification.

[00181] Protein purification techniques are well known to those of skill in the art. These techniques involve, at one level, the crude fractionation of the polypeptide and non-polypeptide fractions. Further purification using chromatographic and electrophoretic techniques to achieve partial or complete purification (or purification to homogeneity) is frequently desired. Analytical methods particularly suited to the preparation of a pure fusion protein are ion-exchange chromatography; exclusion chromatography; polyacrylamide gel electrophoresis; and isoelectric focusing. Particularly efficient methods of purifying peptides are fast protein liquid chromatography and HPLC.

[00182] Certain aspects of the present disclosure concern the purification, and in particular embodiments, the substantial purification, of a fusion protein. The term "purified fusion protein" as used herein, is intended to refer to a composition, isolatable from other components, wherein the fusion protein is purified to any degree relative to its naturally obtainable state. A purified fusion protein therefore also refers to a fusion protein, free from the environment in which it may naturally occur.

[00183] Generally, "purified" will refer to a fusion protein composition that has been subjected to fractionation to remove various other components, and which composition substantially retains its expressed biological activity. Where the term "substantially purified" is used, this designation refers to a fusion binding protein composition in which the fusion protein forms the major component of the composition, such as constituting about 50%, about 60%, about 70%, about 80%, about 90%, about 95%, about 99% or more of the protein, by weight, in the composition.

[00184] Various methods for quantifying the degree of purification are known to those of skill in the art in light of the present disclosure. These include, for example, determining the specific binding activity of an active fraction, or assessing the amount of fusion protein in a fraction by SDS/PAGE analysis. A preferred method for assessing the purity of a protein fraction is to calculate the binding activity of the fraction, to compare it to the binding activity of the initial extract, and to thus calculate the degree of purification, herein assessed by a "-fold purification number." The actual units used to represent the amount of binding activity will, of course, be dependent upon the particular assay technique chosen to follow the purification and whether or not the expressed fusion protein exhibits a detectable binding activity.

[00185] Various techniques suitable for use in protein purification are well known to those of skill in the art. These include, for example, precipitation with ammonium sulfate, PEG, antibodies and the like, or by heat denaturation, followed by centrifugation;

chromatography steps such as ion exchange, gel filtration, reverse phase, hydroxylapatite, and affinity chromatography; isoelectric focusing; gel electrophoresis; and combinations of these and other techniques. As is generally known in the art, it is believed that the order of conducting the various purification steps may be changed, or that certain steps may be omitted, and still result in a suitable method for the preparation of a substantially purified protein.

[00186] There is no general requirement that the fusion protein always be provided in its most purified state. Indeed, it is contemplated that less substantially purified proteins will have utility in certain embodiments. Partial purification may be accomplished by using fewer purification steps in combination, or by utilizing different forms of the same general purification scheme. For example, it is appreciated that a cation-exchange column chromatography performed utilizing an HPLC apparatus will generally result in greater purification than the same technique utilizing a low pressure chromatography system. Methods exhibiting a lower degree of relative purification may have advantages in total recovery of protein product, or in maintaining binding activity of an expressed protein.

[00187] It is known that the migration of a polypeptide can vary, sometimes significantly, with different conditions of SDS/PAGE (Capaldi et al. (1977) Biochem. Biophys. Res. Comm. 76:425). It will therefore be appreciated that under differing electrophoresis conditions, the apparent molecular weights of purified or partially purified fusion protein expression products may vary.

Polynucleotides, Expression Vectors, and Host Cells

[00188] This disclosure provides polynucleotides (isolated or purified or pure polynucleotides) encoding the multi-specific fusion protein of this disclosure, vectors (including cloning vectors and expression vectors) comprising such polynucleotides, and cells (*e.g.*, host cells) transformed or transfected with a polynucleotide or vector according to this disclosure.

[00189] In certain embodiments, a polynucleotide (DNA or RNA) encoding a binding domain of this disclosure, or a multi-specific fusion protein containing one or more such binding domains is contemplated. Expression cassettes encoding multi-specific fusion protein constructs are provided in the examples appended hereto.

[00190] The present disclosure also relates to vectors that include a polynucleotide of this disclosure and, in particular, to recombinant expression constructs. In one embodiment, this disclosure contemplates a vector comprising a polynucleotide encoding a multi-specific

fusion protein containing a TGFβ antagonist domain and an IL6 or IL6/IL6R binding domain of this disclosure, along with other polynucleotide sequences that cause or facilitate transcription, translation, and processing of such multi-specific fusion protein-encoding sequences.

[00191] Appropriate cloning and expression vectors for use with prokaryotic and eukaryotic hosts are described, for example, in Sambrook *et al.*, Molecular Cloning: A Laboratory Manual, Second Edition, Cold Spring Harbor, NY, (1989). Exemplary cloning/expression vectors include cloning vectors, shuttle vectors, and expression constructs, that may be based on plasmids, phagemids, phasmids, cosmids, viruses, artificial chromosomes, or any nucleic acid vehicle known in the art suitable for amplification, transfer, and/or expression of a polynucleotide contained therein

[00192] As used herein, "vector" means a nucleic acid molecule capable of transporting another nucleic acid to which it has been linked. Exemplary vectors include plasmids, yeast artificial chromosomes, and viral genomes. Certain vectors can autonomously replicate in a host cell, while other vectors can be integrated into the genome of a host cell and thereby are replicated with the host genome. In addition, certain vectors are referred to herein as "recombinant expression vectors" (or simply, "expression vectors"), which contain nucleic acid sequences that are operatively linked to an expression control sequence and, therefore, are capable of directing the expression of those sequences.

[00193] In certain embodiments, expression constructs are derived from plasmid vectors. Illustrative constructs include modified pNASS vector (Clontech, Palo Alto, CA), which has nucleic acid sequences encoding an ampicillin resistance gene, a polyadenylation signal and a T7 promoter site; pDEF38 and pNEF38 (CMC ICOS Biologics, Inc.), which have a CHEF1 promoter; and pD18 (Lonza), which has a CMV promoter. Other suitable mammalian expression vectors are well known (*see, e.g.*, Ausubel et al., 1995; Sambrook *et al.*, supra; *see also*, *e.g.*, catalogs from Invitrogen, San Diego, CA; Novagen, Madison, WI; Pharmacia, Piscataway, NJ). Useful constructs may be prepared that include a dihydrofolate reductase (DHFR)-encoding sequence under suitable regulatory control, for promoting enhanced production levels of the fusion proteins, which levels result from gene amplification following application of an appropriate selection agent (*e.g.*, methotrexate).

[00194] Generally, recombinant expression vectors will include origins of replication and selectable markers permitting transformation of the host cell, and a promoter derived from a highly-expressed gene to direct transcription of a downstream structural sequence, as

described above. A vector in operable linkage with a polynucleotide according to this disclosure yields a cloning or expression construct. Exemplary cloning/expression constructs contain at least one expression control element, *e.g.*, a promoter, operably linked to a polynucleotide of this disclosure. Additional expression control elements, such as enhancers, factor-specific binding sites, terminators, and ribosome binding sites are also contemplated in the vectors and cloning/expression constructs according to this disclosure. The heterologous structural sequence of the polynucleotide according to this disclosure is assembled in appropriate phase with translation initiation and termination sequences. Thus, for example, the fusion protein-encoding nucleic acids as provided herein may be included in any one of a variety of expression vector constructs as a recombinant expression construct for expressing such a protein in a host cell.

[00195] The appropriate DNA sequence(s) may be inserted into a vector, for example, by a variety of procedures. In general, a DNA sequence is inserted into an appropriate restriction endonuclease cleavage site(s) by procedures known in the art. Standard techniques for cloning, DNA isolation, amplification and purification, for enzymatic reactions involving DNA ligase, DNA polymerase, restriction endonucleases and the like, and various separation techniques are contemplated. A number of standard techniques are described, for example, in Ausubel *et al*. (*Current Protocols in Molecular Biology*, Greene Publ. Assoc. Inc. & John Wiley & Sons, Inc., Boston, MA, 1993); Sambrook *et al*. (*Molecular Cloning*, Second Ed., Cold Spring Harbor Laboratory, Plainview, NY, 1989); Maniatis *et al*. (*Molecular Cloning*, Cold Spring Harbor Laboratory, Plainview, NY, 1982); Glover (Ed.) (*DNA Cloning* Vol. I and II, IRL Press, Oxford, UK, 1985); Hames and Higgins (Eds.) (*Nucleic Acid Hybridization*, IRL Press, Oxford, UK, 1985); and elsewhere.

[00196] The DNA sequence in the expression vector is operatively linked to at least one appropriate expression control sequence (*e.g.*, a constitutive promoter or a regulated promoter) to direct mRNA synthesis. Representative examples of such expression control sequences include promoters of eukaryotic cells or their viruses, as described above. Promoter regions can be selected from any desired gene using CAT (chloramphenicol transferase) vectors or other vectors with selectable markers. Eukaryotic promoters include CMV immediate early, HSV thymidine kinase, early and late SV40, LTRs from retrovirus, and mouse metallothionein-I. Selection of the appropriate vector and promoter is well within the level of ordinary skill in the art, and preparation of certain particularly preferred recombinant expression constructs comprising at least one promoter or regulated promoter

operably linked to a nucleic acid encoding a protein or polypeptide according to this disclosure is described herein.

[00197] Variants of the polynucleotides of this disclosure are also contemplated. Variant polynucleotides are at least 90%, and preferably 95%, 99%, or 99.9% identical to one of the polynucleotides of defined sequence as described herein, or that hybridizes to one of those polynucleotides of defined sequence under stringent hybridization conditions of 0.015M sodium chloride, 0.0015M sodium citrate at about 65-68°C or 0.015M sodium chloride, 0.0015M sodium citrate, and 50% formamide at about 42°C. The polynucleotide variants retain the capacity to encode a binding domain or fusion protein thereof having the functionality described herein.

[00198] The term "stringent" is used to refer to conditions that are commonly understood in the art as stringent. Hybridization stringency is principally determined by temperature, ionic strength, and the concentration of denaturing agents such as formamide. Examples of stringent conditions for hybridization and washing are 0.015M sodium chloride, 0.0015M sodium citrate at about 65-68°C or 0.015M sodium chloride, 0.0015M sodium citrate, and 50% formamide at about 42°C (*see* Sambrook *et al.*, *Molecular Cloning: A Laboratory Manual*, 2nd Ed., Cold Spring Harbor Laboratory, Cold Spring Harbor, N.Y., 1989).

[00199] More stringent conditions (such as higher temperature, lower ionic strength, higher formamide, or other denaturing agent) may also be used; however, the rate of hybridization will be affected. In instances wherein hybridization of deoxyoligonucleotides is concerned, additional exemplary stringent hybridization conditions include washing in 6x SSC, 0.05% sodium pyrophosphate at 37°C (for 14-base oligonucleotides), 48°C (for 17-base oligonucleotides), 55°C (for 20-base oligonucleotides), and 60°C (for 23-base oligonucleotides).

[00200] A further aspect of this disclosure provides a host cell transformed or transfected with, or otherwise containing, any of the polynucleotides or vector/expression constructs of this disclosure. The polynucleotides or cloning/expression constructs of this disclosure are introduced into suitable cells using any method known in the art, including transformation, transfection and transduction. Host cells include the cells of a subject undergoing *ex vivo* cell therapy including, for example, *ex vivo* gene therapy. Eukaryotic host cells contemplated as an aspect of this disclosure when harboring a polynucleotide, vector, or protein according to this disclosure include, in addition to a subject's own cells (*e.g.*, a human patient's own cells), VERO cells, HeLa cells, Chinese hamster ovary (CHO)

cell lines (including modified CHO cells capable of modifying the glycosylation pattern of expressed multivalent binding molecules, *see* US Patent Application Publication No. 2003/0115614), COS cells (such as COS-7), W138, BHK, HepG2, 3T3, RIN, MDCK, A549, PC12, K562, HEK293 cells, HepG2 cells, N cells, 3T3 cells, *Spodoptera frugiperda* cells (*e.g.*, Sf9 cells), *Saccharomyces cerevisiae* cells, and any other eukaryotic cell known in the art to be useful in expressing, and optionally isolating, a protein or peptide according to this disclosure. Also contemplated are prokaryotic cells, including *Escherichia coli*, *Bacillus subtilis*, *Salmonella typhimurium*, a Streptomycete, or any prokaryotic cell known in the art to be suitable for expressing, and optionally isolating, a protein or peptide according to this disclosure. In isolating protein or peptide from prokaryotic cells, in particular, it is contemplated that techniques known in the art for extracting protein from inclusion bodies may be used. The selection of an appropriate host is within the scope of those skilled in the art from the teachings herein. Host cells that glycosylate the fusion proteins of this disclosure are contemplated.

[00201] The term "recombinant host cell" (or simply "host cell") refers to a cell containing a recombinant expression vector. It should be understood that such terms are intended to refer not only to the particular subject cell but to the progeny of such a cell. Because certain modifications may occur in succeeding generations due to either mutation or environmental influences, such progeny may not, in fact, be identical to the parent cell, but are still included within the scope of the term "host cell" as used herein.

[00202] Recombinant host cells can be cultured in a conventional nutrient medium modified as appropriate for activating promoters, selecting transformants, or amplifying particular genes. The culture conditions for particular host cells selected for expression, such as temperature, pH and the like, will be readily apparent to the ordinarily skilled artisan. Various mammalian cell culture systems can also be employed to express recombinant protein. Examples of mammalian expression systems include the COS-7 lines of monkey kidney fibroblasts, described by Gluzman (1981) Cell 23:175, and other cell lines capable of expressing a compatible vector, for example, the C127, 3T3, CHO, HeLa and BHK cell lines. Mammalian expression vectors will comprise an origin of replication, a suitable promoter and, optionally, enhancer, and also any necessary ribosome binding sites, polyadenylation site, splice donor and acceptor sites, transcriptional termination sequences, and 5′-flanking nontranscribed sequences, for example, as described herein regarding the preparation of multivalent binding protein expression constructs. DNA sequences derived from the SV40 splice, and polyadenylation sites may be used to provide the required nontranscribed genetic

elements. Introduction of the construct into the host cell can be effected by a variety of methods with which those skilled in the art will be familiar, including calcium phosphate transfection, DEAE-Dextran-mediated transfection, or electroporation (Davis *et al*. (1986) Basic Methods in Molecular Biology).

[00203] In one embodiment, a host cell is transduced by a recombinant viral construct directing the expression of a protein or polypeptide according to this disclosure. The transduced host cell produces viral particles containing expressed protein or polypeptide derived from portions of a host cell membrane incorporated by the viral particles during viral budding.

Compositions and Methods of Use

[00204] To treat human or non-human mammals suffering a disease state associated with TGFβ, IL6, IL10, GITR, VEGF, TNF, HGF, TWEAK, IGF1 or IGF2 dysregulation, a multi-specific fusion protein of this disclosure is administered to the subject in an amount that is effective to ameliorate symptoms of the disease state following a course of one or more administrations. Being polypeptides, the multi-specific fusion proteins of this disclosure can be suspended or dissolved in a pharmaceutically acceptable diluent, optionally including a stabilizer of other pharmaceutically acceptable excipients, which can be used for intravenous administration by injection or infusion, as more fully discussed below.

[00205] A pharmaceutically effective dose is that dose required to prevent, inhibit the occurrence of, or treat (alleviate a symptom to some extent, preferably all symptoms of) a disease state. The pharmaceutically effective dose depends on the type of disease, the composition used, the route of administration, the type of subject being treated, the physical characteristics of the specific subject under consideration for treatment, concurrent medication, and other factors that those skilled in the medical arts will recognize. For example, an amount between 0.1 mg/kg and 100 mg/kg body weight (which can be administered as a single dose, or in multiple doses given hourly, daily, weekly, monthly, or any combination thereof that is an appropriate interval) of active ingredient may be administered depending on the potency of a binding domain polypeptide or multi-specific protein fusion of this disclosure.

[00206] In certain aspects, compositions of fusion proteins are provided by this disclosure. Pharmaceutical compositions of this disclosure generally comprise one or more type of binding domain or fusion protein in combination with a pharmaceutically acceptable carrier, excipient, or diluent. Such carriers will be nontoxic to recipients at the dosages and

concentrations employed. Pharmaceutically acceptable carriers for therapeutic use are well known in the pharmaceutical art, and are described, for example, in Remington's Pharmaceutical Sciences, Mack Publishing Co. (A.R. Gennaro (Ed.) 1985). For example, sterile saline and phosphate buffered saline at physiological pH may be used. Preservatives, stabilizers, dyes and the like may be provided in the pharmaceutical composition. For example, sodium benzoate, sorbic acid, or esters of *p*-hydroxybenzoic acid may be added as preservatives. *Id*. at 1449. In addition, antioxidants and suspending agents may be used. *Id*. The compounds of the present invention may be used in either the free base or salt forms, with both forms being considered as being within the scope of the present invention.

[00207] Pharmaceutical compositions may also contain diluents such as buffers; antioxidants such as ascorbic acid, low molecular weight (less than about 10 residues) polypeptides, proteins, amino acids, carbohydrates (*e.g.*, glucose, sucrose, or dextrins), chelating agents (*e.g.*, EDTA), glutathione or other stabilizers or excipients. Neutral buffered saline or saline mixed with nonspecific serum albumin are exemplary appropriate diluents. Preferably, product is formulated as a lyophilizate using appropriate excipient solutions as diluents.

[00208] Compositions of this disclosure can be used to treat disease states in human and non-human mammals that are a result of or associated with TGFβ or IL6 dysregulation. Increased production or activity of TGFβ has been implicated in various disease processes, including tumorigenesis, angiogenesis, metastasis, metastatic migration, and epithelial and mesenchymal cancers (*see*, *e.g.*, Oft et al. (1998) Curr. Biol. 8:1243; Pardali & Mousaka (2007) Biochim. Biophys. Acta 1775:21). In addition, TGFβ signal transduction has been associated with angiogenesis and the development of vascular disorders (Bertolino et al. (2005) Chest 128:585S).

[00209] It has been suggested that IL10 may play a key role in the occurrence of lyphocytic diseases (US Patent No. 5,639,600) and that IL10 may increase proliferation of non-Hodgkin's lymphoma cells (Voorzanger et al. (1996) Cancer Res. 56:5499). More recently it has been proposed that TGFβ and IL10 work together to ensure a controlled inflammatory response (Li & Flavell, (2008) Immunity 28:468). It has been suggested that tumor-expressed GITRL mediates immunosubversion in humans (Baltz et al. (2007) FASEB J. 21:2442). Overexpression of VEGF and TGFβ has been associated with the development of cervical cancer (Baritaki et al. (2007) Int. J. Oncol. 31:69). TNFα has been associated with the development of renal cell carcinoma (Harrison et al. (2007) J. Clin. Oncol. 25:4542-

9). TGFβ has been shown to promote HGF-dependent invasion of squamous carcinoma cells (Lewis et al. (2004) Br. J. Cancer, 90:822), and HGF has been shown to stimulate cell growth and enhance expression of TGFα in human pancreatic cancer cells (Ohba et al. (1999) J. Gastroenterol. 34:498-504). In addition, TGFβ and HGF have been shown to stimulate the invasivenss of gastric cancer cells (Inoue et al., (197) Jpn. J. Cancer Res. 88:152). IGF1R has been identified in the treatment of cancers, including sarcomas (Scotlandi & Picci (2008) Curr. Opin. Oncol. 20:419-27; Yuen & Macaulay (2008) Expert Opin. Ther. Targets 12:589-603).

[00210] IL-6 trans-signaling has been implicated in malignancies, such as colon cancer, while IL6 cis-signaling has been implicated in malignancies including hormone-independent prostate cancer, B-cell proliferative disorders such as B cell non-Hodgkin's lymphoma, and advanced cancers of kidney, breast, colon, lung, brain, and other tissues (*see, e.g.*, Sansone *et al*. (2007) J. Clin Invest. 117:3988). Thus, multi-specific fusion proteins of this disclosure are useful in treating various TGFβ related autoimmune disorders (such as systemic lupus erythematosus (SLE) or rheumatoid arthritis), Alzheimer's disease or hyperproliferative diseases or malignant disorders, including polycystic kidney disease, lung cancer, colon cancer, urothelial cancer, bladder cancer, renal cell cancer, breast cancer, ovarian cancer, Rhabdomyosarcoma, Ewing's sarcoma, osteosarcoma, neuroblastoma, head & neck cancer, melanoma, glioblastoma, pancreatic cancer, or hepatocarcinoma, or the like.

[00211] "Pharmaceutically acceptable salt" refers to a salt of a binding domain polypeptide or fusion protein of this disclosure that is pharmaceutically acceptable and that possesses the desired pharmacological activity of the parent compound. Such salts include the following: (1) acid addition salts, formed with inorganic acids such as hydrochloric acid, hydrobromic acid, sulfuric acid, nitric acid, phosphoric acid, and the like; or formed with organic acids such as acetic acid, propionic acid, hexanoic acid, cyclopentanepropionic acid, glycolic acid, pyruvic acid, lactic acid, malonic acid, succinic acid, malic acid, maleic acid, fumaric acid, tartaric acid, citric acid, benzoic acid, 3-(4-hydroxybenzoyl)benzoic acid, cinnamic acid, mandelic acid, methanesulfonic acid, ethanesulfonic acid, 1,2-ethane-disulfonic acid, 2-hydroxyethanesulfonic acid, benzenesulfonic acid, 4-chlorobenzenesulfonic acid, 2-naphthalenesulfonic acid, 4-toluenesulfonic acid, camphorsulfonic acid, 4-methylbicyclo[2.2.2]-oct-2-ene-1-carboxylic acid, glucoheptonic acid, 3-phenylpropionic acid, trimethylacetic acid, tertiary butylacetic acid, lauryl sulfuric acid, gluconic acid, glutamic acid, hydroxynaphthoic acid, salicylic acid, stearic acid,

muconic acid, and the like; or (2) salts formed when an acidic proton present in the parent compound either is replaced by a metal ion, *e.g.*, an alkali metal ion, an alkaline earth ion, or an aluminum ion; or coordinates with an organic base such as ethanolamine, diethanolamine, triethanolamine, N-methylglucamine, or the like.

[00212] In particular illustrative embodiments, a polypeptide or fusion protein of this disclosure is administered intravenously by, for example, bolus injection or infusion. Routes of administration in addition to intravenous include oral, topical, parenteral (*e.g.*, sublingually or buccally), sublingual, rectal, vaginal, and intranasal. The term parenteral as used herein includes subcutaneous injections, intravenous, intramuscular, intrasternal, intracavernous, intrathecal, intrameatal, intraurethral injection, perispinal or infusion techniques. The pharmaceutical composition is formulated so as to allow the active ingredients contained therein to be bioavailable upon administration of the composition to a patient. Compositions that will be administered to a patient take the form of one or more dosage units, where for example, a tablet may be a single dosage unit, and a container of one or more compounds of this disclosure in aerosol form may hold a plurality of dosage units.

[00213] For oral administration, an excipient and/or binder may be present, such as sucrose, kaolin, glycerin, starch dextrans, cyclodextrins, sodium alginate, ethyl cellulose, and carboxy methylcellulose. Sweetening agents, preservatives, dye/colorant, flavor enhancer, or any combination thereof may optionally be present. A coating shell may also optionally be used.

[00214] In a composition intended to be administered by injection, one or more of a surfactant, preservative, wetting agent, dispersing agent, suspending agent, buffer, stabilizer, isotonic agent, or any combination thereof may optionally be included.

[00215] For nucleic acid-based formulations, or for formulations comprising expression products according to this disclosure, about 0.01 μg/kg to about 100 mg/kg body weight will be administered, for example, by the intradermal, subcutaneous, intramuscular, or intravenous route, or by any route known in the art to be suitable under a given set of circumstances. A preferred dosage, for example, is about 1 μg/kg to about 20 mg/kg, with about 5 μg/kg to about 10 mg/kg particularly preferred. It will be evident to those skilled in the art that the number and frequency of administration will be dependent upon the response of the host.

[00216] The pharmaceutical compositions of this disclosure may be in any form that allows for administration to a patient, such as, for example, in the form of a solid, liquid, or

gas (aerosol). The composition may be in the form of a liquid, *e.g.*, an elixir, syrup, solution, emulsion or suspension, for administration by any route described herein.

[00217] A liquid pharmaceutical composition as used herein, whether in the form of a solution, suspension or other like form, may include one or more of the following components: sterile diluents such as water for injection, saline solution (*e.g.*, physiological saline), Ringer's solution, isotonic sodium chloride, fixed oils such as synthetic mono- or digylcerides that may serve as the solvent or suspending medium, polyethylene glycols, glycerin, propylene glycol or other solvents; antibacterial agents such as benzyl alcohol or methyl paraben; antioxidants such as ascorbic acid or sodium bisulfite; buffers such as acetates, citrates or phosphates; chelating agents such as ethylenediaminetetraacetic acid; and agents for the adjustment of tonicity such as sodium, chloride, or dextrose. The parenteral preparation can be enclosed in ampoules, disposable syringes or multiple dose vials made of glass or plastic. Physiological saline is a preferred additive. An injectable pharmaceutical composition is preferably sterile.

[00218] It may also be desirable to include other components in the preparation, such as delivery vehicles including aluminum salts, water-in-oil emulsions, biodegradable oil vehicles, oil-in-water emulsions, biodegradable microcapsules, and liposomes. Examples of adjuvants for use in such vehicles include N-acetylmuramyl-L-alanine-D-isoglutamine (MDP), lipopolysaccharides (LPS), glucan, IL-12, GM-CSF, γ-interferon, and IL-15.

[00219] While any suitable carrier known to those of ordinary skill in the art may be employed in the pharmaceutical compositions of this disclosure, the type of carrier will vary depending on the mode of administration and whether a sustained release is desired. For parenteral administration, the carrier may comprise water, saline, alcohol, a fat, a wax, a buffer, or any combination thereof. For oral administration, any of the above carriers or a solid carrier, such as mannitol, lactose, starch, magnesium stearate, sodium saccharine, talcum, cellulose, glucose, sucrose, magnesium carbonate, or any combination thereof, may be employed.

[00220] Also contemplated is the administration of multi-specific fusion protein compositions of this disclosure in combination with a second agent. A second agent may be one accepted in the art as a standard treatment for a particular disease state, such as inflammation, autoimmunity, and cancer. Exemplary second agents contemplated include cytokines, growth factors, steroids, NSAIDs, DMARDs, chemotherapeutics, radiotherapeutics, or other active and ancillary agents.

[00221] This disclosure contemplates a dosage unit comprising a pharmaceutical composition of this disclosure. Such dosage units include, for example, a single-dose or a multi-dose vial or syringe, including a two-compartment vial or syringe, one comprising the pharmaceutical composition of this disclosure in lyophilized form and the other a diluent for reconstitution. A multi-dose dosage unit can also be, *e.g.*, a bag or tube for connection to an intravenous infusion device.

[00222] This disclosure also contemplates a kit comprising a pharmaceutical composition in a unit dose or multi-dose container, *e.g.*, a vial, and a set of instructions for administering the composition to patients suffering a disorder as described herein.

[00223] All U.S. patents, U.S. patent application publications, U.S. patent applications, foreign patents, foreign patent applications, non-patent publications, tables, sequences, webpages, or the like referred to in this specification, are incorporated herein by reference, in their entirety. The following examples are intended to illustrate, but not limit, this disclosure.

EXAMPLES

Xceptor Sequences

[00224] Exemplary IL6 antagonist variable region (V_L and V_H) binding sequences (SEQ ID NO:373-496) are disclosed herein. Also disclosed are amino acid sequences and nucleic acid expression cassettes for exemplary Xceptor fusion proteins comprising a TGFβR2 ectodomain and an anti-IL6xR binding domain. Xceptor fusion proteins having a TGFβR2 ectodomain at the amino-terminus and an anti-IL6xR binding domain at the carboxy terminus, are referred to herein as TRU(XB6)-1019.1 and TRU(XB6)-1019.2 (amino acid sequences provided in SEQ ID NO:737 and 738, respectively, with the corresponding nucleotide sequences being provided in SEQ ID NO:741 and 742, respectively). The Xceptor fusion proteins in the reverse orientation – that is, having an anti-IL6xR binding domain at the amino-terminus and a TGFβR2 ectodomain at the carboxy terminus, are referred to herein as TRU(X6B)-1019.1 and TRU(X6B)-1019.2 (amino acid sequences provided in SEQ ID NO:735 and 736, respectively, with the corresponding nucleotide sequences being provided in SEQ ID NO:739 and 740, respectively).

Activity Examples

[00225] Various Xceptor fusion proteins described herein were tested for activity as described below. Abbreviations used in the following examples include the following terms, except where indicated otherwise:

PBS-T: PBS, pH 7.2-7.4 and 0.1% Tween®20

Working buffer: PBS-T with 1% BSA

Blocking buffer (PBS-T with 3% BSA

EXAMPLE 1

TGFβ BINDING DOMAINS

[00226] A phage library of Fab binding domains is screened for binding domains specific for either a TGFβ or an IL6xR complex essentially as described by Hoet *et al*. (2005) Nature Biotechnol. 23:344. The binding domains are cloned by PCR amplification. Briefly, the VL and VH regions from the Fab library clones are amplified using PCR SuperMix (Invitrogen, San Diego, CA) and appropriate primers that create the G_4S linker via overlap, with an initial anneal at 56°C for 9 cycles, then 62 °C for an additional 20 cycles. The PCR products are separated on an agarose gel and purified using a Qiagen (Chatsworth, CA) PCR Purification column. The second round sewing reaction involves mixing a molar equivalent of VL and VH products with Expand buffer and water, denaturing at 95 °C for 5 sec, then cooling slowly to room temperature. To amplify, a mix of dNTPs is added with Expand enzyme and incubated at 72 °C for 10 sec. The outside primers are added (5' VH and 3' VL) and the mix is cycled 35 times with an anneal at 62°C and a 45 min extension reaction. The resulting 750 basepair product is gel purified, digested with EcoRI and NotI, and cloned in plasmid pD28 (for more details, see US Patent Application Publication No. 2005/0136049 and PCT Application Publication No. WO 2007/146968).

EXAMPLE 2

XCEPTOR BINDING TO IL6 AND HYPER IL6 BY ELISA

[00227] Hyper-IL6 (HIL6 or IL6xR), recombinant human IL6 (rhIL6), and human soluble IL6R binding activity was examined for exemplary Xceptors TRU(XT6)-1002, 1019, 1025, 1042, 1058, and TRU(X6T)-1019 (SEQ ID NO:608, 625, 631, 648, 664 and 670,

respectively), substantially as follows. Each of these Xceptors includes a TNFRSF1B ectodomain and an anti-IL6xR binding domain.

HIL6 and IL6 Binding

[00228] Added to each well of a 96-well plate was 100 µl goat anti-human IgG-Fc (Jackson ImmunoResearch, West Grove, PA) from a 2 µg/ml solution in PBS, pH 7.2-7.4. The plate was covered, and incubated overnight at 4°C. After washing four times with PBS (pH 7.2-7.4) and 0.1% Tween®20 (PBS-T), 250 µl Blocking buffer (PBS-T with 3% BSA or 10% normal goat serum) was added to each well, the plate was covered, and incubated at room temperature for 2 hours (or at 4°C overnight). After washing the plate three times with PBS-T, added in duplicate wells to the anti-human IgG-Fc coated plate was 100 µl / well Xceptor TNFRSF1B::anti-HIL6 samples and human gp130-Fc chimera (R&D Systems, Minneapolis, MN) serially diluted three-fold in Working buffer starting at 300 ng/ml, the plate was covered, and incubated at room temperature for about 1 to 2 hours. After washing the plate five times with PBS-T, added in duplicate wells was 100 µl/well human Hyper IL-6 or recombinant human IL-6 from a 150 pM solution in Working buffer, the plate was covered, and incubated at room temperature for about 1 to 2 hours. After washing the plate five times with PBS-T, 100 µl/well anti-human IL-6-biotin (R&D Systems) from a 150 ng/ml solution in Working buffer, the plate was covered, and incubated at room temperature for about 1 to 2 hours. After washing the plate five times with PBS-T, 100 µl per well horse radish peroxidase-conjugated streptavidin (Zymed, San Francisco, CA) diluted 1:4,000 in Working buffer was added, the plate was covered, and incubated at room temperature for 30 minutes. After washing the plate six times with PBS-T, 100 µl per well 3,3,5,5-tetramentylbenzidine (TMB) substrate solution (Pierce, Rockford, IL) was added for about 3 to 5 minutes and then the reaction was stopped with 50 µl Stop buffer (1N H_2SO_4) per well. The absorbance of each well was read at 450 nm.

sIL6R Binding

[00229] Added to each well of a 96-well plate was 100 µl goat anti-human IgG-Fc (ICN Pharmaceuticals, Costa Mesa, CA) from a 2 µg/ml solution in PBS, pH 7.2-7.4, The plates were covered, and incubated overnight at 4°C. After washing four times with PBS-T, 250 µl Blocking buffer (PBS-T with 3% BSA or 10% normal goat serum) was added to each well, the plate was covered, and incubated at room temperature for 2 hours (or at 4°C overnight). After washing the plate three times with PBS-T, added in duplicate wells to the anti-human IgG-Fc coated plate was 100 µl/well Xceptor TNFRSF1B::anti-HIL6 samples,

positive control anti-human IL-6R (R&D Systems, Minneapolis, MN) and negative controls human IgG or human gp130-Fc chimera (R&D Systems), each serially diluted three-fold in Working buffer starting at 300 ng/ml, the plate was covered, and incubated at room temperature for about 1 to 2 hours. After washing the plate five times with PBS-T, added in duplicate wells was 100 µl/well recombinant human sIL-6R (R&D Systems) from a 75 pM solution in Working buffer, the plate was covered, and incubated at room temperature for about 1 to 2 hours. After washing the plate five times with PBS-T, added 100 µl/well anti-human IL-6R-biotin (R&D Systems) from a 100 ng/ml solution in Working buffer, the plate was covered, and incubated at room temperature for about 1 to 2 hours. After washing the plate five times with PBS-T, 100 µl per well horse radish peroxidase-conjugated streptavidin (Zymed, San Francisco, CA) diluted 1:4,000 in Working buffer was added, the plate was covered, and incubated at room temperature for 30 minutes. After washing the plate six times with PBS-T, 100 µl per well 3,3,5,5-tetramentylbenzidine (TMB) substrate solution (Pierce, Rockford, IL) was added for about 3 to 5 minutes and then the reaction was stopped with 50 µl Stop buffer (1N H_2SO_4) per well. The absorbance of each well was read at 450 nm.

[00230] The data in Figures 1A-1C demonstrate that all Xceptor fusion proteins, whether the TNFRSF1B ectodomain was on the amino- or carboxy terminus of the fusion protein molecules, can bind HIL6. Furthermore, these assays show that the Xceptor proteins have specificity for the IL6xR complex because only two of the Xceptors bind rhIL6 (Figure 1B) and none bind sIL6R (Figure 1C). In related studies, the xceptor TRU(XT6)-1002 and the SMIP TRU(S6)-1002 were found to cross-react with IL6 from the non-human primate Mucaca mulatta.

EXAMPLE 3

XCEPTOR BINDING TO TNF-α BY ELISA

[00231] TNF-α binding activity was examined for Xceptors TRU(XT6)-1002, 1042, 1058, 1019, and TRU(X6T)-1019 (SEQ ID NO:608, 648, 664, 625 and 670, respectively), substantially as follows.

[00232] Added to each well of a 96-well plate was 100 µl goat anti-human IgG-Fc (ICN Pharmaceuticals, Costa Mesa, CA) from a 2 µg/ml solution in PBS, pH 7.2-7.4. The plate was covered, and incubated overnight at 4°C. After washing four times with PBS-T, 250 µl Blocking buffer was added to each well, the plate was covered, and incubated at room

temperature for 2 hours (or at 4°C overnight). After washing the plate three times with PBS-T, added in duplicate wells to the anti-human IgG-Fc coated plate was 100 µl/well Xceptor TNFRSF1B::anti-HIL6 samples, positive controls Enbrel® (etanercept) and recombinant human TNFR2 (TNFRSF1B)-Fc chimera (R&D Systems, Minneapolis, MN), and negative controls human IgG or human gp130-Fc chimera (R&D Systems), each serially diluted three-fold in Working bufferstarting at 300 ng / ml, the plate was covered, and incubated at room temperature for about 1 to 2 hours. After washing the plate five times with PBS-T, added in duplicate wells was 100 µl/well recombinant human TNF-α (R&D Systems) from a 2 ng/ml solution in Working buffer, the plate was covered, and incubated at room temperature for about 1 to 2 hours. After washing the plate five times with PBS-T, added 100 µl/well anti-human TNF-α-biotin (R&D Systems) from a 200 ng/ml solution in Working buffer, the plate was covered, and incubated at room temperature for about 1 to 2 hours. After washing the plate five times with PBS-T, 100 µl per well horse radish peroxidase-conjugated streptavidin (Jackson ImmunoResearch, West Grove, PA) diluted 1:1,000 in Working buffer was added, the plate was covered, and incubated at room temperature for 30 minutes. After washing the plate six times with PBS-T, 100 µl per well 3,3,5,5-tetramentylbenzidine (TMB) substrate solution (Pierce, Rockford, IL) was added for about 3 to 5 minutes and then the reaction was stopped with 50 µl Stop buffer (1N H_2SO_4) per well. The absorbance of each well was read at 450 nm.

[00233] The data in Figure 2 shows that all Xceptor fusion proteins tested can bind TNF-α, whether the TNFRSF1B ectodomain was on the amino- or carboxy terminus of the fusion protein.

EXAMPLE 4

XCEPTOR DUAL LIGAND BINDING BY ELISA

[00234] Concurrent binding to TNF-α and to IL6xR complex was examined for Xceptor fusion protein TRU(XT6)-1006 (SEQ ID NO:612), substantially as follows.

[00235] Added to each well of a 96-well plate was 100 µl human HIL-6 solution (5 µg/ml in PBS, pH 7.2-7.4). The plate was covered, and incubated overnight at 4°C. After washing four times with PBS-T, then 250 µl Blocking buffer was added to each well, the plate was covered, and incubated at room temperature for 2 hours (or at 4°C overnight). After washing the plate three times with PBS-T, added in duplicate wells to the HIL-6 coated plate was 100 µl/well Xceptor TNFRSF1B::HIL6 samples serially diluted three-fold in

Working buffer starting at 300 ng / ml. Negative controls included human gp130-Fc chimera (R&D Systems, Minneapolis, MN), Enbrel® (etanercept), and Working buffer only. The plate was covered and incubated at room temperature for 1.5 hours. After washing the plate five times with PBS-T, 100 µl per well recombinant human TNF-α (R&D Systems, Minneapolis, MN) to 2 ng / ml in Working buffer was added, the plate was covered, and incubated at room temperature for 1.5 hr. After washing the plate five times with PBS-T, 100 µl per well anti-human TNF-α-biotin (R&D Systems) to 200 ng/ml in Working buffer was added, the plate was covered, and incubated at room temperature for 1.5 hr. After washing the plate five times with PBS-T, 100 µl per well horse radish peroxidase-conjugated streptavidin (Jackson ImmunoResearch, West Grove, PA) diluted 1:1000 in Working buffer was added, the plate was covered, and incubated at room temperature for 30 minutes. After washing the plate six times with PBS-T, 100 µl per well 3,3,5,5-tetramentylbenzidine (TMB) substrate solution (Pierce, Rockford, IL) was added for 3-5 minutes and then the reaction was stopped with 50 µl Stop buffer (1N H_2SO_4) per well. The absorbance of each well was read at 450 nm.

[00236] The data in Figure 3 demonstrates that Xceptor proteins can bind two ligands simultaneously (in this case TNF-α and Hyper IL6).

EXAMPLE 5

XCEPTOR BLOCKING OF HYPER IL6 BINDING TO GP130 BY ELISA

[00237] Blocking of Hyper IL6 (IL6xR) binding to soluble gp130 receptor by Xceptor fusion proteins TRU(XT6)-1004, 1006, 1007, 1008, 1013, and 1019 (SEQ ID NO:610, 612, 613, 614, 619 and 625, respectively), was examined substantially as follows.

[00238] Added to each well of a 96-well plate was 100 µl human gp130-Fc chimera (R&D Systems, Minneapolis, MN) from of 0.25 – 0.5 µg/ml solution in PBS, pH 7.2-7.4. The plates were covered, and incubated overnight at 4°C. After washing four times with PBS-T, 250 µl Blocking buffer (PBS-T with 3% BSA or 10% normal goat serum) was added to each well, the plate was covered, and incubated at room temperature for 2 hours (or at 4°C overnight). Serial five-fold dilutions in Working buffer starting at 50 µg/ml were made of the following samples: Xceptor TNFRSF1B::anti-HIL6 samples, positive controls human gp130-Fc chimera (R&D Systems) and anti-human IL-6R (R&D Systems), and negative controls anti-human IL-6 (R&D Systems), human IgG or Enbrel® (etanercept). Equal volumes of the serially diluted Xceptor samples were mixed with Hyper IL-6 (final Hyper IL-6 concentration

of 2.5 ng/ml) and incubated at room temperature for 1 hour. After washing the plate three times with PBS-T, added in duplicate wells to the human gp130-Fc coated plate was 100 µl/well of the serially dilutions of Xceptor / HIL6 mixtures, human gp130-Fc chimera, anti-human IL-6R, anti-human IL-6, human IgG, and Enbrel® (etanercept), the plate was covered, and incubated at room temperature for about 1.5 hours. After washing the plate five times with PBS-T, 100 µl per well horse radish peroxidase-conjugated anti-mouse IgG-Fc (Pierce, Rockford, IL) diluted 1:10,000 in Working buffer was added, the plate was covered, and incubated at room temperature for 1 hour. After washing the plate six times with PBS-T, 100 µl per well 3,3,5,5-tetramentylbenzidine (TMB) substrate solution (Pierce) was added for about 5 to 15 minutes and then the reaction was stopped with 50 µl Stop buffer (1N H_2SO_4) per well. The absorbance of each well was read at 450 nm.

[00239] The data in Figure 4 demonstrate that Xceptor proteins comprising an anti-IL6xR binding domain can block soluble gp130 from binding to HIL6.

EXAMPLE 6

XCEPTOR BLOCKING OF IL6 AND HYPER IL6 INDUCED CELL PROLIFERATION

[00240] Blocking of IL6 or Hyper IL6 (IL6xR) induced cell proliferation of TF-1 cells was examined for Xceptor fusion proteins TRU(XT6)-1011, 1014, 1025, 1026, 1002, and TRU(X6T)-1019 (SEQ ID NO:617, 620, 631, 632, 608 and 670, respectively), substantially as follows.

[00241] Added to each well of a 96-well flat bottom plate were 0.3 $x10^6$ TF-1 cells (human erythroleukemia cells) in the fresh growth medium (10% FBS-RPMI 1640; 2mM L-glutamine; 100 units/ml penicillin; 100 µg/ml streptomycin; 10 mM HEPES; 1mM sodium pyruvate; and 2 ng/ml Hu GM-CSF) one day before use in proliferation assay. The cells were then harvested and washed twice with assay medium (same as growth medium except without GM-CSF, cytokine-free), then resuspended at 1 x 10^5 cells/ml in assay medium. For blocking IL-6 activity, serial dilutions of a TNFSFR1B::anti-HIL-6 Xceptor of interest or antibody was pre-incubated with a fixed concentration of recombinant human IL-6 (rhIL-6) (R&D Systems, Minneapolis, MN) or hyper IL-6 (HIL-6) in 96-well plates for 1 hour at 37°C, 5%CO_2. Controls used included human IgG; human gp130-Fc chimera (R&D Systems); anti-hIL-6 antibody (R&D Systems); and anti-hIL-6R antibody (R&D Systems). After the pre-incubation period, $1x10^4$1cells (in 100 µl) was added to each well. The final assay mixture, in a total volume of 200 µL/well, containing TNFSFR1B::HIL-6, rhIL-6, or

HIL-6 and cells was incubated at 37°C, 5%CO_2 for 72 hours. During the last 4-6 hours of culture, ^{3}H-thymidine (20 μCi/ml in assay medium, 25 μL/well) was added. The cells were harvested onto UniFilter-96 GF/c plates and incorporated ^{3}H-Thymidine was determined using TopCount reader (Packard). The data are presented as the Mean of cpm ± SD of triplicates. The percentage of blocking = 100 - (test cpm – control cpm /maximum cpm-control cpm)*100.

[00242] The data in Figure 5A and Figure 5B demonstrate that all Xceptor proteins, whether the TNFRSF1B ectodomain was on the amino- or carboxy terminus of the fusion protein molecules, can block cell proliferation induced by IL6 or Hyper IL6, respectively, or both.

EXAMPLE 7

XCEPTOR BLOCKING OF TNF-α BINDING TO TNFR BY ELISA

[00243] Blocking of TNF-α binding to TNF receptor by Xceptor fusion proteins TRU(XT6)-1004, 1006, 1007, 1008, 1013, and 1019 (SEQ ID NO:610, 612, 613, 614, 619 and 625, respectively) was examined substantially as follows.

[00244] Added to each well of a 96-well plate was 100 μL recombinant human TNFR2-Fc chimera (R&D Systems, Minneapolis, MN) from of 0.25 – 0.5 μg/ml solution in PBS, pH 7.2-7.4. The plates were covered, and incubated overnight at 4°C. After washing four times with PBS-T, 250 μL Blocking buffer (PBS-T with 3% BSA or 10% normal goat serum) was added to each well, the plate was covered, and incubated at room temperature for 2 hours (or at 4°C overnight). Serial five-fold dilutions in Working buffer starting at 50 to 250 μM were made of the following samples: Xceptor TNFRSF1B::anti-HIL6 samples, positive controls Enbrel® (etanercept) and anti-TNF-α (R&D Systems), and negative controls human gp130-Fc chimera (R&D Systems) and human IgG. Equal volumes of the serially diluted Xceptor samples were mixed with TNF-α (final TNF-α concentration of 2.5 ng/ml) and incubated at room temperature for 1 hour. After washing the plate three times with PBS-T, added in duplicate wells to the recombinant human TNFR2-Fc coated plate was 100 μl/well of the serially dilutions of Xceptor / TNF-α mixture, Enbrel® (etanercept), anti-TNF-α, human gp130-Fc chimera, and human IgG, the plate was covered, and incubated at room temperature for about 1.5 hours. After washing the plate five times with PBS-T, 100 μL per well of anti-human TNF-α-biotin (R&D Systems) from a 200 ng/ml solution in

Working buffer was added, the plate was covered, and incubated at room temperature for 1 to 2 hours. After washing the plate five times with PBS-T, 100 µL per well horse radish peroxidase-conjugated streptavidin (Jackson ImmunoResearch, West Grove, PA) diluted 1:1,000 in Working buffer was added, the plate was covered, and incubated at room temperature for 30 minutes. After washing the plate six times with PBS-T, 100 µL per well 3,3,5,5-tetramentylbenzidine (TMB) substrate solution (Pierce, Rockford, IL) was added for about 3 to 5 minutes and then the reaction was stopped with 50 µl Stop buffer (1N H_2SO_4) per well. The absorbance of each well was read at 450 nm.

[00245] The data in Figure 6 show that Xceptor proteins blocked TNF-α binding to TNF receptor, which was approximately equivalent to blocking by TNFR-Fc.

EXAMPLE 8

XCEPTOR BLOCKING OF TNF-α INDUCED CELL KILLING

[00246] Blocking of TNF-α induced killing of L929 cells was examined for Xceptor fusion proteins TRU(XT6)-1011, 1014, 1025, 1026, 1002, and TRU(X6T)-1019 (SEQ ID NO:617, 620, 631, 632, 608 and 670, respectively), substantially as follows.

[00247] A suspension of L929 mouse fibroblast cells (ATCC, Manassas, VA) was prepared at a density of 2 x 10^5 cells/ml in culture medium (10% FBS-RPMI 1640; 2 mM L-glutamine; 100 units/ml penicillin; 100 µg/ml streptomycin; and 10 mM HEPES), then 100 µl was added to each well of a 96-well flat bottom black plate and incubated overnight at 37°C, 5% CO_2 in a humidified incubator. Xceptor TNFRSF1B::anti-HIL6 samples serially diluted in assay medium (same as culture medium but supplemented with 2% FBS) were mixed with an equal volume of recombinant human TNF-α (rhTNF-α; R&D Systems, Minneapolis, MN), and incubated at 37°C, 5% CO_2 in a humidified incubator for 1 hour. Positive controls (*i.e.*, those agents that block TNF-α induced killing of L929 cells) included Enbrel® (etanercept), rhTNFR2-Fc chimera (R&D Systems, Minneapolis, MN), and anti-TNF-α antibody (R&D Systems, Minneapolis, MN). Negative controls included assay medium alone (no TNF-α added) and antibody hIgG (with TNF-α added). To analyze TNF-α activity, culture medium was removed from the L929 cells and then each well received 50 µl of a TNF-α/Xceptor or control mixture, and 50 µl actinomycin D (Sigma-Aldrich, St. Louis, MO) (from a freshly prepared working solution of 4 µg/ml). The cells were then incubated for 24 hrs at 37°C, 5% CO_2 in a humidified incubator. To measure cell viability, added to each well was 100µl ATPlite 1 Step Reagent (PerkinElmer, Waltham, MA) according to the manufacturer's

instructions, shaken for two minutes, and then luminescence is measured using a TopCount reader (Packard).

[00248] The data in Figure 9 demonstrate that all Xceptor proteins, whether the TNFRSF1B ectodomain was on the amino- or carboxy terminus of the fusion protein molecules, can block TNF-α induced cell killing in this assay.

EXAMPLE 9

XCEPTOR BINDING TO TGFβ BY ELISA

[00249] TGFβ binding activity was examined for Xceptors X6B and XB6, substantially as follows.

[00250] Added to each well of a 96-well plate was 100 µl goat anti-human IgG-Fc (ICN Pharmaceuticals, Costa Mesa, CA) from a 2 µg/ml solution in PBS, pH 7.2-7.4. The plate was covered, and incubated overnight at 4°C. After washing four times with PBS-T, 250 µl Blocking buffer (PBS-T with 10% NGS) was added to each well, the plate was covered, and incubated at room temperature for 2 hours. After washing the plate three times with PBS-T, added in duplicate wells to the anti-human IgG-Fc coated plate was 100 µl/well Xceptor TGFβR2::anti-HIL6 samples, positive control recombinant human TGFβRII-Fc chimera (R&D Systems, Minneapolis, MN), and negative control recombinant human TNFR2 (TNFRSF1B)-Fc chimera (R&D Systems), each diluted to 300ng/ml in Working buffer (PBS-T with 1% BSA). The plate was covered, and incubated at room temperature for about 1 hour. After washing the plate five times with Wash buffer (PBS/0.1% Tween 20 (PBS-T)), added was 100 µl/well TGFβ-1 ligand (R&D Systems), serially diluted two-fold in Working buffer starting at 4 ng/ml. The plate was covered, and incubated at room temperature for 1 hour. After washing the plate five times with Wash buffer, added was 100 µl/well biotinylated anti-TGFβ-1 (R&D Systems) from a 200 ng/ml solution in Working buffer. The plate was covered and incubated at room temperature for 1 hour. After washing the plate five times with Wash buffer, 100 µl per well horse radish peroxidase-conjugated streptavidin (Pierce Rockford, IL) diluted 1:20,000 in Working buffer was added, the plate was covered, and incubated at room temperature for 30 minutes. After washing the plate five times with Wash buffer, 100 µl per well QuantaBlu Fluorogenic Peroxidase Substrate solution (Pierce, Rockford, IL; prepared by mixing 9 ml substrate solution with 1 ml peroxide solution) was added, and the plate was covered and incubated at room temperature for 20

min. The reaction was stopped with 50 µl QuantaBlu Stop Solution per well. The absorbance of each well was read at 325 nm.

[00251] The data in Figure 8 shows that the Xceptor fusion proteins tested bound TGFβ-1, whether the TGFβR2 ectodomain was on the amino- or carboxy terminus of the fusion protein.

EXAMPLE 10

EXPRESSION OF XCEPTOR FUSION PROTEINS

[00252] Expression of certain of the Xceptor fusion proteins disclosed herein in 293 cells was performed using the FreeStyle™ 293 Expression System (Invitrogen, Carlsbad, CA) according to the manufacturer's instructions.

[00253] For each 30 ml transfection, 3 x 10^7 cells in 28 ml of FreeStyle™ 293 Expression Medium were used. On the day of transfection, a small aliquot of the cell suspension was transferred to a microcentrifuge tube, and the viability and the amount of cell clumping determined using the trypan blue dye exclusion method. The suspension was vigorously vortexed for 45 seconds to break up cell clumps and total cell counts determined using a Coulter Counter or a hemacytometer. The viability of the cells was over 90%. A shaker flask containing the required cells was placed in a 37°C incubator on an orbital shaker.

[00254] For each transfection sample, lipid-DNA complexes were prepared as follows. 30 µg of plasmid DNA was diluted in Opti-MEM® I to a total volume of 1 ml and mixed gently. 60 µl of 293fectin™ was diluted in Opti-MEM® I to a total volume of 1 ml, mixed gently, and incubated for 5 minutes at room temperature. After the 5 minute incubation, the diluted DNA was added to the diluted 293fectin™ to obtain a total volume of 2 ml and mixed gently. The resulting solution was incubated for 20-30 minutes at room temperature to allow DNA- 293fectin™ complexes to form.

[00255] While the DNA-293fectin™ complexes were incubating, the cell suspension was removed from the incubator and the appropriate volume of cell suspension was placed in a sterile, disposable 125 ml Erlenmeyer shaker flasks. Fresh, pre-warmed FreeStyle™ 293 Expression Medium was added up to a total volume of 28 ml for a 30 ml transfection.

[00256] After the DNA-293fectin™ complex incubation was complete, 2 ml of DNA-293fectin™ complex was added to the shaker flasks. 2 ml of Opti-MEM® I was added to the negative control flask, instead of DNA-293fectin™ complex. Each flask contained a total volume of 30 ml, with a final cell density of approximately 1 x 10^6 viable cells/ml. The

cells were incubated in a 37°C incubator with a humidified atmosphere of 8% CO_2 in air on an orbital shaker rotating at 125 rpm. Cells were harvested at approximately 7 days post-transfection and assayed for recombinant protein expression.

[00257] Xceptor molecules having a TNFRSF1B ectodomain and a TGFβRII ectodomain were expressed in 293 cells as described above.

EXAMPLE 11

XCEPTOR BINDING TO LIGANDS BY ELISA

[00258] The ability of xceptor molecules comprising a TNFRSF1B ectodomain and either a TWEAKR ectodomain, an OPG ectodomain, a TGFβRII ectodomain or an IL7R ectodomain to bind to the ligands TWEAK, RANKL, TGFβ or IL7, respectively, was examined substantially as follows.

[00259] Mouse and human ligands (R&D Systems, Minnesota, MN) were added to wells of a 96-well plate at a concentration of 1μg/ml in PBS (100 μL/well). Plates were incubated at 4°C overnight. After washing five times with PBS-T, 250 μL Blocking Buffer (PBS-T with 3% BSA) was added to each well, and the plate covered and incubated at room temperature (RT) for 2 hours. Serial three fold dilutions of xceptors were made in Working Buffer (PBS-T with 1% BSA) starting at 300ng/ml. As a negative control, an irrelevant xceptor was used. The plate was incubated at RT for 1 hour. After washing five times with PBS-T, 100 μL per well of HRP-conjugated anti-human IgG-Fc (1:5000 in Working buffer) was added, the plate covered, and incubated at RT for 1 hour. After washing five times with PBS-T, 100 μL of Quant-Blu substrate (Pierce, Rockford, IL) was added to each well. The plate was incubated at RT for 10-30 minutes, and fluorescence measured at 325/420nm.

[00260] The results are shown in Table 3 below. The binding of the TNFRxTGFβRII to mouse TGFβ was not tested, however it is noted that mouse and human TGFβ are 99% identical.

Table 3. Xceptor binding to Ligands

TNFR x R	Ligand	Mouse ligand binding	Human ligand binding
TNFR x TWEAKR	TWEAK	+++	+++
TNFR x OPG	RANKL	+++	+++
TNFR x TGFβRII	TGFβ	homologous	+++
TNFR x IL7R	IL7	ND	+

ND = Not Done

EXAMPLE 12

XCEPTOR BLOCKING OF TGFβ-1-INDUCED INHIBITION OF CELL PROLIFERATION

[00261] Blocking of TGFβ-1 induced inhibition of IL-4 proliferation of HT2 cells was examined for the Xceptor of SEQ ID NO:1236 using the method described by Tsang et al. (Tsang, M. et al. (1995) Cytokine 7:389).

[00262] Briefly, in a 96 well plate, Xceptor TNFR::TGFβRII samples were serially diluted in culture medium (RPMI, 10% FCS, 0.05 mM beta-mercaptoethanol) containing 1 ng/ml of human TGFβ-1; 100 ul per well. The plate was incubated at 37° C, 5% CO_2 in a humidified incubator for 1.5 hours. Negative controls included an irrelevant xceptor protein (with TGFβ-1 added) and culture medium (with and without TGFβ-1 added). The positive control was a recombinant TGFβRII-Fc chimera (R&D Systems, Minneapolis, MN). Following incubation, $1x10^4$ HT2 cells (ATCC, Manassas, VA) in 100 ul of culture medium containing 15 ng/ml mIL4 (R&D Systems, Minneapolis, MN) was added to each well. The plate was then incubated at 37°C, 5% CO_2 in a humidified incubator for 72 hours.

[00263] To analyze TGFβ-1 activity by measuring cell viability, 100 ul of culture medium was removed from each well and replaced with 10 μL WST-8 reagent (Dojindo Molecular Technologies, Rockville, MD). The plate was incubated for 2 hours at 37°C, and absorbance for each well read at 450nM.

[00264] The data in Figure 9 shows that the xceptor protein blocked TGFβ-1 inhibition of IL4-mediated proliferation of HT2 cells.

EXAMPLE 13

SPECIFICITY OF BINDING TO HYPER IL6 AND NOT OTHER GP130 CYTOKINES

[00265] The effect of Xceptor fusion proteins on induction of TF-1 cell proliferation by IL6 and the gp130 cytokines IL-11, leukemia inhibitory factor (LIF), oncostatin M (OSM) and cardiotrophin-1 (CT-1) was examined substantially as follows.

[00266] Added to each well of a 96-well flat bottom plate was $0.3x10^6$ TF-1 cells (human erythroleukemia cells) in fresh growth medium (10% FBS-RPMI 1640, 2mM L-glutamine, 100 units/ml penicillin, 100 μg/ml streptomycin, 10 mM HEPES, 1mM sodium pyruvate and 2 ng/ml Hu GM-CSF) one day before use in the proliferation assay. The cells

were harvested and washed twice with assay medium (same as growth medium except without GM-CSF, cytokine-free), then resuspended at 1 x 10^5 cells/ml in assay medium. For examining blocking of LIF, OSM, and CT-1 activity, serial dilutions of a TNFSFR1B::anti-HIL-6 xceptors TRU(XT6)-1002 (SEQ ID NO:608), TRU(XT6)-1019 (SEQ ID NO:625), TRU(XT6)-1022 (SEQ ID NO:628), and TRU(XT6)-1025 (SEQ ID NO:631) were pre-incubated with a fixed concentration of each gp130 cytokine individually or hyper IL-6 (HIL-6) in 96-well plates for 1 hour at 37°C, 5% CO_2. After the pre-incubation period, 1x10^4 cells (in 100 µl) were added to each well. The final assay mixture, in a total volume of 200 µL/well, containing TNFSFR1B::HIL-6, gp130 cytokine or HIL-6 and cells, was incubated at 37°C, 5% CO_2 for 72 hours. During the last 4-6 hours of culture, ^{3}H-thymidine (20 µCi/ml in assay medium, 25 µL/well) was added. The cells were harvested onto UniFilter-96 GF/c plates and incorporated ^{3}H-Thymidine was determined using TopCount reader (Packard). The percentage of blocking = 100 - (test cpm – control cpm /maximum cpm- control cpm)*100.

[00267] The results showed that the xceptor blocked IL6 activity but not IL-11, LIF, OSM or CT-1 (data not shown), and therefore bound to hyper IL6 but had no effect on the other gp130 cytokines tested.

EXAMPLE 14

SMIP AND XCEPTOR BINDING TO IL6R ON LIVER CELLS

[00268] The ability of TRU(S6)-1002, TRU(XT6)-1019 and the anti-IL6 antibody hu-PM1 to bind to IL6R on the liver-derived HepG2 cells was examined as follows.

[00269] HepG2 cells were washed in FACS Buffer and adjusted to 2 x 10^6 cells/mL in FACS Buffer (PBS + 3% FBS). To wells of a 96-well plate were added 50 µL of this solution (10^5 cells/well). The plates were held at 37°C until ready to add diluted test molecules. Serial dilutions of the test molecules were prepared in FACS Buffer to give a 2X working stock which was diluted to 1X when added to cells. The diluted test molecules were added to cells (50 µL/well) and the cells incubated for 20 min on ice. Whole IgG was used as a control. The cells were then washed two times with FACS Buffer and resuspended in phycoerythrin-conjugated goat anti-human antibody (Jackson Labs; diluted 1:200 in FACS Buffer). After being incubated for 20 min on ice in the dark, the cells were washed two times with FACS buffer, resuspended in 200ul PBS and read on a LSRII™ flow cytometer (BD Biosciences, San Jose, CA).

[00270] As shown in Fig. 10, TRU(S6)-1002 and TRU(XT6)-1029 showed essentially no binding to HepG2 cells.

EXAMPLE 15

SMIP AND XCEPTOR BLOCKING OF IL-6 AND TNF ACTIVITY IN MICE

[00271] The ability of SMIP and Xceptor fusion proteins disclosed herein to block IL-6 or TNF-induced production of serum amyloid A (SAA) protein in mice was examined as described below. SAA is one of the major acute-phase proteins in humans and mice. Prolonged elevation of plasma SAA levels is found in chronic inflammation and leads to amyloidosis which affects the liver, kidney and spleen (Rienhoff et al., (1990) Mol. Biol. Med. 7:287). Both IL-6 and TNF have been shown to induce SAA when administered alone (Benigni et al., (1996) Blood 87:1851; Ramadori et al., (1988) Eur. J. Immunol. 18:1259).

(a) Blocking of hyperIL-6 activity

[00272] Female BALB/C mice were injected retro-orbitally with 0.2 ml PBS, or Enbrel® (200 ug), TRU(S6)-1002 (200 ug) or TRU(XT6)-1002 (300 ug or 500ug) in PBS. One hour later, the mice were injected IP with 0.2 ml PBS or 2 μg human hyper-IL6 in PBS. Mouse serum was collected at 2 hours and 24 hours after the IP injection. The serum concentration of SAA was determined by ELISA, and concentration of sgp130 was determined by a Luminex-based mouse soluble receptor assay. As shown in Figs. 11 and 12, TRU(S6)-1002 and TRU(XT6)-1002 blocked hyperIL6-induced expression of both sgp130 and SAA.

(b) Blocking of TNF activity

[00273] Female BALB/C mice were injected retro-orbitally with 0.2 ml PBS, or Enbrel® (200 μg), TRU(S6)-1002 (200 μg) or TRU(XT6)-1002 (300 μg) in PBS. One hour later, the mice were injected IP with 0.2 ml PBS or 0.5 ug mouse TNF-α in PBS. Mouse serum was collected at 2 hours and 24 hours after the IP injection. The serum concentration of SAA was determined by ELISA, and concentration of sgp130 was determined by a Luminex-based mouse soluble receptor assay. As shown in Figs. 13A and B, the Xceptor TRU(XT6)-1002 blocked TNFα-induced expression of SAA, with the level of SAA observed at 2 hours post-injection being similar to that seen with Enbrel®.

EXAMPLE 16

XCEPTOR ACTIVITY *IN VIVO*

[00274] The therapeutic efficacy of Xceptor molecules described herein is examined in animal models of disease as described below.

(a) Multiple Myeloma

[00275] The activity of Xceptor molecules is examined in at least one of two well characterized mouse models of multiple myeloma, namely the 5T2 multiple myeloma (5T2MM) model and the 5T33 multiple myeloma (5T33MM) model. In the 5T33 model, mice are treated with Xceptors from the time of injection of tumor cells (prophylactic mode). In the 5T2MM model, mice are treated from the onset of the disease (therapeutic mode). The effect of treatment on tumor development and angiogenesis is assessed in both models, with bone studies also being performed in the 5T2MM model.

[00276] The 5TMM murine model of myeloma was initially developed by Radl et al. (J. Immunol. (1979) 122:609; *see also* Radl et al. Am. J. Pathol. (1988) 132:593; Radl J. Immunol. Today (1990) 11:234). Its clinical characteristics resemble the human disease closely: the tumor cells are located in the bone marrow, the serum paraprotein concentration is a measure of disease development, neovascularization is increased in both the 5T2MM and 5T33MM models (Van Valckenborgh et al., Am. J. Pathol. (1988) 132:593), and in certain lines a clear osteolytic bone disease develops. The 5T2MM model includes moderate tumor growth and the development of osteolytic bone lesions. These lesions are associated with a decrease in cancellous bone volume, decreased bone mineral density and increased numbers of osteoclasts (Croucher et al., Blood (2001) 98:3534). The 5T33MM model has a more rapid tumor take and, in addition to the bone marrow, tumor cells also grow in the liver (Vanderkerken et al., Br. J. Cancer (1997) 76:451).

[00277] The 5T2 and 5T33MM models have been extensively characterized. Specific monoclonal antibodies have been raised against the idiotype of both 5T2 and 5T33MM allowing the detection, with great sensitivity, of the serum paraprotein by ELISA, and the specific staining of the tumor cells both by FACS analysis and immunostaining of histological sections (Vanderkerken et al., Br. J. Cancer (1997) 76:451). The sequence analysis of the VH gene enables the detection of cells by RT-PCR and Northern blot analysis (Zhu et al., Immunol. (1998) 93:162). The 5TMM models, which can be used for both *in vitro* and *in vivo* experiments, generate a typical MM disease and different methods are

available to assess tumor load in the bone marrow, serum paraprotein concentrations, bone marrow angiogenesis (by measuring the microvessel density) and osteolytic bone lesions (by a combination of radiography, densitometry and histomorphometry). The investigation of these latter parameters allow the use of the 5TMM models in a preclinical setting and study of the growth and biology of the myeloma cells in a complete syngeneic microenvironment. Both molecules targeting the MM cells themselves and molecules targeting the bone marrow microenvironment can be studied. Specifically, while the 5T33MM model can be used to study both the microenvironment and the MM cells themselves, the 5T2MM model can also be used to study the myeloma associated bone disease.

[00278] To study the prophylactic efficacy of the Xceptor molecules disclosed herein, C57BL/KaLwRij mice are injected with 2 x 10^6 5T33 MM cells and with Xceptor on day 0. Mice are sacrificed at day 28 and tumor development is assessed by determining serum paraprotein concentration and the percentage of tumor cells on isolated bone marrow cells (determined by flow cytometry with anti-idiotype antibodies or by cytosmears). The weight of spleen and liver is determined and these organs are fixed in 4% formaldehyde for further analysis. Bone samples are fixed for further processing including CD31 immunostaining on paraffin sections and quantification of microvessel density.

[00279] To study the therapeutic efficacy of the Xceptor molecules disclosed herein, mice are injected with 5T2MM cells on day 0, and Xceptor is administered following the onset of disease, as determined by the presence of detectable levels of serum paraprotein. Mice are sacrificed approximately five weeks following administration of Xceptor, and tumor development is assessed as described above for the prophylactic study. In addition, bone analysis is performed using X-rays to determine the number of bone lesions and trabecular bone area, and TRAP staining to assess the number of osteoclasts.

(b) Rheumatoid Arthritis

[00280] The therapeutic efficacy of the Xceptor molecules disclosed herein is examined in at least one of two murine models of rheumatoid arthritis (RA), namely the collagen induced arthritis (CIA) and glucose-6-phosphate isomerase (G6PI) models. Each of these models has been shown by others to be useful for predicting efficacy of certain classes of therapeutic drugs in RA (*see* Holmdahl (2000) Arthritis Res. 2:169; Holmdahl (2006) Immunol. Lett. 103:86; Holmdahl (2007) Methods Mol. Med. 136:185; McDevitt (2000) Arthritis Res. 2:85; Kamradt and Schubert (2005) Arthritis Res. Ther. 7:20).

(i) CIA Model

[00281] The CIA model is the best characterized mouse model of arthritis in terms of its pathogenesis and immunological basis. In addition, it is the most widely used model of RA and, although not perfect for predicting the ability of drugs to inhibit disease in patients, is considered by many to be the model of choice when investigating potential new therapeutics for RA (Jirholt, J. et al. (2001) Arthritis Res. 3:87-97; Van den Berg, W.B. (2002) Curr. Rheumatol. Rep. 4:232-239; Rosloniec, E. (2003) Collagen-Induced Arthritis. In Current Protocols in Immunology, eds. Coligan et al., John Wiley & Sons, Inc, Hoboken, NJ).

[00282] In the CIA model, arthritis is induced by immunization of male DBA/1 mice with collagen II (CII) in Complete Freund's Adjuvant (CFA). Specifically, mice are injected intradermally/ subcutaneously with CII in CFA on Day -21 and boosted with CII in Incomplete Freund's Adjuvant (IFA) on Day 0. Mice develop clinical signs of arthritis within days of the boost with CII/IFA. A subset of mice (0% to 10%) immunized with CII/CFA develop signs of arthritis on or around Day 0 without a boost and are excluded from the experiments. In some CIA experiments, the boost is omitted and mice are instead treated with Xceptor or control starting 21 days after immunization with CII/CFA (i.e. the day of first treatment is Day 0).

[00283] Mice are treated with Xceptor, vehicle (PBS), or negative or positive control in a preventative and/or therapeutic regimen. Preventative treatment starts on Day 0 and continues through the peak of disease in control (untreated) mice. Therapeutic treatment starts when the majority of mice show mild signs of arthritis. Enbrel®, which has been shown to have good efficacy in both the CIA and G6PI-induced models of arthritis, is used as a positive control. Data collected in every experiment includes clinical scores and cumulative incidence of arthritis. Clinical signs of arthritis in the CIA model are scored using a scale from 0 to 4 as shown in Table 4 below:

Table 4.

Score	Observations
0	No apparent swelling or redness
1	Swelling/redness in one to three digits
2	Redness and/or swelling in more than three digits, mild swelling extending into the paw, swollen or red ankle, or mild swelling/redness of forepaw
3	Swollen paw with mild to moderate redness
4	Extreme redness and swelling in entire paw

(ii) G6PI Model

[00284] In the G6PI model, arthritis is induced by immunization of DBA/1 mice with G6PI in adjuvant (Kamradt, T. and D. Schubert (2005) Arthritis Res. Ther. 7:20-28; Schubert, D. et al. (2004) J. Immunol. 172:4503-4509; Bockermann, R. et al. (2005) Arthritis Res. Ther. 7:R1316-1324; Iwanami, K. et al. (2008) Arthritis Rheum. 58:754-763; Matsumoto, I. et al. (2008) Arthritis Res. Ther. 10:R66). G6PI is an enzyme present in virtually all cells in the body and it is not known why immunization induces a joint specific disease. A number of agents, such as CTLA4-Ig, TNF antagonists (e.g. Enbrel®) and anti-IL6 receptor monoclonal antibody, have been shown to inhibit development of arthritis in the G6PI model.

[00285] Male DBA/1 mice are immunized with G6PI in Complete Freund's Adjuvant (CFA) in order to induce arthritis. Specifically, mice are injected intradermally/subcutaneously with G6PI in CFA on Day 0 and develop clinical signs of arthritis within days of the immunization. As with the CIA model discussed above, mice are treated with Xceptor, vehicle (PBS), or negative or positive control in a preventative and/or therapeutic regimen. Preventative treatment starts on Day 0 and continues through the peak of disease in control mice. Therapeutic treatment starts when the majority of mice show mild signs of arthritis. Enbrel®, which has been shown to have good efficacy in both the CIA and G6PI-induced models of arthritis, is used as a positive control. Data collected in every experiment includes clinical scores and cumulative incidence of arthritis. Clinical signs of arthritis in the G6PI model are scored using a scale similar to that employed for the CIA model.

(c) Polycystic Kidney Disease

[00286] The efficacy of an xceptor fusion protein (preferably containing a TNF antagonist and a TGFβ antagonist, as disclosed herein) in the treatment of polycystic kidney disease is tested in murine models as described in Gattone et al., Nat. Med. (2003) 9:1323-6; Torres et al. Nat. Med. (2004) 10:363-4; Wang et al. J. Am. Soc. Nephrol. (2005) 16:846-851; and Wilson (2008) Curr. Top. Dev. Biol. 84:311-50.

[00287] SEQ ID NOS:1-1255 are set out in the attached Sequence Listing. The codes for nucleotide sequences used in the attached Sequence Listing, including the symbol "n," conform to WIPO Standard ST.25 (1998), Appendix 2, Table 1.

CLAIMS

We claim:

1. A multi-specific fusion protein having one of the following structures from amino terminus to carboxy terminus:

(a) BD-ID-ED;

(b) ED-ID-BD; or

(c) ED1-ID-ED2

wherein:

ED is a TGFβ antagonist and ED1 and ED2 are different antagonists wherein ED1 or ED2 is a TGFβ antagonist;

ID is an intervening domain; and

BD is a TNF antagonist, IL6 antagonist, IL10 antagonist, VEGF antagonist, HGF antagonist, IGF antagonist, or a GITR agonist.

2. The multi-specific fusion protein of claim 1, wherein the binding domain is an immunoglobulin variable binding domain.

3. The multi-specific fusion protein of claim 1 or 2, wherein the ectodomain is a receptor ligand binding domain.

4. The multi-specific fusion protein of any of the preceding claims, wherein the intervening domain has the following structure:

-L1-CH2CH3-,

wherein:

L1 is an immunoglobulin hinge linker, optionally an IgG1 hinge having the first cysteine substituted with a different amino acid;

-CH2CH3- is the CH2CH3 region of an IgG1 Fc domain, optionally mutated to eliminate FcγRI-III interaction while retaining FcRn interaction.

5. The multi-specific fusion protein of any of the preceding claims, wherein the BD is connected to the intervening domain by a first linker and the ED is connected to the intervening domain by a second linker and wherein the first and second linkers may be the same or different.

6. The multi-specific fusion protein of claim 5, wherein the first and second linkers are selected from SEQ ID NO:497-604 and 1223-1228, optionally wherein the first linker is SEQ ID NO:576 and the second linker is SEQ ID NO:1223.

7. The multi-specific fusion protein of any of the preceding claims, comprising an amino acid sequence as set forth in any one of SEQ ID NOS:735-742.

8. A composition comprising one or more multi-specific fusion proteins according to any of the preceding claims and a pharmaceutically acceptable carrier, diluent, or excipient.

9. A composition of claim 8 wherein the multi-specific fusion protein exists as a dimer or a multimer in the composition.

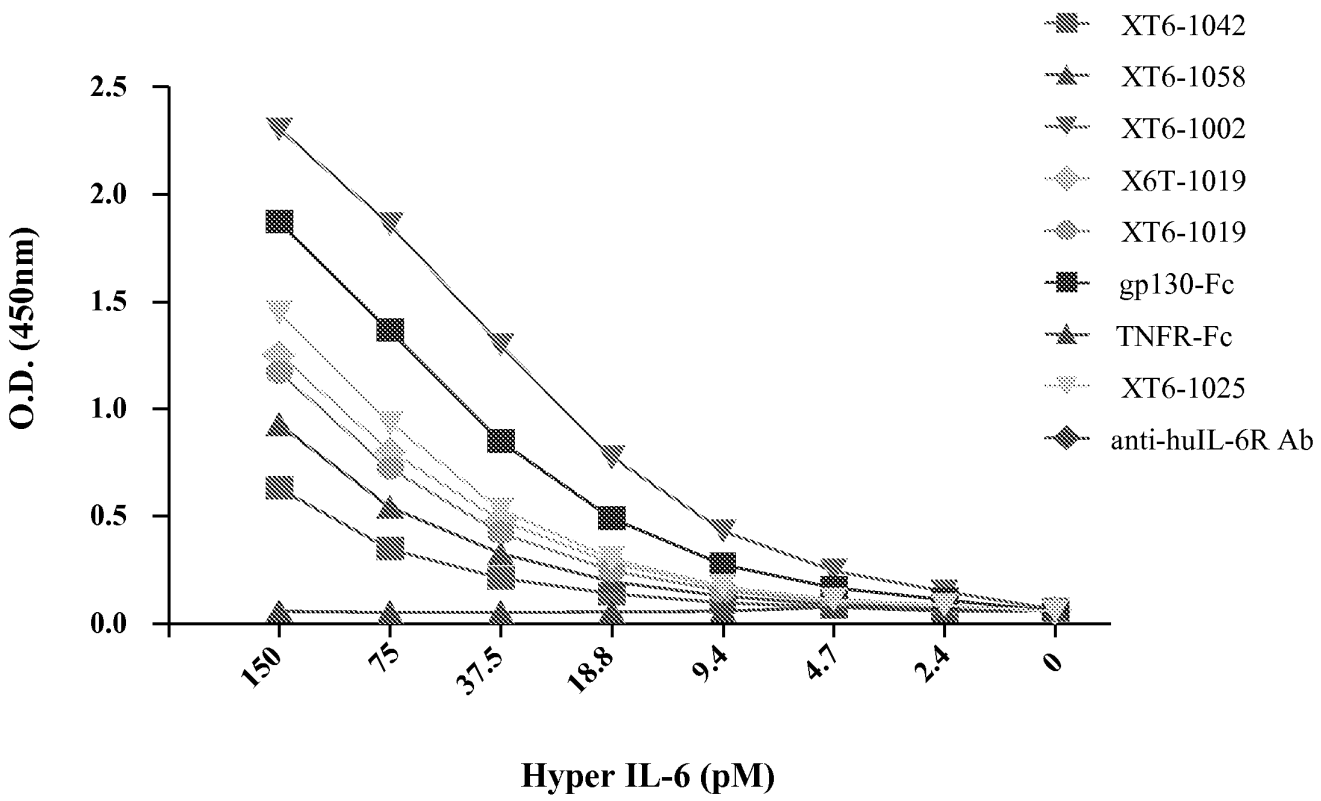
10. A polynucleotide encoding a multi-specific fusion protein according to any one of claims 1-7.

11. An expression vector comprising a polynucleotide according to claim 10 operably linked to an expression control sequence.

12. A host cell comprising an expression vector according to claim 11.

13. A method for treating a subject with a malignant condition comprising the administration of a therapeutically effective amount of a multi-specific fusion protein or composition thereof of any of the preceding claims.

14. The method of claim 13 wherein the malignant condition is breast cancer, renal cell carcinoma, melanoma or prostate cancer.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XT6-1058
XT6-1002
X6T-1019
XT6-1019
gp130-Fc
TNFR-Fc
XT6-1025
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O.D. (450nm)
2.5
2.0
1.5
1.0
0.5
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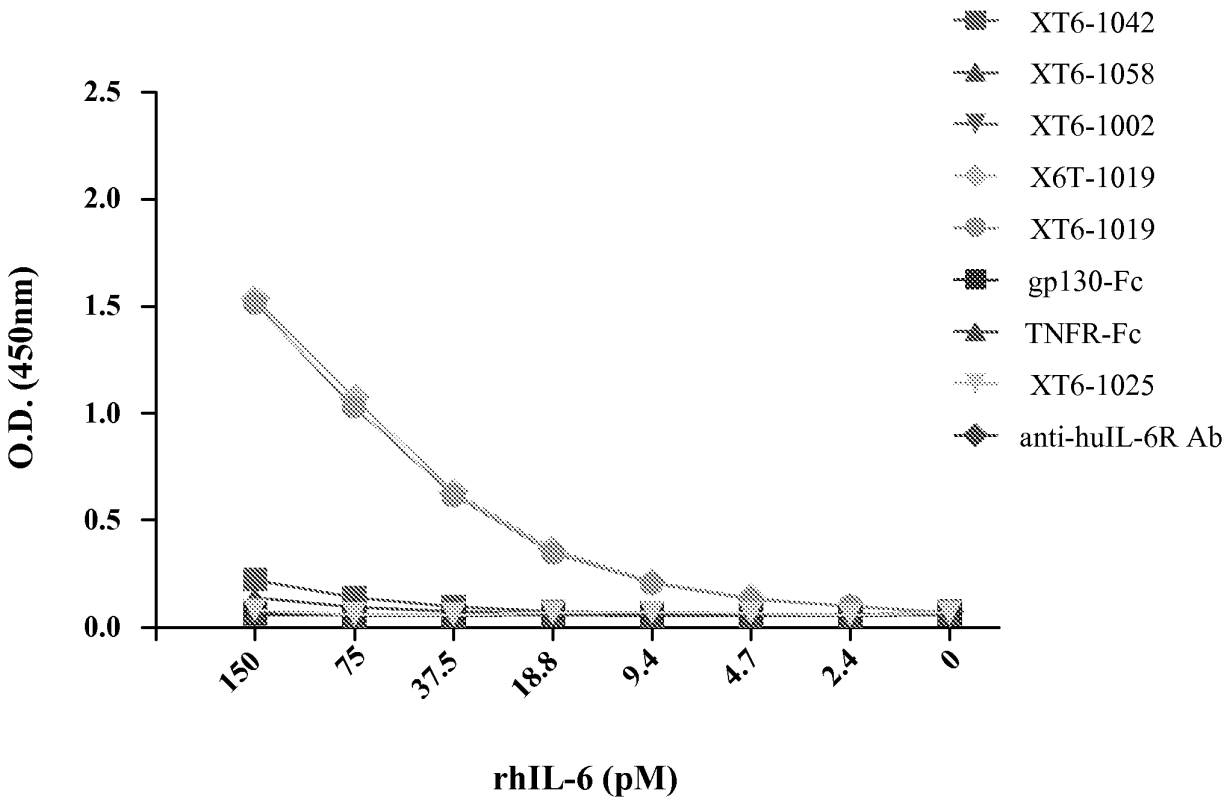
75
37.5
18.8
9.4
4.7
2.4
0
Hyper IL-6 (pM)

Fig. 1A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gp130-Fc
TNFR-Fc
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anti-huIL-6R Ab
O.D. (450nm)
2.5
2.0
1.5
1.0
0.5
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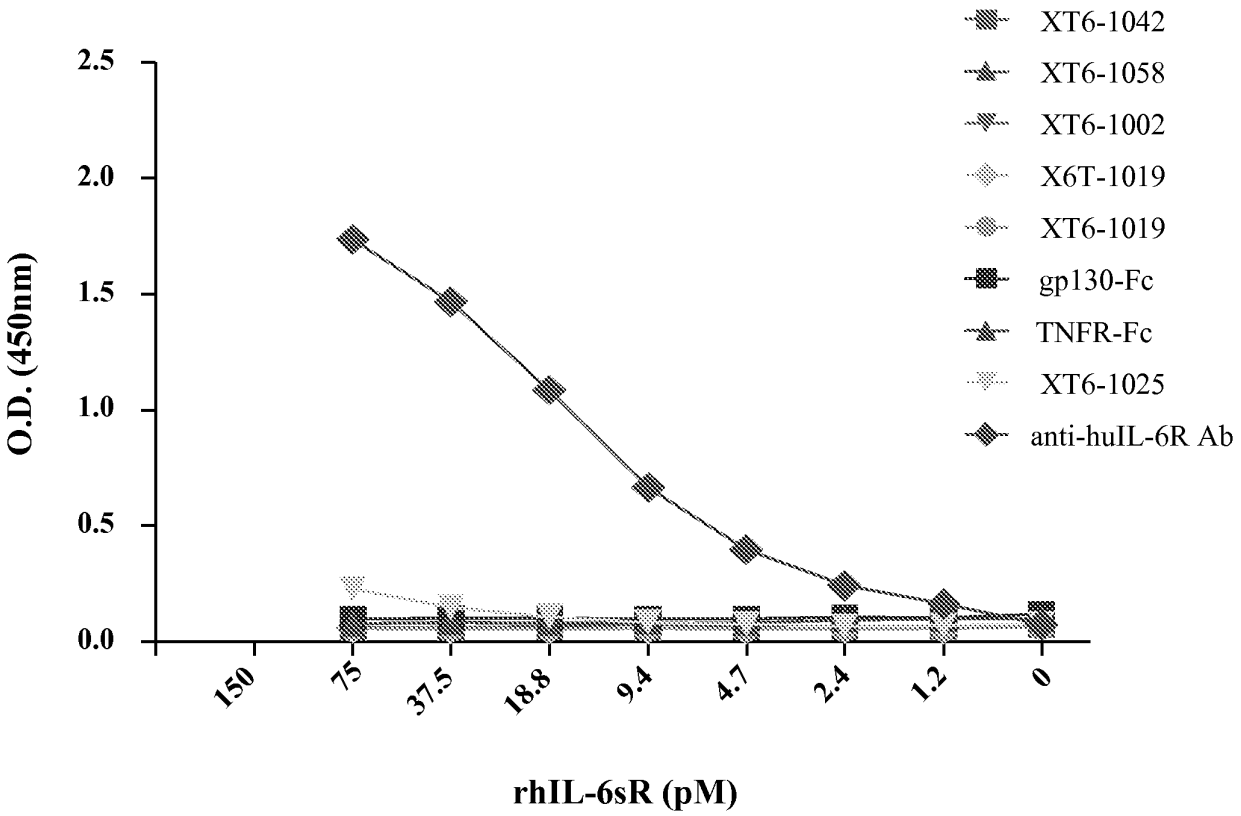
150
75
37.5
18.8
9.4
4.7
2.4
0
rhIL-6 (pM)

Fig. 1B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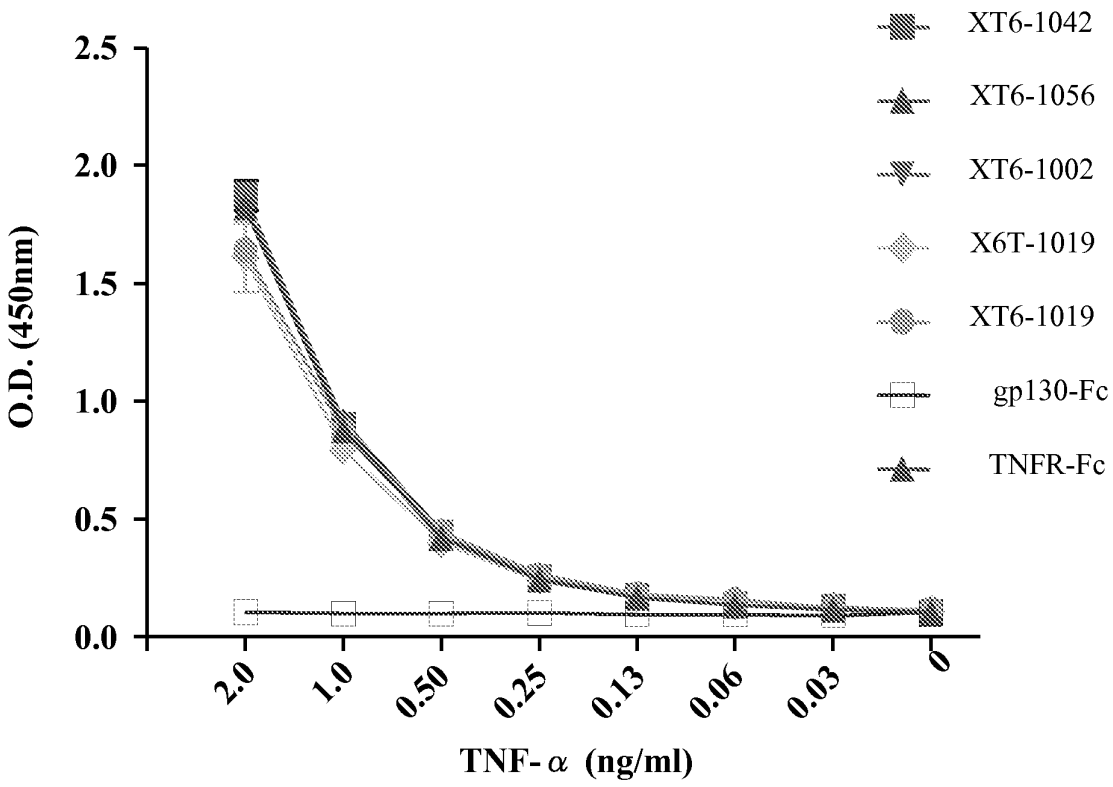
XT6-1058
XT6-1002
X6T-1019
XT6-1019
gp130-Fc
TNFR-Fc
XT6-1025
anti-huIL-6R Ab
O.D. (450nm)
2.5
2.0
1.5
1.0
0.5
0.0
150
75
37.5
18.8
9.4
4.7
2.4
1.2
0
rhIL-6sR (pM)

Fig. 1C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X6T-1019
XT6-1019
gp130-Fc
TNFR-Fc
O.D. (450nm)
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2.0
1.5
1.0
0.5
0.0
2.0
1.0
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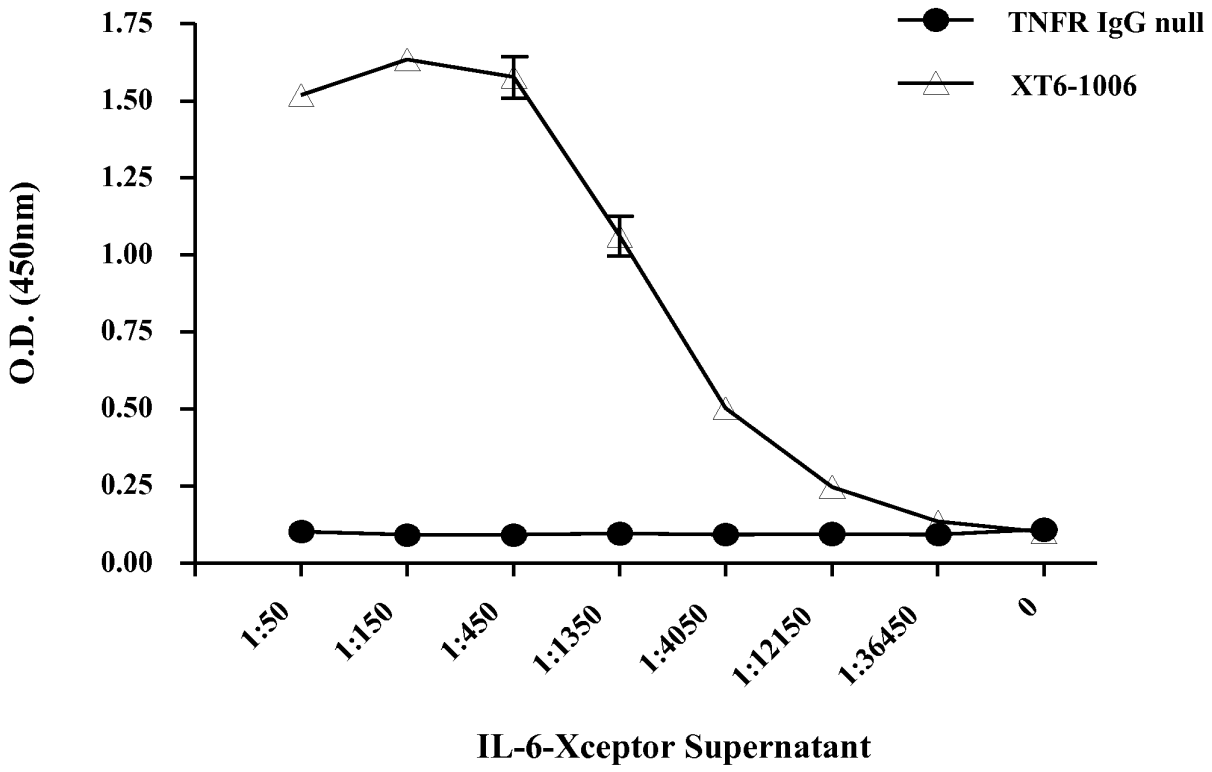
0.06
0.03
0
TNF-α (ng/ml)

Fig. 2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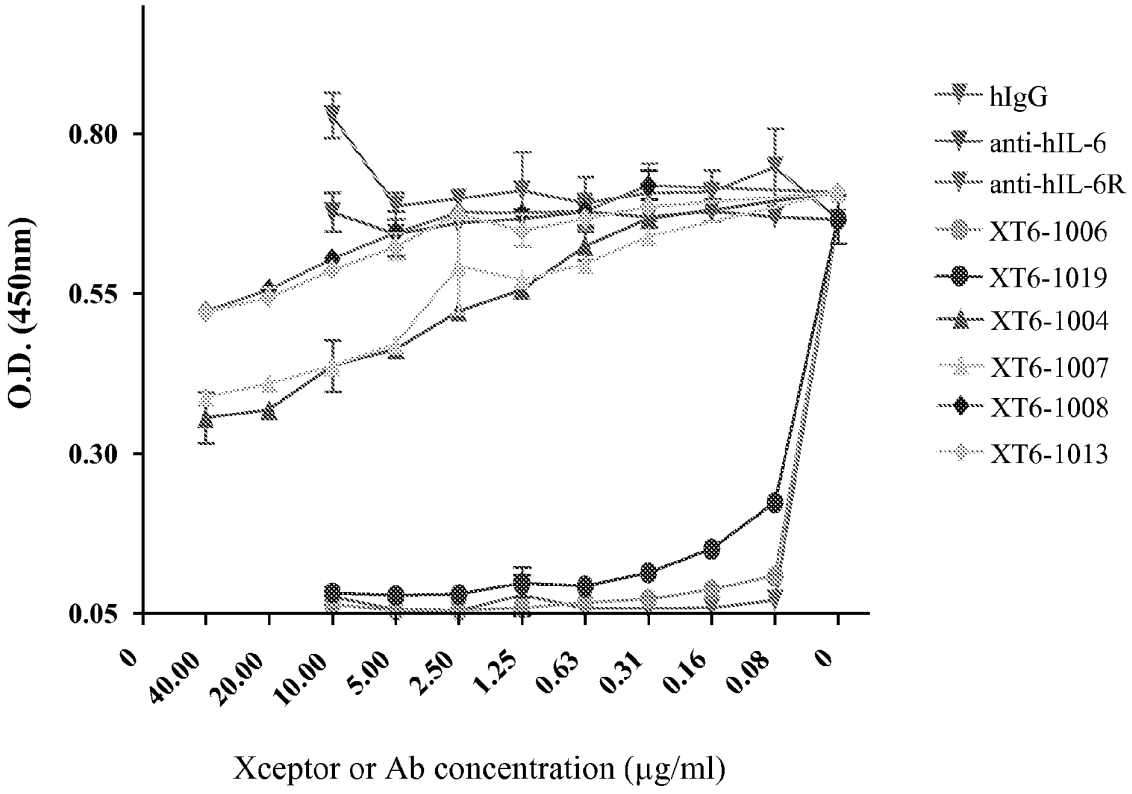
1.50
1.25
1.00
0.75
0.50
0.25
0.00
1:50
1:150
1:450
1:1350
1:4050
1:12150
1:36450
0
IL-6-Xceptor Supernatant

Fig. 3


O.D. (450nm)
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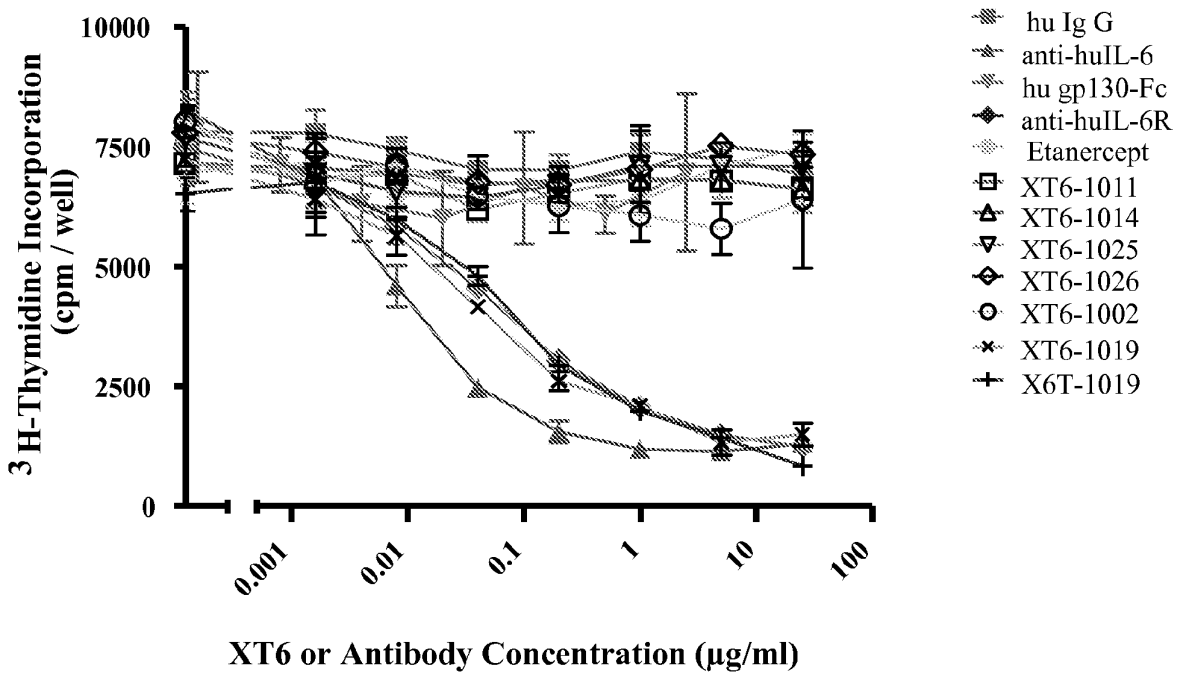
0.55
0.30
0.05
0
40.00
20.00
10.00
5.00
2.50
1.25
0.63
0.31
0.16
0.08
0
Xceptor or Ab concentration (μg/ml)
hIgG
anti-hIL-6
anti-hIL-6R
XT6-1006
XT6-1019
XT6-1004
XT6-1007
XT6-1008
XT6-1013

Fig. 4


10000
7500
5000
2500
0
3 H-Thymidine Incorporation (cpm / well)
0.001
0.01
0.1
1
10
100
XT6 or Antibody Concentration (µg/ml)
hu Ig G
anti-huIL-6
hu gp130-Fc
anti-huIL-6R
Etanercept
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XT6-1014
XT6-1025
XT6-1026
XT6-1002
XT6-1019
X6T-1019

Fig. 5A

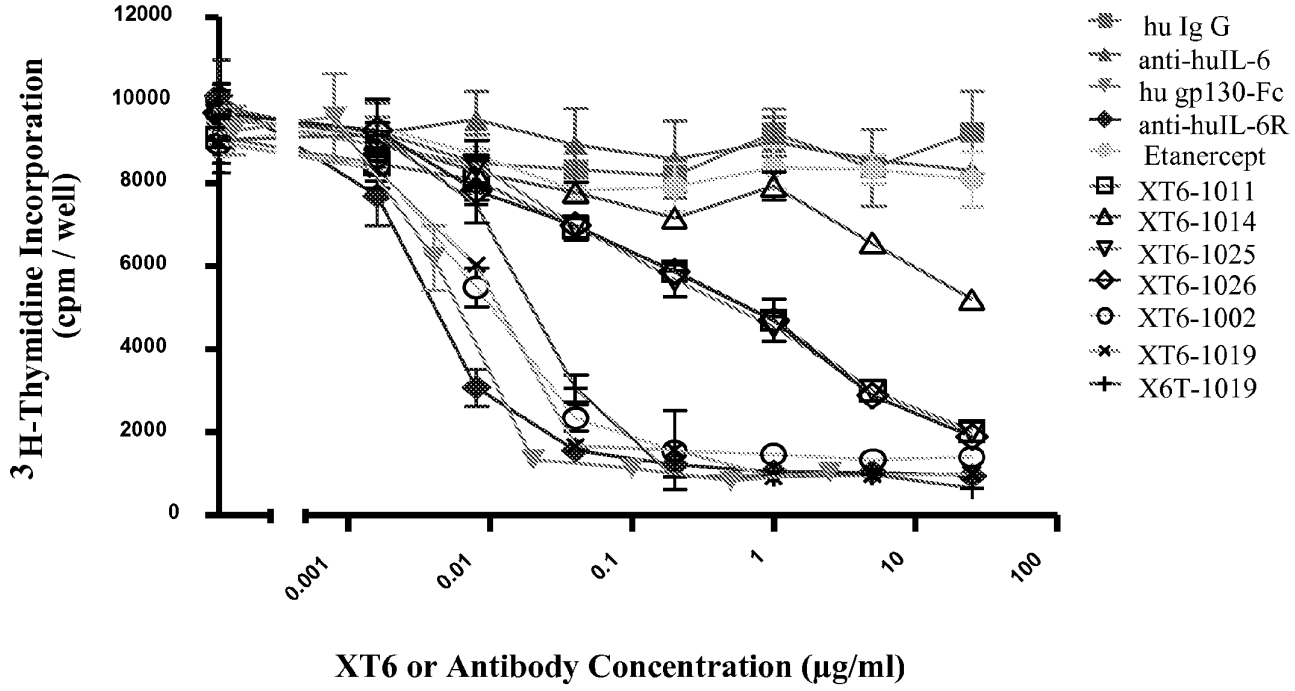

12000
10000
8000
6000
4000
2000
0
3H-Thymidine Incorporation (cpm / well)
0.001
0.01
0.1
1
10
100
XT6 or Antibody Concentration (µg/ml)
hu Ig G
anti-huIL-6
hu gp130-Fc
anti-huIL-6R
Etanercept
XT6-1011
XT6-1014
XT6-1025
XT6-1026
XT6-1002
XT6-1019
X6T-1019

Fig. 5B

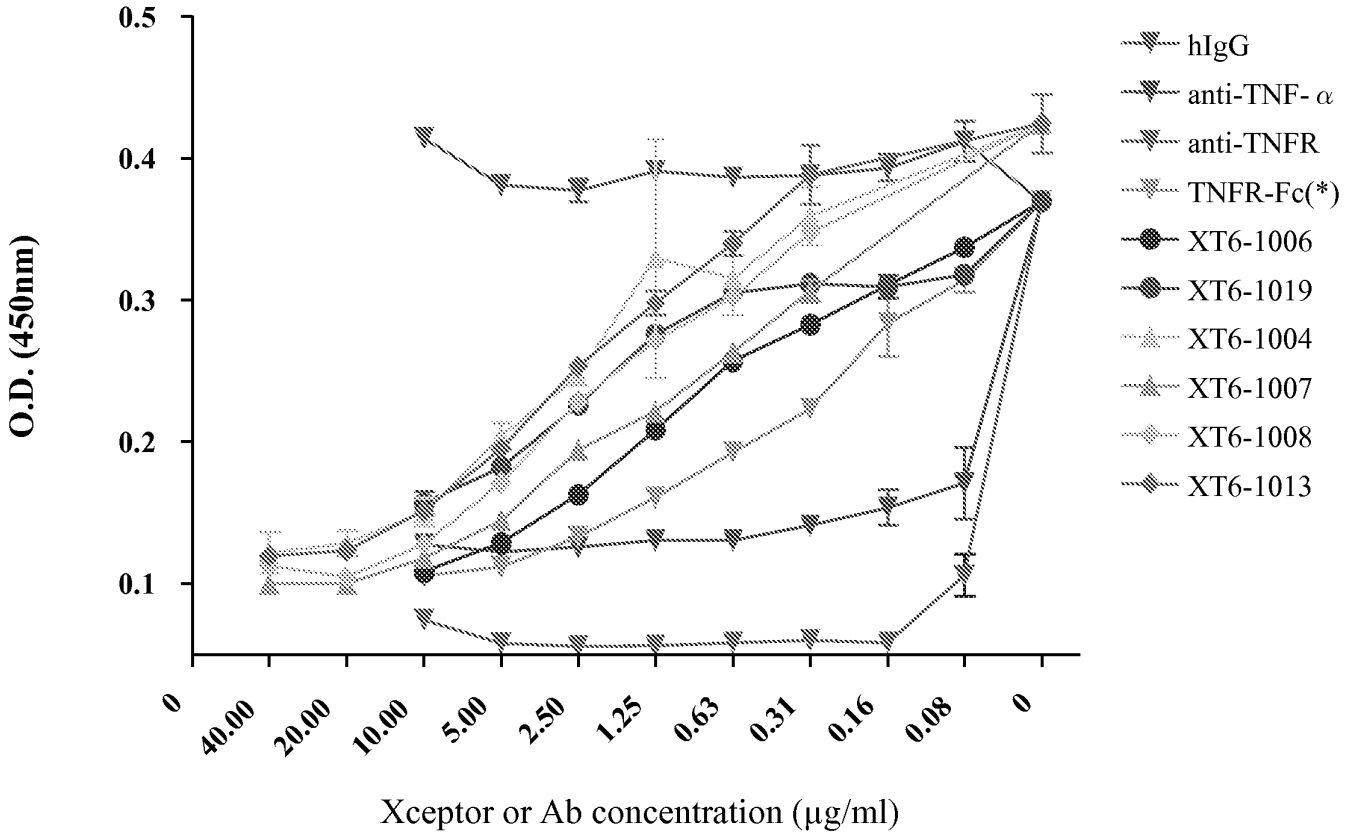

0.5
0.4
0.3
0.2
0.1
O.D. (450nm)
0
40.00
20.00
10.00
5.00
2.50
1.25
0.63
0.31
0.16
0.08
0
Xceptor or Ab concentration (μg/ml)
hIgG
anti-TNF- α
anti-TNFR
TNFR-Fc(*)
XT6-1006
XT6-1019
XT6-1004
XT6-1007
XT6-1008
XT6-1013

Fig. 6

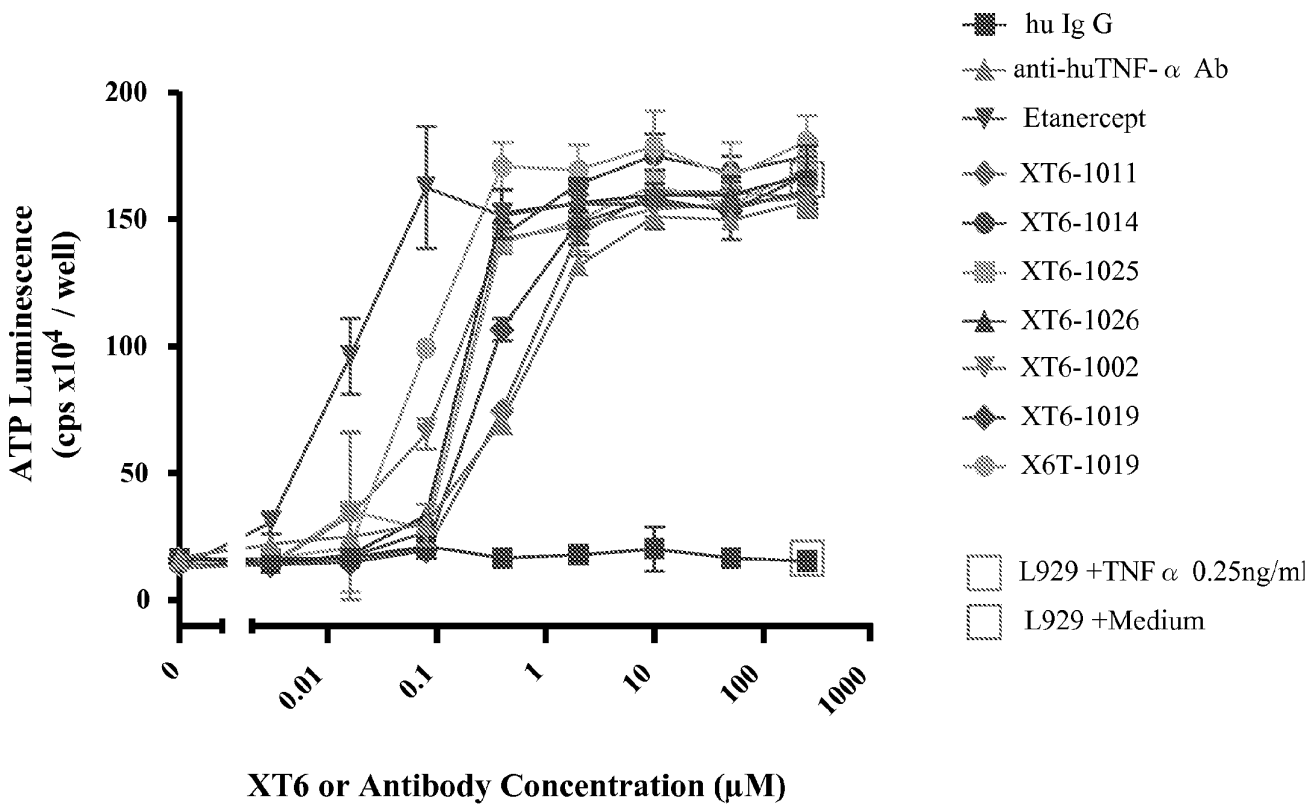

ATP Luminescence (cps x10^4 / well)
200
150
100
50
0
0
0.01
0.1
1
10
100
1000
XT6 or Antibody Concentration (μM)
hu Ig G
anti-huTNF- α Ab
Etanercept
XT6-1011
XT6-1014
XT6-1025
XT6-1026
XT6-1002
XT6-1019
X6T-1019
L929 +TNF α 0.25ng/ml
L929 +Medium

Fig. 7

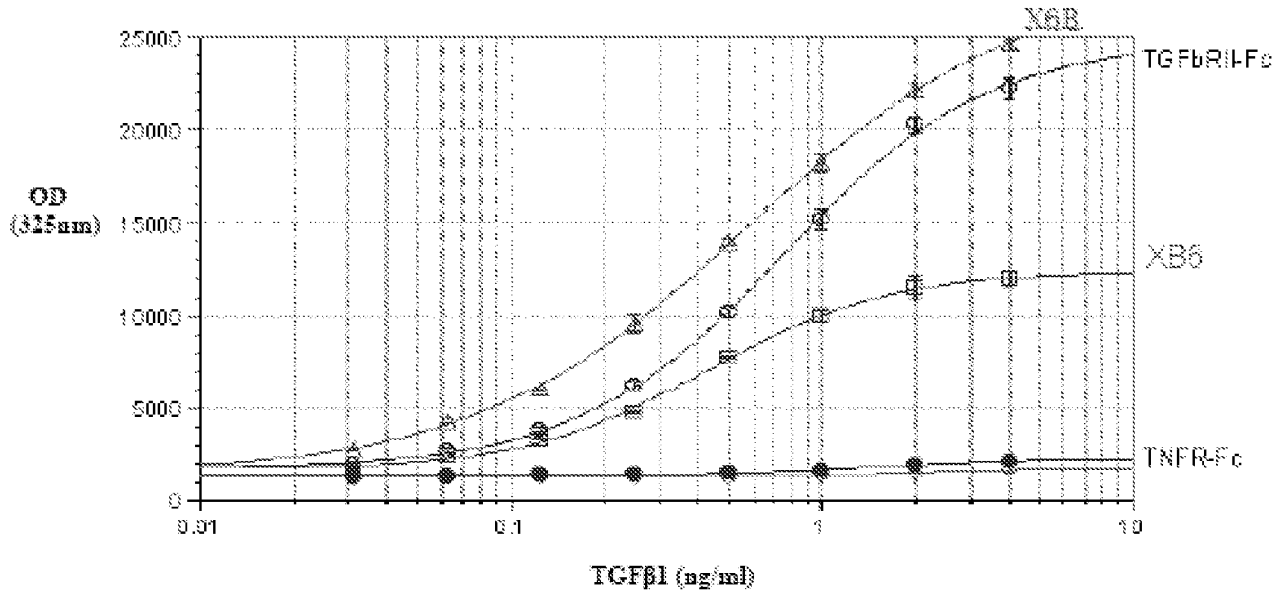

X6B
TGFbRII-Fc
XB6
TNFR-Fc
OD
(325nm)
25000
20000
15000
10000
5000
0
0.01
0.1
1
10
TGFβ1 (ng/ml)

Fig. 8

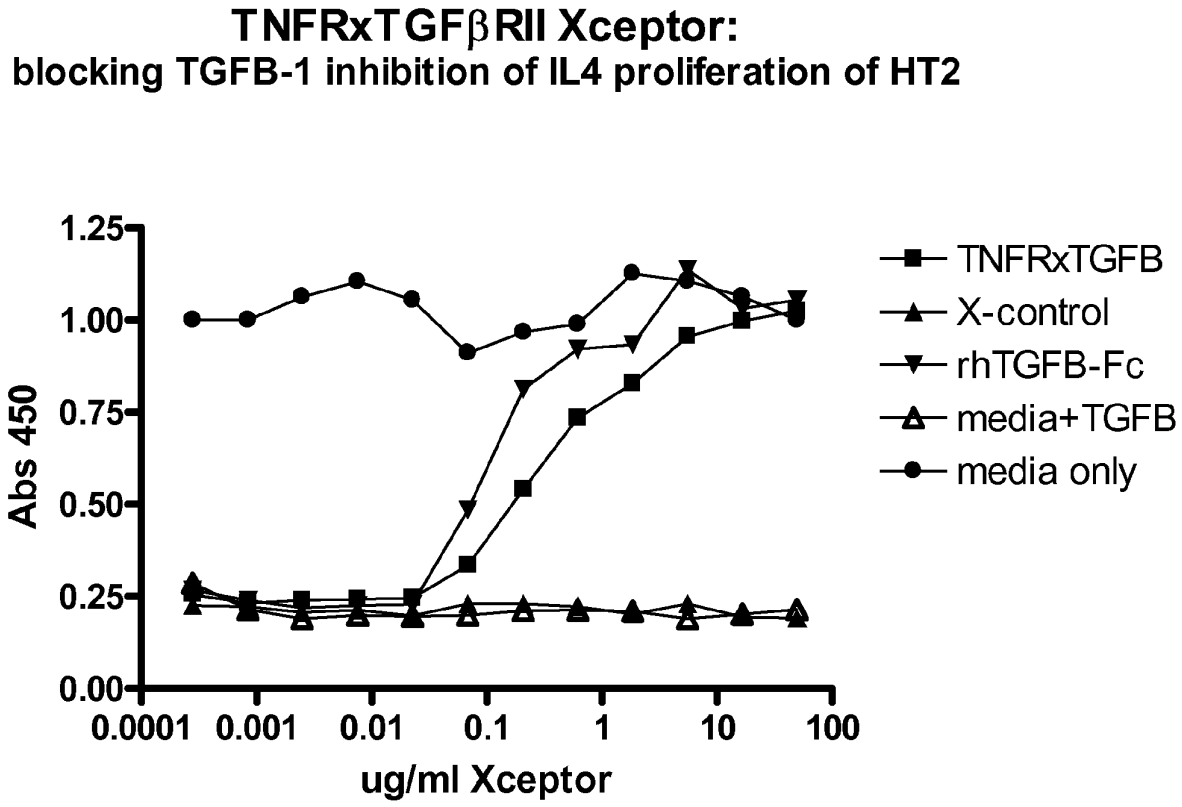

TNFRxTGFβRII Xceptor:
blocking TGFB-1 inhibition of IL4 proliferation of HT2
Abs 450
1.25
1.00
0.75
0.50
0.25
0.00
0.0001
0.001
0.01
0.1
1
10
100
ug/ml Xceptor
TNFRxTGFB
X-control
rhTGFB-Fc
media+TGFB
media only

Fig. 9

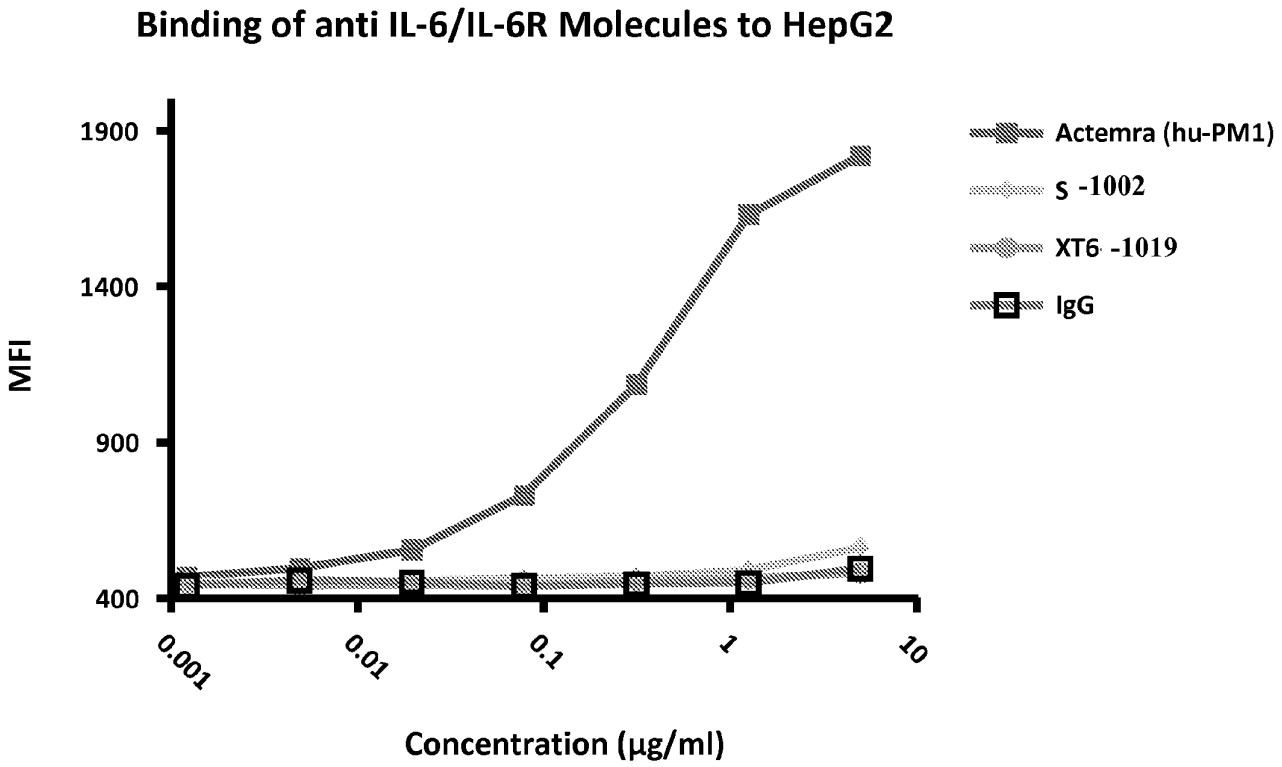

Binding of anti IL-6/IL-6R Molecules to HepG2
1900
1400
900
400
MFI
0.001
0.01
0.1
1
10
Concentration (µg/ml)
Actemra (hu-PM1)
S -1002
XT6 -1019
IgG

Fig. 10

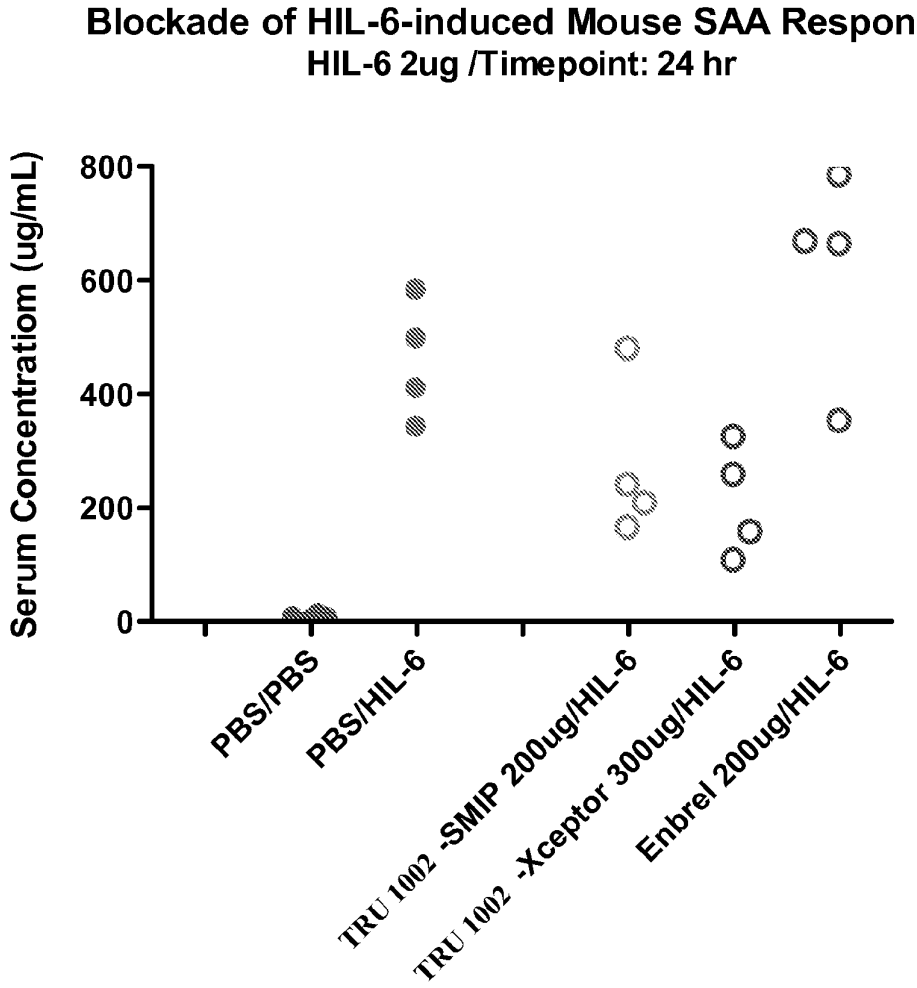

Blockade of HIL-6-induced Mouse SAA Response
HIL-6 2ug /Timepoint: 24 hr
Serum Concentratiom (ug/mL)
800
600
400
200
0
PBS/PBS
PBS/HIL-6
TRU 1002 -SMIP 200ug/HIL-6
TRU 1002 -Xceptor 300ug/HIL-6
Enbrel 200ug/HIL-6

Fig. 11

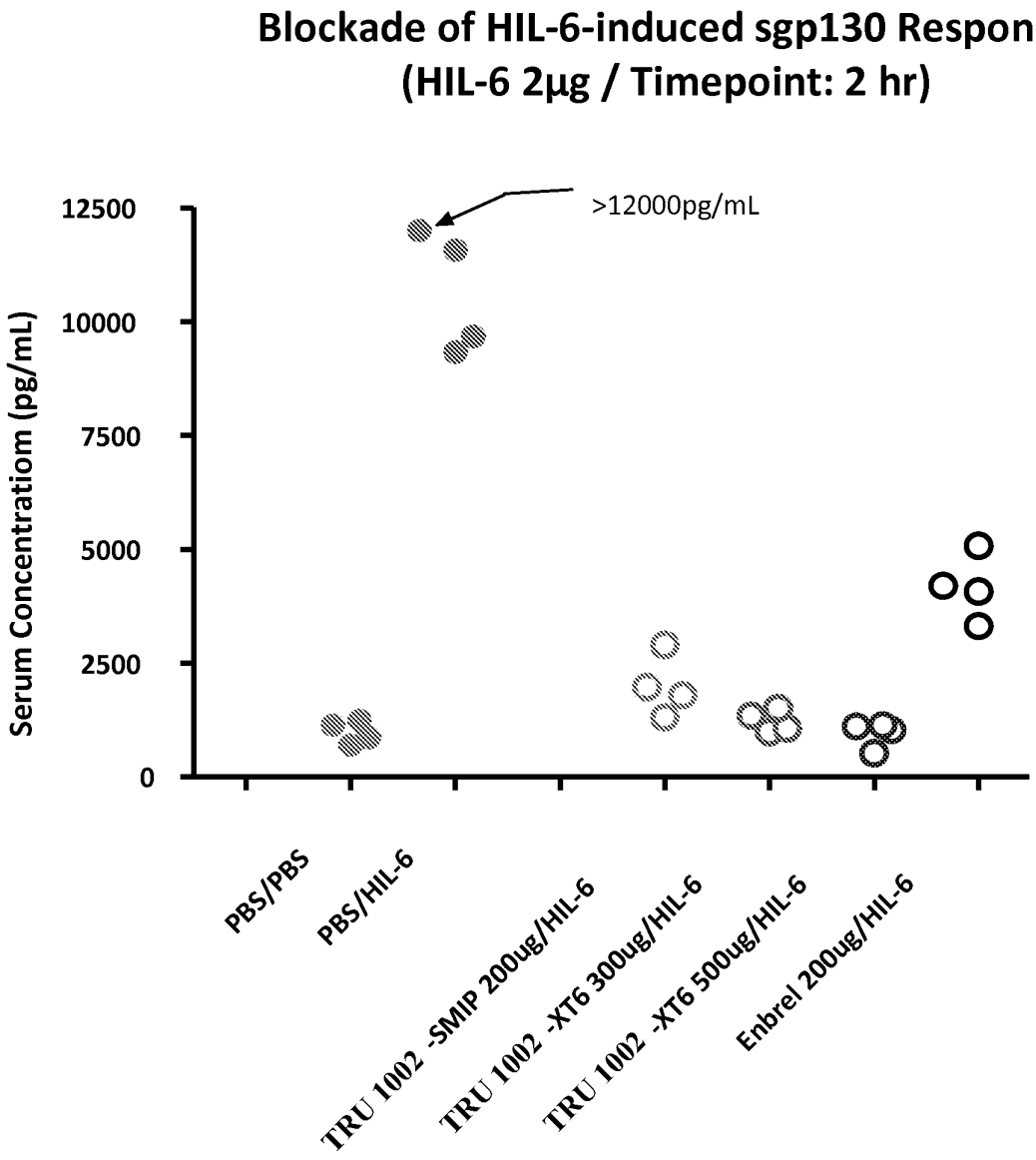

Blockade of HIL-6-induced sgp130 Response
(HIL-6 2µg / Timepoint: 2 hr)
>12000pg/mL
Serum Concentratiom (pg/mL)
12500
10000
7500
5000
2500
0
PBS/PBS
PBS/HIL-6
TRU 1002 -SMIP 200ug/HIL-6
TRU 1002 -XT6 300ug/HIL-6
TRU 1002 -XT6 500ug/HIL-6
Enbrel 200ug/HIL-6

Fig. 12

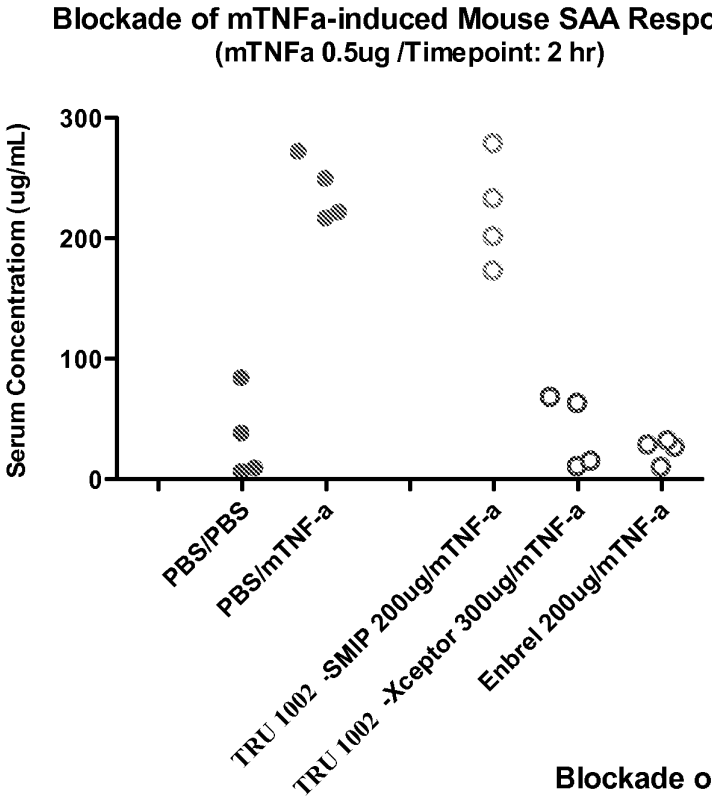
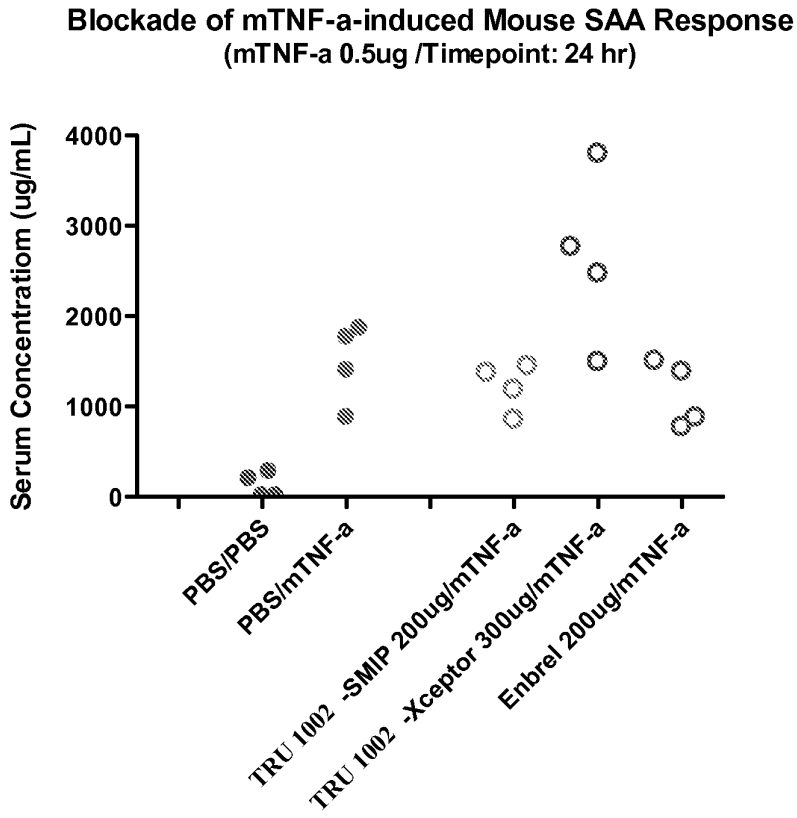


Fig. 13A

Fig. 13B



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Baum, Peter Robert
Thompson, Peter Armstrong
Misher, Lynda

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 1   5   10

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<210> 102
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<210> 108
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<210> 109
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 1   5

<210> 111
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<210> 114
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Gln Gln Tyr Asn Ala Tyr Pro Phe Ile
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<210> 123
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Gln Gln Ala Asn Ser Phe Pro Leu Thr
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<400> 126
Gln Gln Ser Tyr Ser Thr Pro Tyr Thr
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<400> 128
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<210> 129
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<210> 130
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 1   5   10

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<210> 132
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<210> 133
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 1   5

<210> 135
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<210> 136
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 1   5   10

<210> 137
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<400> 137
Gln Ala Ser Thr Leu Glu Ser
 1   5

<210> 138
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<400> 138
Gln Gln Ala Asn Ser Phe Pro Ile Thr
 1   5

<210> 139
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 1   5

<210> 141
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Gln Gln Tyr Asp Thr Leu His Pro Ser
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<210> 142
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<210> 143
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<210> 144
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<400> 144
Gly Ser Tyr Arg Ala Ser Ser Ser Tyr Val
 1   5   10

<210> 145
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Ala Ala Ser Thr Leu Glu Ser
 1   5

<210> 147
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Ser Gly Asp Lys Leu Gly Glu Lys Phe Ala Ser
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 1   5

<210> 150
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Gln Ala Trp Gly Gly Ser Thr Ala Tyr Val
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Arg Ala Ser Gln Ser Val Thr Thr Tyr Leu Ala
 1   5   10

<210> 152
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<400> 152
Asp Ala Ser Asn Arg Ala Thr
 1   5

<210> 153
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Gln Gln Arg Ser Asn Trp Pro Pro Ser Ile Thr
 1   5   10

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Thr Gly Thr Ser Ser Asp Val Gly Ser Tyr Asn Leu Val Ser
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Glu Gly Ser Lys Arg Pro Ser
 1   5

<210> 156
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<220>
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<400> 156
Cys Ser Tyr Ala Gly Arg Ser Thr Tyr Val
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Ser Gly Asn Arg Leu Glu Asp Lys Tyr Val His
 1   5   10

<210> 158
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<400> 158
Gln Asp Asn Lys Arg Pro Ser
 1   5

<210> 159
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<400> 159
Gln Ala Trp Asp Ser Ser Thr Arg Glu Val
 1   5   10

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 1   5   10

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<400> 161
Gly Ala Ser Ser Leu Gln Thr
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<210> 162
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Gln Gln Ala His Ser Phe Pro Phe Thr
 1   5

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 1   5   10

<210> 164
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<400> 164
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<210> 165
<211> 10
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<213> Artificial Sequence

<220>
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<400> 165
Gln Gln Tyr Gly Ser Ser Leu Thr Trp Thr
 1   5   10

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<220>
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<400> 166
Arg Ala Ser Gln Ser Val Ser Gly Asn Tyr Leu Ala
 1   5   10

<210> 167
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<400> 167
Gly Ala Ser Ser Arg Ala Thr
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<210> 168
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<400> 168
Leu Gln His Asn Ser Tyr Pro Leu Thr
 1   5

<210> 169
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<400> 169
Gly Gly Ile Asn Ile Gly Ser Lys Ser Val His
 1   5   10

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<400> 170
Tyr Phe Asp Ser Asp Arg Pro Ser
 1   5

<210> 171
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<400> 171
Gln Val Trp Asp Ser Arg Ser Asp Gln Tyr Val
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Arg Ala Ser Gln Ser Ile Ser Ser Trp Leu Ala
 1   5   10

<210> 173
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<220>
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<400> 173
Lys Ala Ser Thr Leu Glu Ser
 1   5

<210> 174
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<400> 174
Gln Gln Tyr Asn Ser Tyr Ser Leu Thr
 1   5

<210> 175
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<400> 175
Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn
 1   5   10

<210> 176
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<400> 176
Ala Ala Ser Ser Leu Gln Ser
 1   5

<210> 177
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<400> 177
Gln Gln Ser Tyr Ser Thr Pro Leu Thr
 1   5

<210> 178
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Arg Ala Ser Gln Ser Ile Asn Asn Tyr Leu Asn
 1   5   10

<210> 179
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Thr Ala Ser Thr Leu His Ser
 1   5

<210> 180
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<400> 180
Gln Gln Ser Tyr Ala Thr Leu Arg Thr
 1   5

<210> 181
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<400> 181
Ser Gly Ser Ser Ser Asp Val Gly His Tyr Asp Tyr Val Ser
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<400> 182
Asp Val Ser Asn Arg Pro Ser
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<210> 183
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<400> 183
Ser Ser Tyr Thr Ser Ser Gly Thr Arg Val
 1   5   10

<210> 184
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<400> 184
Arg Ala Ser Gln Ser Val Asn Asn Trp Val Ala
 1   5   10

<210> 185
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<400> 185
Ala Ala Ser Ser Leu Gln Ser
 1   5

<210> 186
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<400> 186
Gln Gln Ser Tyr Ser Met Pro Leu Thr
 1   5

<210> 187
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<220>
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<400> 187
Lys Tyr Ser Met His
 1   5

<210> 188
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<220>
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<400> 188
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Gly

<210> 189
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<212> PRT
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<223> Made in a lab

<400> 189
Gly Gly Tyr Tyr Tyr Ala Leu Asp Tyr
 1   5

<210> 190
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<220>
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<400> 190
Phe Tyr Gln Met His
 1   5

<210> 191
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<400> 191
Gly Ile Tyr Pro Ser Gly Gly Tyr Thr Lys Tyr Ala Asp Ser Val Lys
 1   5   10   15
Gly

<210> 192
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<220>
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<400> 192
Asp Leu Gly Tyr Gly Ser Ser Trp Tyr Tyr Phe Asp Tyr
 1   5   10

<210> 193
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<400> 193
Lys Tyr Ser Met His
 1   5

<210> 194

<211> 16
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<400> 194
Gly Ile Ser Pro Ser Gly Tyr Thr Arg Tyr Ala Asp Ser Val Lys Gly
 1   5   10   15

<210> 195
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<400> 195
Asp Gln Leu Leu Glu Ala Phe Asp Ile
 1   5

<210> 196
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<400> 196
Glu Tyr Pro Met Asn
 1   5

<210> 197
<211> 17
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<220>
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<400> 197
Gly Ile Tyr Ser Ser Gly Gly Leu Thr Lys Tyr Ala Asp Ser Val Lys
 1   5   10   15
Gly

<210> 198
<211> 10
<212> PRT
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<220>
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<400> 198
Asp His Tyr Gly Asp Tyr Ala Phe Asp Tyr
 1   5   10

<210> 199
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<220>
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<400> 199
Leu Tyr Glu Met Val
 1   5

<210> 200
<211> 17
<212> PRT
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<220>
<223> Made in a lab

<400> 200
Gly Ile Trp Pro Ser Gly Gly Trp Thr Gln Tyr Ala Asp Ser Val Lys
 1   5   10   15
Gly

<210> 201
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 201
Asp Leu Ala Val Ala Gly Trp Asp Tyr Tyr Tyr Tyr Tyr Gly Met Asp
 1   5   10   15
Val

<210> 202
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
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<400> 202
Gln Tyr Asn Met Ile
 1   5

<210> 203

<211> 16
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<220>
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<400> 203
Trp Ile Ser Ser Ser Gly Gly Thr Glu Tyr Ala Asp Ser Val Lys Gly
 1   5   10   15

<210> 204
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 204
Asp Arg Gly Tyr Gly Ser Gly Ser Tyr Gly Ala Tyr Asp Ala Phe Asp
 1   5   10   15
Ile

<210> 205
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
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<400> 205
His Tyr Ser Met Gly
 1   5

<210> 206
<211> 17
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<220>
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<400> 206
Ser Ile Tyr Pro Ser Gly Gly Ser Thr Leu Tyr Ala Asp Ser Val Lys
 1   5   10   15
Gly

<210> 207
<211> 9
<212> PRT
<213> Artificial Sequence

<220>

<223> Made in a lab

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Trp Tyr Ser Met Trp
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Gly

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Gly

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Leu Tyr Ser Met Asn
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Ser Ile Ser Ser Ser Gly Gly Ala Thr Leu Tyr Ala Asp Ser Val Lys
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Gly

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Gly

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Phe Asp Tyr

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Trp Tyr Ser Met Val
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1 5 10 15
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<210> 324
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<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 324
Val Ser Gly Phe Tyr Ala Ala Phe Asp Tyr
 1   5   10

<210> 325
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 325
Trp Tyr Trp Met Thr
 1   5

<210> 326
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 326
Ser Ile Ser Pro Ser Gly Gly His Thr Ser Tyr Ala Asp Ser Val Lys
 1   5   10   15
Gly

<210> 327
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 327
Ser Ser Gly Trp Tyr Glu Asp Tyr Phe Asp Tyr
 1   5   10

<210> 328
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 328

Pro Tyr Glu Met Ala
1 5

<210> 329
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 329
Val Ile Gly Pro Ser Gly Gly Tyr Thr Glu Tyr Ala Asp Ser Val Lys
1 5 10 15
Gly

<210> 330
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 330
Gly Tyr Asp Phe Trp Ser Gly Tyr Tyr Asp Ala Phe Asp Ile
1 5 10

<210> 331
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 331
Ser Tyr Phe Met Gly
1 5

<210> 332
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 332
Ser Ile Trp Pro Ser Gly Gly Asn Thr Thr Tyr Ala Asp Ser Val Lys
1 5 10 15
Gly

<210> 333
<211> 10

<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 333
His Val Gly Trp Gly Arg Tyr Phe Asp Tyr
 1   5   10

<210> 334
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 334
Ala Tyr Arg Met Ile
 1   5

<210> 335
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 335
Tyr Ile Ser Ser Ser Gly Gly Arg Thr Asp Tyr Ala Asp Ser Val Lys
 1   5   10   15
Gly

<210> 336
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 336
Gly Gly Leu Arg Tyr Phe Asp Trp Leu Ala Pro Ser Met Asp Tyr
 1   5   10   15

<210> 337
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 337

Ala Tyr Ser Met Val
 1   5

<210> 338
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 338
Tyr Ile Tyr Pro Ser Gly Gly Ile Thr Thr Tyr Ala Asp Ser Val Lys
 1   5   10   15
Gly

<210> 339
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 339
Glu Gly Gln Val Phe Asp Ile
 1   5

<210> 340
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 340
Asn Tyr Ala Met Gly
 1   5

<210> 341
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 341
Arg Ile Val Pro Ser Gly Gly Met Thr Ser Tyr Ala Asp Ser Val Lys
 1   5   10   15
Gly

<210> 342
<211> 9

<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 342
Asp Asp Phe Trp Ser Gly Met Asp Val
 1   5

<210> 343
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 343
Leu Tyr Asn Met Gln
 1   5

<210> 344
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 344
Gly Ile Ser Leu Ser Gly Gly Lys Thr Phe Tyr Ala Asp Ser Val Lys
 1   5   10   15
Gly

<210> 345
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 345
Asp Tyr Gly Val Ala Thr Leu Asp Ala Phe Asp Ile
 1   5   10

<210> 346
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 346

Ala Tyr Thr Met His
 1   5

<210> 347
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 347
Ser Ile Tyr Pro Ser Gly Gly Thr Thr Pro Tyr Ala Asp Ser Val Lys
 1   5   10   15
Gly

<210> 348
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 348
Val Val Asn Ile Asp Phe Trp Ser Gly Tyr Asn Met Arg Ser Ala Phe
 1   5   10   15
Asp Ile

<210> 349
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 349
Asp Tyr Leu Met Gly
 1   5

<210> 350
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 350
Val Ile Ser Ser Ser Gly Gly Pro Thr Ala Tyr Ala Asp Ser Val Lys
 1   5   10   15
Gly

<210> 351
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 351
Val Gly Leu Asp Tyr Gly Ile Leu Gly Ala Phe Asp Ile
 1   5   10

<210> 352
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 352
Glu Tyr Gly Met Ser
 1   5

<210> 353
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 353
Ser Ile Arg Ser Ser Gly Gly Trp Thr Lys Tyr Ala Asp Ser Val Lys
 1   5   10   15
Gly

<210> 354
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 354
Gly Leu Gly Ala Thr Ser Gly Glu Phe Asp Tyr
 1   5   10

<210> 355
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 355
Lys Tyr Asp Met Trp
 1   5

<210> 356
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 356
Ser Ile Trp Pro Ser Gly Gly Trp Thr Ser Tyr Ala Asp Ser Val Lys
 1   5   10   15
Gly

<210> 357
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 357
Ser Arg Gly Ser Pro Trp Tyr Gly Asp Phe Asp His
 1   5   10

<210> 358
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 358
Met Tyr Thr Met His
 1   5

<210> 359
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 359
Trp Ile Ser Pro Ser Gly Gly Trp Thr Lys Tyr Ala Asp Ser Val Lys
 1   5   10   15
Gly

<210> 360
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 360
Ser Pro Trp Gly Gly Pro Phe Asp Tyr
 1   5

<210> 361
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 361
Gln Tyr Phe Met Met
 1   5

<210> 362
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 362
Ser Ile Ser Pro Ser Gly Gly Tyr Thr Gln Tyr Ala Asp Ser Val Lys
 1   5   10   15
Gly

<210> 363
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 363
Thr Gly Asp Tyr Thr Arg Tyr Tyr Ser Tyr Gly Met Asp Val
 1   5   10

<210> 364
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 364
Gly Tyr Ser Met Ala
 1   5

<210> 365
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 365
Gly Ile Tyr Ser Ser Gly Gly Trp Thr Trp Tyr Ala Asp Ser Val Lys
 1   5   10   15
Gly

<210> 366
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 366
Asp Gln Ser Phe Ser Tyr Asp Ser Ser Leu Asp Ala Phe Asp Ile
 1   5   10   15

<210> 367
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 367
Leu Tyr Gly Met His
 1   5

<210> 368
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 368
Ser Ile Val Pro Ser Gly Gly Leu Thr Arg Tyr Ala Asp Ser Val Lys
 1   5   10   15
Gly

<210> 369
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 369
Leu Ala Tyr Tyr Asp Phe Trp Ser Gly Arg Asp Ala Phe Asp Ile
 1   5   10   15

<210> 370
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 370
His Tyr Gly Met Asp
 1   5

<210> 371
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 371
Ser Ile Tyr Ser Ser Gly Gly Tyr Thr Leu Tyr Ala Asp Ser Val Lys
 1   5   10   15
Gly

<210> 372
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 372
Arg Thr Trp Ala Asp Ala Phe Asp Val
 1   5

<210> 373
<211> 105
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 373
Gln Ser Glu Leu Thr Gln Pro Pro Ser Val Ser Val Ser Pro Gly Gln
 1   5   10   15
Thr Ala Thr Ile Thr Cys Ser Gly Glu Lys Leu Gly Asp Ile Tyr Ala
            20   25   30
Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Val Leu Val Ile Tyr
        35   40   45
Gln Asp Thr Lys Arg Pro Ser Gly Ile Pro Val Arg Phe Ser Gly Ser
    50   55   60
Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr Gln Ala Met
65   70   75   80
Asp Glu Ala Asp Tyr Tyr Cys Gln Ala Trp Asp Ser Ser Thr Val Phe
                85   90   95
Gly Gly Gly Thr Lys Leu Thr Val Leu
            100   105

<210> 374
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 374
Gln Ser Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln
 1   5   10   15
Ser Ile Thr Ile Ser Cys Ser Gly Thr Asp Ser Asp Val Gly Gly Tyr
            20   25   30
Asn His Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Leu
        35   40   45
Ile Ile Tyr Asp Val Asp His Arg Pro Ser Gly Ile Ser Asn Arg Phe
    50   55   60
Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu
65   70   75   80
Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ser Ser Tyr Arg Ser Gly
                85   90   95
Ser Thr Tyr Val Phe Gly Thr Ala Thr Lys Val Thr Val Leu
            100   105   110

<210> 375
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 375
Gln Asp Ile Gln Met Thr Gln Ser Pro Leu Ser Leu Ser Ala Ser Val
 1   5   10   15
Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser
            20   25   30
Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Glu Ala Pro Lys Leu Leu
        35   40   45
Ile Tyr Ala Ala Ser Ala Leu Gln Ser Gly Val Pro Ser Arg Phe Ser

```
    50                  55                  60
Gly Ser Gly Leu Gly Thr Val Phe Thr Leu Thr Ile Thr Ser Leu Gln
65                  70                  75                  80
Pro Glu Asp Ser Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Pro Pro
                85                  90                  95
Val Thr Phe Gly Gly Gly Thr Lys Val Asp Ile Lys
            100                 105

<210> 376
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 376
Gln Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val
 1               5                  10                  15
Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser
            20                  25                  30
Trp Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu
        35                  40                  45
Ile Tyr Lys Ala Ser Ser Leu Glu Ser Gly Val Pro Ser Arg Phe Ser
    50                  55                  60
Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln
65                  70                  75                  80
Pro Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser Tyr Trp
                85                  90                  95
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
            100                 105

<210> 377
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 377
Gln Asp Ile Gln Met Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro
 1               5                  10                  15
Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val 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 Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser
    50                  55                  60
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu
65                  70                  75                  80
Pro Glu Asp Ser Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asn Trp Pro
                85                  90                  95
Pro Phe Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100                 105

<210> 378
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<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 378
Gln Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
 1   5   10   15
Gly Asp Arg Val Thr Ile Thr Cys Gln Thr Ser Gln Ser Ile Asp Arg
            20   25   30
Tyr Leu Asn Trp Tyr Gln Gln Lys Ala Gly Glu Ala Pro Lys Leu Leu
        35   40   45
Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser
    50   55   60
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln
65   70   75   80
Pro Glu Asp Phe Ala Ser Tyr Tyr Cys Gln Gln Ser Tyr Arg Thr Pro
                85   90   95
Arg Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
            100   105

<210> 379
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 379
Gln Asp Ile Gln Met Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro
 1   5   10   15
Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser
            20   25   30
Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu
        35   40   45
Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe
    50   55   60
Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu
65   70   75   80
Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser
                85   90   95
Pro Leu Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
            100   105   110

<210> 380
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 380
Gln Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val

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 1               5                  10                  15
Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser
            20                  25                  30
Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu
        35                  40                  45
Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser
    50                  55                  60
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln
65                  70                  75                  80
Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro
                85                  90                  95
Arg Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
            100                 105
```

<210> 381
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 381

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Gln Asp Ile Gln Met Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro
 1               5                  10                  15
Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Ile Ser Thr
            20                  25                  30
Ser Leu Ala Trp Tyr Gln Gln Ile Pro Gly Gln Ala Pro Arg Leu Leu
        35                  40                  45
Met Tyr Asp Ala Ser Lys Arg Ala Ser Gly Ile Pro Ala Arg Phe Ser
    50                  55                  60
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu
65                  70                  75                  80
Pro Glu Asp Ser Ala Val Tyr Tyr Cys Gln Leu Arg Ile Asn Trp Pro
                85                  90                  95
Pro Glu Phe Thr Phe Gly Pro Gly Thr Lys Val Glu Ile Lys
            100                 105                 110
```

<210> 382
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 382

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Gln Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val
 1               5                  10                  15
Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Arg Gly Val Ile Thr
            20                  25                  30
Trp Leu Asn Trp Tyr Gln Gln Lys Pro Gly Arg Val Pro Ser Pro Leu
        35                  40                  45
Ile Phe Gly Ala Ser Thr Leu Gln Thr Gly Val Pro Ser Arg Phe Ser
    50                  55                  60
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Asp Leu Gln
65                  70                  75                  80
```

```
Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Thr His Ser Phe Pro
                85                  90                  95
Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100                 105

<210> 383
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 383
Gln Ser Ala Leu Thr Gln Pro Pro Ser Val Ser Val Ser Pro Gly Gln
 1               5                  10                  15
Thr Ala Arg Ile Thr Cys Ser Gly Asp Lys Leu Gly Glu Lys Tyr Val
            20                  25                  30
Ser Trp Tyr Gln Gln Arg Ser Gly Gln Ser Pro Leu Leu Val Ile Ser
        35                  40                  45
Gln Asp Thr Lys Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
    50                  55                  60
Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Ala Gln Ala Ala
65                  70                  75                  80
Asp Glu Ala Asp Tyr Tyr Cys Gln Thr Trp Asp Ser Asp Thr Tyr Val
                85                  90                  95
Phe Gly Ser Gly Ser Thr Val Thr Val Leu
            100                 105

<210> 384
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 384
Gln Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
 1               5                  10                  15
Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser
            20                  25                  30
Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu
        35                  40                  45
Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser
    50                  55                  60
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln
65                  70                  75                  80
Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Leu
                85                  90                  95
Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
            100                 105

<210> 385
<211> 108
<212> PRT
<213> Artificial Sequence
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<220>
<223> Made in a lab

<400> 385
Gln Asp Ile Gln Met Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro
 1   5   10   15
Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg 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 Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser
    50   55   60
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Thr Ser Leu Gln
65   70   75   80
Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asp Asn Leu Pro
                85   90   95
Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100   105

<210> 386
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 386
Gln Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Phe Val
 1   5   10   15
Gly Asp Arg Val Thr Ile Thr Cys Arg Thr Ser Gln Ser Val Ala Thr
            20   25   30
Tyr Val Asn Trp Tyr Gln Gln Lys Pro Gly Glu Gly Pro Lys Leu Leu
        35   40   45
Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Arg
    50   55   60
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Gly Ser Leu Gln
65   70   75   80
Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Val Pro
                85   90   95
Ile Thr Phe Gly Gln Gly Thr Arg Leu Asp Ile Lys
            100   105

<210> 387
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 387
Gln Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val
 1   5   10   15
Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Met Ser Asn
            20   25   30

Trp Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu
35 40 45
Ile Tyr Asp Val Phe Thr Leu Lys Ser Gly Val Pro Ser Arg Phe Ser
50 55 60
Gly Ser Arg Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln
65 70 75 80
Pro Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Asp Tyr Ser
85 90 95
Gly Ile Thr Phe Gly Pro Gly Thr Glu Val Asp Ile Arg
100 105

<210> 388
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 388
Gln Ser Val Leu Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln
1 5 10 15
Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ser Lys
20 25 30
Val Val Tyr Trp Tyr Gln Gln Val Pro Gly Thr Ala Pro Lys Leu Leu
35 40 45
Ile Tyr Arg Asn Asp Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
50 55 60
Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Arg
65 70 75 80
Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu
85 90 95
Ser Gly Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105 110

<210> 389
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 389
Gln Asp Ile Gln Met Thr Gln Ser Pro Ala Thr Leu Ser Ala Ser Val
1 5 10 15
Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser
20 25 30
Trp Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu
35 40 45
Ile Tyr Lys Ala Ser Gly Leu Glu Ser Gly Val Pro Ser Arg Phe Ser
50 55 60
Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln
65 70 75 80
Pro Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser Tyr Pro
85 90 95
Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys

100 105

<210> 390
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 390
Gln Asp Ile Gln Met Thr Gln Ser Pro Leu Ser Leu Ser Ala Ser Val
1 5 10 15
Gly Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Arg Asp Ile Ser Ile
20 25 30
Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Val Pro Lys Leu Leu
35 40 45
Ile Phe Gly Ala Ser Thr Leu Arg Ser Gly Val Pro Ser Arg Phe Ser
50 55 60
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Thr Ser Leu Gln
65 70 75 80
Pro Glu Asp Val Ala Thr Tyr Tyr Cys Gln Lys Tyr Asn Ser Ala Pro
85 90 95
Tyr Thr Phe Gly Pro Gly Thr Lys Val Glu Ile Arg
100 105

<210> 391
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 391
Gln Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val
1 5 10 15
Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Ser
20 25 30
Trp Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu
35 40 45
Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser
50 55 60
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln
65 70 75 80
Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ala Asn Ser Phe Pro
85 90 95
Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 392
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 392
Gln Asp Ile Gln Met Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro
 1   5   10   15
Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Ile Asn Thr
            20   25   30
Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly His Pro Pro Arg Leu Leu
        35   40   45
Ile Tyr Asp Ala Ser Asn 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 Val Val Tyr Tyr Cys Gln Gln Tyr Gly Arg Ser Arg
                85   90   95
Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100   105

<210> 393
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 393
Gln Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
 1   5   10   15
Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Asn
            20   25   30
Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Val Pro Lys Leu Leu
        35   40   45
Ile Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser
    50   55   60
Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln
65   70   75   80
Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Asp Asn Ile Pro
                85   90   95
Tyr Thr Phe Gly Leu Gly Thr Lys Leu Glu Ile Lys
            100   105

<210> 394
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 394
Gln Ser Glu Leu Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln
 1   5   10   15
Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn
            20   25   30
Thr Val Asn Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
        35   40   45
Ile Tyr Ser Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser

```
    50                  55                  60
Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln
65                  70                  75                  80
Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu
                85                  90                  95
Asn Gly Tyr Val Phe Gly Ile Gly Thr Lys Val Thr Val Leu
            100                 105                 110

<210> 395
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 395
Gln Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
 1               5                  10                  15
Gly Asp Ser Val Thr Ile Ala Cys Arg Ala Ser Gln Ser Ile Ser Thr
            20                  25                  30
Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Lys Leu Leu
        35                  40                  45
Ile Tyr Glu Ala Thr Asn Leu Gln Ser Gly Val Pro Ser Arg Phe Ser
    50                  55                  60
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln
65                  70                  75                  80
Pro Glu Asp Val Ala Thr Tyr Tyr Cys Gln Gln Ala Asn Asn Phe Pro
                85                  90                  95
Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
            100                 105

<210> 396
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 396
Gln Ser Val Leu Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln
 1               5                  10                  15
Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Gly Asn
            20                  25                  30
Ala Val Asn Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Val
        35                  40                  45
Leu Tyr Ser Ser Asn His Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
    50                  55                  60
Gly Ser Arg Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln
65                  70                  75                  80
Ser Gln Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu
                85                  90                  95
Asn Gly Pro Leu Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100                 105                 110

<210> 397
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<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 397
Gln Ser Glu Leu Thr Gln Pro Pro Ser Val Ser Val Ser Pro Gly Gln
 1   5   10   15
Thr Ala Thr Ile Ser Cys Ser Gly Glu Lys Leu Gly Asp Arg Tyr Ala
            20   25   30
Trp Trp Tyr Gln Gln Lys Ala Gly Gln Ser Pro Val Leu Val Ile Tyr
        35   40   45
Gln Asp Thr Lys Arg Pro Ser Gly Val Pro Asp Arg Phe Ser Gly Ser
    50   55   60
Asn Ser Gly Thr Ser Ala Ser Leu Val Ile Ser Gly Leu Gln Ser Glu
65   70   75   80
Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu Lys Gly
                85   90   95
Val Val Phe Gly Gly Gly Ser Lys Leu Thr Val Leu
            100   105

<210> 398
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 398
Gln Ser Glu Leu Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln
 1   5   10   15
Arg Val Thr Ile Ser Cys Ser Gly Arg Ser Ser Asn Ile Gly Ser Asn
            20   25   30
Ser Val Asn Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
        35   40   45
Ile Tyr Ser Asn Asn His Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
    50   55   60
Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln
65   70   75   80
Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu
                85   90   95
Tyr Gln Gly Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100   105   110

<210> 399
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 399
Gln Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val

```
 1               5                  10                  15
Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser
            20                  25                  30
Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu
        35                  40                  45
Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Lys Phe Ser
    50                  55                  60
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Leu
65                  70                  75                  80
Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Glu Tyr Phe Pro
                85                  90                  95
Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
            100                 105
```

<210> 400
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 400

```
Gln Asp Ile Gln Met Thr Gln Ser Pro Asp Ser Leu Ser Leu Ser Pro
 1               5                  10                  15
Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser
            20                  25                  30
Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu
        35                  40                  45
Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe
    50                  55                  60
Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu
65                  70                  75                  80
Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser
                85                  90                  95
Ser Leu Thr Phe Gly Gly Gly Thr Glu Val Glu Ile Lys
            100                 105
```

<210> 401
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 401

```
Gln Asp Ile Gln Met Thr Gln Ser Pro Ala Thr Leu Ser Ala Ser Val
 1               5                  10                  15
Gly Asp Arg Val Thr Ile Thr Cys Arg Ser Ser Gln Arg Ile Ser Gly
            20                  25                  30
Tyr Leu Asn Trp Tyr Gln Gln Gln Pro Gly Lys Ala Pro Lys Leu Leu
        35                  40                  45
Ile Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Ile Ser
    50                  55                  60
Gly Ser Gly Ser Gly Thr Asp Phe Ser Leu Ile Ile Ser Ser Leu Gln
65                  70                  75                  80
```

```
Pro Glu Asp Val Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Pro Pro
                85                  90                  95
Phe Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
            100                 105

<210> 402
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 402
Gln Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val
 1               5                  10                  15
Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Thr
            20                  25                  30
Trp Leu Ala Trp Phe Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu
        35                  40                  45
Ile Tyr Lys Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser
    50                  55                  60
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln
65                  70                  75                  80
Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Lys Ser Tyr Pro
                85                  90                  95
Phe Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100                 105

<210> 403
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 403
Gln Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
 1               5                  10                  15
Gly Asp Ser Val Thr Ile Thr Cys Gln Ala Ser Gln Asp Ile Arg Ser
            20                  25                  30
Tyr Leu Asn Trp Phe Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu
        35                  40                  45
Ile Tyr Asp Thr Val Asn Leu Gln Thr Gly Val Pro Ser Arg Phe Ser
    50                  55                  60
Gly Ser Gly Ser Gly Thr Asp Tyr Ser Phe Thr Ile Asn Asn Leu Gln
65                  70                  75                  80
Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Glu Tyr Leu Pro
                85                  90                  95
Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
            100                 105

<210> 404
<211> 108
<212> PRT
<213> Artificial Sequence
```

<220>
<223> Made in a lab

<400> 404
Gln Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
 1   5   10   15
Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Asn
            20   25   30
Tyr Leu Asn Trp Tyr Gln Gln Lys Ser Gly Lys Ala Pro Asn Leu Leu
        35   40   45
Met Tyr Ala Ala Ser Ser Leu His Ser Gly Val Ser Ser Arg Phe Ser
    50   55   60
Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln
65   70   75   80
Pro Glu Asp Tyr Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Ser
                85   90   95
Gly Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
            100   105

<210> 405
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 405
Gln Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
 1   5   10   15
Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser
            20   25   30
Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu
        35   40   45
Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser
    50   55   60
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln
65   70   75   80
Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro
                85   90   95
Val Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100   105

<210> 406
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 406
Gln Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
 1   5   10   15
Gly Asp Arg Val Ala Ile Thr Cys Arg Ala Ser Gln Ser Ile Asp Thr
            20   25   30

```
Tyr Leu Asn Trp Tyr Gln His Lys Pro Gly Lys Ala Pro Lys Leu Leu
        35                  40                  45
Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser
    50                  55                  60
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Gly Leu Gln
65                  70                  75                  80
Pro Glu Asp Phe Ala Ser Tyr Phe Cys Gln Gln Ser Tyr Ser Ser Pro
                85                  90                  95
Gly Ile Thr Phe Gly Gly Gly Thr Arg Val Glu Ile Lys
            100                 105
```

<210> 407
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 407

```
Gln Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
 1               5                  10                  15
Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Gly Thr
            20                  25                  30
Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Asn Leu Leu
        35                  40                  45
Ile Tyr Gly Thr Ser Ser Leu Gln Arg Gly Val Pro Ser Arg Phe Ser
    50                  55                  60
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Thr Leu Gln
65                  70                  75                  80
Pro Glu Asp Phe Val His Tyr Tyr Cys Gln Gln Ser Tyr Thr Ser Pro
                85                  90                  95
Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Val Lys
            100                 105
```

<210> 408
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 408

```
Gln Tyr Glu Leu Thr Gln Ser Pro Ser Val Ser Val Ser Pro Gly Gln
 1               5                  10                  15
Thr Ala Ser Ile Pro Cys Ser Gly Asp Gln Leu Gly Gly Lys Phe Thr
            20                  25                  30
Ser Trp Tyr Gln Gln Lys Ala Gly Gln Ser Pro Leu Leu Val Ile Tyr
        35                  40                  45
Gln Asp Thr Lys Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
    50                  55                  60
Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Thr Gly Thr Gln Ala Met
65                  70                  75                  80
Asp Glu Ala Asp Tyr Tyr Cys Leu Val Trp Asp Ser Asn Thr Tyr Val
                85                  90                  95
Phe Gly Pro Gly Thr Lys Val Thr Val Leu
```

100 105

<210> 409
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 409
Gln Tyr Glu Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Gln
1 5 10 15
Thr Ala Arg Ile Thr Cys Gly Gly Asn Asn Ile Gly Ser Lys Ser Val
20 25 30
His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Val Tyr
35 40 45
Asp Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
50 55 60
Asn Ser Gly Asn Thr Ala Thr Leu Thr Val Ser Arg Val Glu Ala Gly
65 70 75 80
Asp Glu Ala Asp Tyr Tyr Cys Gln Val Trp Asp Ser Ser Gly Gly Leu
85 90 95
Gln Val Phe Gly Thr Gly Thr Lys Val Thr Val Leu
100 105

<210> 410
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 410
Gln Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val
1 5 10 15
Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser
20 25 30
Trp Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu
35 40 45
Ile Tyr Lys Ala Ser Asn Leu Glu Ser Glu Val Pro Ser Arg Phe Ser
50 55 60
Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln
65 70 75 80
Pro Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ala Tyr Pro
85 90 95
Phe Ile Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
100 105

<210> 411
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 411
Gln Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val
 1   5   10   15
Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser
            20   25   30
Trp Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu
        35   40   45
Ile Tyr Lys Ala Ser Ser Leu Glu Ser Gly Val Pro Ser Arg Phe Ser
    50   55   60
Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln
65   70   75   80
Pro Asp Asp Phe Ala Thr Tyr His Cys Gln Gln Tyr Lys Ser Tyr Trp
                85   90   95
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
            100   105

<210> 412
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 412
Gln Ser Glu Leu Thr Gln Pro Pro Ser Val Ser Glu Ala Pro Arg Gln
 1   5   10   15
Arg Val Thr Val Ser Cys Ser Gly Ser Pro Ser Asn Ile Gly Ser Asn
            20   25   30
Ser Val Asn Trp Tyr Gln Gln Leu Pro Gly Lys Ala Pro Lys Val Val
        35   40   45
Ile Tyr Tyr Asp Asp Leu Val Pro Ser Gly Val Ser Asp Arg Phe Ser
    50   55   60
Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln
65   70   75   80
Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Arg Leu
                85   90   95
Asn Gly Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100   105   110

<210> 413
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 413
Gln Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val
 1   5   10   15
Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Ser
            20   25   30
Trp Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu
        35   40   45
Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser

```
    50                  55                  60
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln
65                  70                  75                  80
Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ala Asn Ser Phe Pro
                85                  90                  95
Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100                 105

<210> 414
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 414
Gln Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
 1               5                  10                  15
Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser
            20                  25                  30
Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu
        35                  40                  45
Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser
    50                  55                  60
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln
65                  70                  75                  80
Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro
                85                  90                  95
Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100                 105

<210> 415
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 415
Gln Asp Ile Gln Met Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro
 1               5                  10                  15
Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser
            20                  25                  30
Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu
        35                  40                  45
Leu Ile Tyr Gly Ala Ser Asn Arg Val Thr Gly Ile Pro Asp Arg Phe
    50                  55                  60
Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu
65                  70                  75                  80
Glu Pro Glu Asp Ser Ala Val Tyr Tyr Cys His Gln Tyr Gly Ser Gln
                85                  90                  95
Tyr Thr Phe Gly Pro Gly Thr Lys Leu Glu Ile Lys
            100                 105

<210> 416
```

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

<220>
<223> Made in a lab

<400> 416
Gln Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
 1   5   10   15
Gly Asp Arg Val Thr Ile Ser Cys Gln Ala Ser Gln His Ile Ser Asn
            20   25   30
Phe Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu
        35   40   45
Ile Tyr Asp Thr Ser Asn Leu Arg Ser Gly Val Pro Ser Arg Phe Ser
    50   55   60
Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln
65   70   75   80
Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asp Asn Phe Pro
                85   90   95
Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100   105

<210> 417
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 417
Gln Ser Glu Leu Thr Gln Pro Pro Ser Val Ser Glu Ala Pro Gly Gln
 1   5   10   15
Arg Val Thr Ile Ser Cys Ser Gly Ser Thr Ser Asn Ile Gly Asn Asn
            20   25   30
Ala Val Ile Trp Tyr Gln Gln Leu Pro Gly Lys Ala Pro Lys Leu Leu
        35   40   45
Ile Tyr Tyr Asp Asp Leu Leu Pro Ser Gly Val Ser Asp Arg Phe Ser
    50   55   60
Gly Ser Lys Ser Gly Thr Ser Gly Ser Leu Ala Ile Ser Gly Leu Gln
65   70   75   80
Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ser Trp Asp Asp Asn Leu
                85   90   95
Asn Gly Pro Leu Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100   105   110

<210> 418
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 418
Gln Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val

```
 1               5                  10                  15
Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser
            20                  25                  30
Trp Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu
        35                  40                  45
Ile Tyr Gln Ala Ser Thr Leu Glu Ser Gly Val Pro Ser Arg Phe Ser
    50                  55                  60
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln
65                  70                  75                  80
Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ala Asn Ser Phe Pro
                85                  90                  95
Ile Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Asn
            100                 105
```

<210> 419
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 419

```
Gln Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
 1               5                  10                  15
Gly Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Asp Ile Thr Asn
            20                  25                  30
Tyr Leu Asn Trp Tyr Leu His Lys Pro Gly Lys Ala Pro Lys Leu Leu
        35                  40                  45
Ile Tyr Asp Ala Ser Asn Leu Gln Thr Gly Val Pro Ser Arg Phe Ser
    50                  55                  60
Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Thr Ser Leu Gln
65                  70                  75                  80
Pro Glu Asp Phe Gly Thr Tyr Tyr Cys Gln Gln Tyr Asp Thr Leu His
                85                  90                  95
Pro Ser Phe Gly Pro Gly Thr Thr Val Asp Ile Lys
            100                 105
```

<210> 420
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 420

```
Gln Ser Ala Leu Thr Gln Pro Pro Ser Ala Ser Gly Ser Pro Gly Gln
 1               5                  10                  15
Ser Val Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp Val Gly Val Tyr
            20                  25                  30
Asp Ser Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Leu
        35                  40                  45
Met Ile Tyr Asp Val Ser Asp Arg Pro Ser Gly Val Ser Asn Arg Phe
    50                  55                  60
Ser Gly Ser Lys Ser Gly Tyr Thr Ala Ser Leu Thr Ile Ser Ala Leu
65                  70                  75                  80
```

```
Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gly Ser Tyr Arg Ala Ser
                85                  90                  95
Ser Ser Tyr Val Phe Gly Thr Gly Thr Lys Val Thr Val Leu
            100                 105                 110

<210> 421
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 421
Gln Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
 1               5                  10                  15
Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asn Ile Tyr His
            20                  25                  30
Tyr Leu His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu
        35                  40                  45
Ile Tyr Ala Ala Ser Thr Leu Glu Ser Gly Val Pro Ser Arg Phe Ser
    50                  55                  60
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Ser Leu Gln
65                  70                  75                  80
Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Thr Tyr Asp Thr Pro
                85                  90                  95
Leu Thr Phe Gly Gly Gly Ser Lys Val Glu Val Lys
            100                 105

<210> 422
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 422
Gln Ser Ala Leu Thr Gln Pro Pro Ser Val Ser Val Ser Pro Gly Gln
 1               5                  10                  15
Thr Ala Ser Ile Thr Cys Ser Gly Asp Lys Leu Gly Glu Lys Phe Ala
            20                  25                  30
Ser Trp Tyr Gln Gln Arg Pro Gly Gln Ser Pro Ile Leu Val Ile Tyr
        35                  40                  45
Gln Asp Ser Lys Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
    50                  55                  60
Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr Gln Thr Met
65                  70                  75                  80
Asp Glu Ala Asp Tyr Tyr Cys Gln Ala Trp Gly Gly Ser Thr Ala Tyr
                85                  90                  95
Val Phe Gly Ser Gly Thr Lys Val Thr Val Leu
            100                 105

<210> 423
<211> 110
<212> PRT
<213> Artificial Sequence
```

<220>
<223> Made in a lab

<400> 423
Gln Asp Ile Gln Met Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro
 1   5   10   15
Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Thr Thr
            20   25   30
Tyr Leu Ala Trp Tyr Gln Gln Arg Pro Gly Gln Ala Pro Arg Leu Leu
        35   40   45
Ile Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser
    50   55   60
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Val Glu
65   70   75   80
Pro Glu Asp Tyr Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asn Trp Pro
                85   90   95
Pro Ser Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu Ser Lys
            100   105   110

<210> 424
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 424
Gln Ser Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln
 1   5   10   15
Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp Val Gly Ser Tyr
            20   25   30
Asn Leu Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Val
        35   40   45
Met Ile Tyr Glu Gly Ser Lys Arg Pro Ser Gly Val Ser Asn Arg Phe
    50   55   60
Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu
65   70   75   80
Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Cys Ser Tyr Ala Gly Arg
                85   90   95
Ser Thr Tyr Val Phe Gly Thr Gly Thr Lys Val Thr Val Leu
            100   105   110

<210> 425
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 425
Gln Ser Glu Leu Thr Gln Thr Pro Ser Val Ser Val Ser Pro Gly Gln
 1   5   10   15
Thr Ala Ser Ile Thr Cys Ser Gly Asn Arg Leu Glu Asp Lys Tyr Val
            20   25   30

```
His Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Val Leu Val Leu Tyr
        35                  40                  45
Gln Asp Asn Lys Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
    50                  55                  60
Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Glu Thr Gln Thr Leu
65                  70                  75                  80
Asp Glu Ala Asp Tyr Tyr Cys Gln Ala Trp Asp Ser Ser Thr Arg Glu
                85                  90                  95
Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100                 105
```

<210> 426
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 426

```
Gln Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val
 1               5                  10                  15
Gly Asp Thr Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Val Ser Asp
            20                  25                  30
Trp Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Asn Leu Leu
        35                  40                  45
Ile Tyr Gly Ala Ser Ser Leu Gln Thr Gly Val Pro Ser Arg Phe Ser
    50                  55                  60
Gly Gly Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln
65                  70                  75                  80
Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ala His Ser Phe Pro
                85                  90                  95
Phe Thr Phe Gly Gly Gly Thr Arg Val Glu Ile Lys
            100                 105
```

<210> 427
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 427

```
Gln Asp Ile Gln Met Thr Gln Ser Pro Ala Thr Leu Ser Val Ser Pro
 1               5                  10                  15
Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Asn Ile Asn Thr
            20                  25                  30
His Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
        35                  40                  45
Ile Phe Gly Ala Ser Thr Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser
    50                  55                  60
Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln
65                  70                  75                  80
Ser Glu Asp Phe Thr Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Leu
                85                  90                  95
Thr Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
```

100 105

<210> 428
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 428
Gln Asp Ile Gln Met Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro
1 5 10 15
Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Gly
20 25 30
Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Leu Gly Gln Ala Pro Arg Leu
35 40 45
Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Thr Pro Asp Arg Phe
50 55 60
Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu
65 70 75 80
Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln His Asn Ser Tyr
85 90 95
Pro Leu Thr Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr
100 105

<210> 429
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 429
Gln Ser Glu Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Glu
1 5 10 15
Thr Ala Thr Val Thr Cys Gly Gly Ile Asn Ile Gly Ser Lys Ser Val
20 25 30
His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Val Val Met Tyr
35 40 45
Phe Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
50 55 60
Asn Ser Gly Asp Thr Ala Thr Leu Thr Ile Ser Arg Val Glu Ala Gly
65 70 75 80
Asp Glu Ala Asp Tyr Tyr Cys Gln Val Trp Asp Ser Arg Ser Asp Gln
85 90 95
Tyr Val Phe Gly Phe Gly Thr Lys Val Thr Val Leu
100 105

<210> 430
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 430
Gln Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val
 1   5   10   15
Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser
            20   25   30
Trp Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu
        35   40   45
Ile Tyr Lys Ala Ser Thr Leu Glu Ser Gly Val Pro Ser Arg Phe Ser
    50   55   60
Ala Gly Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln
65   70   75   80
Pro Asp Asp Phe Gly Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser Tyr Ser
                85   90   95
Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Ile
            100   105

<210> 431
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 431
Gln Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
 1   5   10   15
Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser
            20   25   30
Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu
        35   40   45
Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser
    50   55   60
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln
65   70   75   80
Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro
                85   90   95
Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100   105

<210> 432
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 432
Gln Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
 1   5   10   15
Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Asn Asn
            20   25   30
Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu
        35   40   45
Ile Tyr Thr Ala Ser Thr Leu His Ser Gly Val Pro Ser Arg Phe Ser

```
    50                  55                  60
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Asn Leu Gln
65                  70                  75                  80
Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ala Thr Leu
                85                  90                  95
Arg Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
            100                 105

<210> 433
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 433
Gln Ser Val Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln
 1               5                  10                  15
Ser Ile Thr Ile Ser Cys Ser Gly Ser Ser Ser Asp Val Gly His Tyr
            20                  25                  30
Asp Tyr Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Leu
        35                  40                  45
Met Ile Tyr Asp Val Ser Asn Arg Pro Ser Gly Val Ser Asn Arg Phe
    50                  55                  60
Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu
65                  70                  75                  80
Gln Ala Asp Asp Glu Ala Glu Tyr Tyr Cys Ser Ser Tyr Thr Ser Ser
                85                  90                  95
Gly Thr Arg Val Phe Gly Thr Gly Thr Lys Val Thr Val Leu
            100                 105                 110

<210> 434
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 434
Gln Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val
 1               5                  10                  15
Gly Asp Arg Val Thr Phe Thr Cys Arg Ala Ser Gln Ser Val Asn Asn
            20                  25                  30
Trp Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu
        35                  40                  45
Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser
    50                  55                  60
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln
65                  70                  75                  80
Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Met Pro
                85                  90                  95
Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100                 105

<210> 435
```

<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 435
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Lys Tyr
            20   25   30
Ser Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45
Ser Ser Ile Trp Pro Ser Gly Gly Trp Thr Thr 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 Gly Tyr Tyr Tyr Ala Leu Asp Tyr Trp Gly Gln Gly Asn
            100   105   110
Leu Val Thr Val Ser Ser
        115

<210> 436
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 436
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Phe Tyr
            20   25   30
Gln Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45
Ser Gly Ile Tyr Pro Ser Gly Gly Tyr Thr Lys 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 Leu Gly Tyr Gly Ser Ser Trp Tyr Tyr Phe Asp Tyr Trp
            100   105   110
Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 437
<211> 117
<212> PRT
<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 437
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Lys Tyr
            20   25   30
Ser Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45
Ser Gly Ile Ser Pro Ser Gly Tyr Thr Arg Tyr Ala Asp Ser Val Lys
    50   55   60
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
65   70   75   80
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
                85   90   95
Arg Asp Gln Leu Leu Glu Ala Phe Asp Ile Trp Gly Gln Gly Thr Thr
            100   105   110
Val Thr Val Ser Ser
        115

<210> 438
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 438
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Glu Tyr
            20   25   30
Pro Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45
Ser Gly Ile Tyr Ser Ser Gly Gly Leu Thr Lys 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 His Tyr Gly Asp Tyr Ala Phe Asp Tyr Trp Gly Gln Gly
            100   105   110
Thr Leu Val Thr Val Ser Ser
        115

<210> 439
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 439
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1   5   10   15

```
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Leu Tyr
            20                  25                  30
Glu Met Val Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
Ser Gly Ile Trp Pro Ser Gly Gly Trp Thr Gln 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 Leu Ala Val Ala Gly Trp Asp Tyr 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> 440
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 440
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1               5                  10                  15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Gln Tyr
            20                  25                  30
Asn Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
Ser Trp Ile Ser Ser Ser Gly Gly Thr Glu Tyr Ala Asp Ser Val Lys
    50                  55                  60
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
65                  70                  75                  80
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95
Lys Asp Arg Gly Tyr Gly Ser Gly Ser Tyr Gly Ala Tyr Asp Ala Phe
            100                 105                 110
Asp Ile Trp Gly Gln Gly Lys Met Val Thr Val Ser Ser
        115                 120                 125

<210> 441
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 441
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1               5                  10                  15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser His Tyr
            20                  25                  30
Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
Ser Ser Ile Tyr Pro Ser Gly Gly Ser Thr Leu 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 Trp Gly Val Gly Ala Thr Phe Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110
Leu Val Thr Val Ser Ser
        115
```

<210> 442
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 442

```
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1               5                  10                  15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser His Tyr
            20                  25                  30
Met Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
Ser Tyr Ile Tyr Pro Ser Gly Gly Trp Thr Ser 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 Phe Asp Tyr Thr Ile Gly Phe Asp Phe Trp Gly Gln Gly Thr
            100                 105                 110
Leu Val Thr Val Ser Ser
        115
```

<210> 443
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 443

```
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1               5                  10                  15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser His Tyr
            20                  25                  30
Gly Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
Ser Gly Ile Arg Ser Ser Gly Gly Val Thr Asn 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 Gly Ser Gly Trp Ser Lys Ala Phe Asp Ile Trp Gly Gln
            100                 105                 110
Gly Thr Met Val Thr Val Ser Ser
        115                 120

<210> 444
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 444
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1               5                  10                  15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser His Tyr
            20                  25                  30
Asn Met Arg Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
Ser Ser Ile Ser Pro Ser Gly Gly Phe Thr Gly 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 Ile Asn Tyr Tyr Asp Ser Ser Gly Tyr Tyr Pro Pro Val
            100                 105                 110
Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
        115                 120                 125

<210> 445
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 445
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1               5                  10                  15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Trp Tyr
            20                  25                  30
Asn Met Leu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
Ser Ser Ile Ser Pro Ser Gly Gly Tyr Thr Val Tyr Ala Asp Ser Val
    50                  55                  60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
Ala Arg Asp Arg Gly Gly Ser Pro Phe Arg Pro Asp Ala Phe Asp Ile
            100                 105                 110
Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
        115                 120
```

<210> 446
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 446
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Glu Tyr
            20   25   30
Asp Met Leu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45
Ser Ser Ile Trp Pro Ser Gly Gly Phe Thr Gln Tyr Ala Asp Ser Val
    50   55   60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65   70   75   80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95
Ala Arg Asn Tyr Tyr Asp Phe Trp Ser Gly Pro Tyr Tyr Tyr Gly Met
            100   105   110
Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
        115   120   125

<210> 447
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 447
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Gly Tyr
            20   25   30
Val Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45
Ser Ser Ile Ser Pro Ser Gly Gly Tyr Thr Leu Tyr Ala Asp Ser Val
    50   55   60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65   70   75   80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95
Ala Arg Ala Phe Ser Thr Arg Trp Tyr Trp Gly Ala Phe Asp Ile Trp
            100   105   110
Gly Gln Gly Thr Met Val Thr Val Ser Ser
        115   120

<210> 448
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 448
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ile Tyr
            20   25   30
His Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45
Ser Gly Ile Ser Ser Ser Gly Gly Arg Thr Asn 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 Ser Ser Tyr Arg Ala Ala Gly Trp Val Asp Tyr Tyr Tyr Gly Met
            100   105   110
Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
        115   120   125

<210> 449
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 449
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Leu Tyr
            20   25   30
Asp Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45
Ser Arg Ile Tyr Ser Ser Gly Gly Thr Thr Gln 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 Met Tyr Tyr Cys
                85   90   95
Ala Arg Asp Pro Gly Tyr Gly Ser His His Ser Phe Asp Tyr Trp Gly
            100   105   110
Gln Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 450
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 450
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

```
 1               5                  10                  15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30
Tyr Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
Ser Gly Ile Tyr Ser Ser Gly Gly Pro Thr Gln Tyr Ala Asp Ser Val
    50                  55                  60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
Ala Arg Ala Gly Gly Asp Ala Phe Asp Ile Trp Gly Gln Gly Thr Met
            100                 105                 110
Val Thr Val Ser Ser
        115
```

<210> 451
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 451

```
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1               5                  10                  15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30
Glu Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
Ser Ser Ile Ser Pro Ser Gly Gly Tyr Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
Ala Thr Met Thr Thr Ser Gly Phe His Leu Ile Trp Gly Gln Gly Thr
            100                 105                 110
Met Val Thr Val Ser Ser
        115
```

<210> 452
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 452

```
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1               5                  10                  15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
            20                  25                  30
Pro Met Gln Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
```

```
Ser Trp Ile Gly Pro Ser Gly Gly Trp Thr Val 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 Gly Ile Ala Gly Phe Leu Trp Gly Gln Gly Thr Leu
            100                 105                 110
Val Thr Val Ser Ser
        115
```

<210> 453
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 453

```
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1               5                  10                  15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Trp Tyr
            20                  25                  30
Leu Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
Ser Gly Ile Trp Pro Ser Gly Gly His Thr Leu 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 Pro Leu Leu Trp Phe Gly Glu Leu Ser Tyr Asn Trp Phe
            100                 105                 110
Asp Pro Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120                 125
```

<210> 454
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 454

```
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1               5                  10                  15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Tyr Tyr
            20                  25                  30
Glu Asn Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
        35                  40                  45
Val Ser Gly Ile Tyr Pro Ser Gly Gly Leu Thr Tyr Tyr Ala Asp Ser
    50                  55                  60
Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu
65                  70                  75                  80
Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr
```

```
                85                  90                  95
Cys Ala Arg Ser Arg Arg Tyr Tyr Asp Ser Ser Asp Ala Phe Asp Ile
            100                 105                 110
Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
        115                 120

<210> 455
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 455
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1               5                  10                  15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr
            20                  25                  30
Val Met Tyr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
Ser Gly Ile Gly Pro Ser Gly Gly Asn Thr Phe 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 Pro Gly Asp Phe Trp Ser Gly Tyr Tyr Gly Met Asp Val
            100                 105                 110
Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
        115                 120

<210> 456
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 456
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1               5                  10                  15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Phe Tyr
            20                  25                  30
Gly Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
Ser Ser Ile Tyr Pro Ser Gly Gly Tyr Thr Asp Tyr Ala Asp Ser Val
    50                  55                  60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
Ala Arg Ser Ala Gly Gly Trp Ile Gly Gly Gly Ala Phe Asp Ile Trp
            100                 105                 110
Gly Gln Gly Thr Met Val Thr Val Ser Ser
        115                 120
```

<210> 457
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 457
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Lys Tyr
            20   25   30
Pro Met Met Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45
Ser Tyr Ile Tyr Pro Ser Gly Gly Lys Thr Ala Tyr Ala Asp Ser Val
    50   55   60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65   70   75   80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95
Ala Thr Tyr Gly Ser Gly Ser Tyr Tyr Leu Tyr Tyr Tyr Tyr Tyr Tyr
            100   105   110
Met Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
        115   120   125

<210> 458
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 458
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Trp Tyr
            20   25   30
Ser Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45
Ser Tyr Ile Val Pro Ser Gly Gly Glu Thr Ile Tyr Ala Asp Ser Val
    50   55   60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65   70   75   80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95
Ala Lys Asn Leu Gly Glu Gly Phe Trp Ser Asp Tyr Tyr Pro Pro Leu
            100   105   110
Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115   120   125

<210> 459
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 459
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser His Tyr
            20   25   30
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45
Ser Ser Ile Tyr Pro Gly Met Thr Gln Tyr Ala Asp Ser Val Lys Gly
    50   55   60
Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln
65   70   75   80
Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
                85   90   95
Asp Arg Gly Ser Gly Ile Asp Ala Phe Asp Ile Trp Gly Gln Gly Thr
            100   105   110
Met Val Thr Val Ser Ser
        115

<210> 460
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 460
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Trp Tyr
            20   25   30
Asp Met Leu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45
Ser Val Ile Ser Pro Ser Gly Gly Arg Thr Phe 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 Val Thr Arg Ser Met Tyr Ser Ser Ser Trp Tyr Gly Ala Pro Pro
            100   105   110
Thr His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115   120   125

<210> 461
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 461

```
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1               5                  10                  15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Trp Tyr
            20                  25                  30
Lys Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
Ser Gly Ile Ser Ser Ser Gly Gly Leu Thr Lys 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
Thr Thr Glu Arg Arg Gly Asp Gly Gly Ala Phe Asp Ile Trp Gly Gln
            100                 105                 110
Gly Thr Met Val Thr Val Ser Ser
        115                 120
```

<210> 462
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 462

```
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1               5                  10                  15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Glu Tyr
            20                  25                  30
Thr Met Tyr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
Ser Tyr Ile Ser Pro Ser Gly Gly Thr Thr Asn Tyr Ala Asp Ser Val
    50                  55                  60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
Ala Lys Gly Ala Trp Gly Asp Ile Tyr Tyr Tyr Gly Met Asp Val Trp
            100                 105                 110
Gly Gln Gly Thr Thr Val Thr Val Ser Ser
        115                 120
```

<210> 463
<211> 115
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 463

```
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1               5                  10                  15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30
Trp Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
```

```
        35                  40                  45
Ser Ser Ile Tyr Pro Ser Gly Gly Ser Thr Glu Tyr Ala Asp Ser Val
    50                  55                  60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
Ala Lys Gly Ile Trp Phe Asp Pro Trp Gly Gln Gly Thr Leu Val Thr
            100                 105                 110
Val Ser Ser
        115

<210> 464
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 464
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1               5                  10                  15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Tyr
            20                  25                  30
Gly Met Met Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
Ser Tyr Ile Ser Ser Ser Gly Gly Phe Thr Arg 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 Val Gly Gly Tyr Ser Tyr Gly Pro His Phe Asp Phe Trp Gly
            100                 105                 110
Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120

<210> 465
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 465
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1               5                  10                  15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Trp Tyr
            20                  25                  30
His Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
Ser Trp Ile Ser Pro Ser Gly Gly Phe Thr Lys 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 Tyr Asp Ser Arg Ala Ala Ala Gly Thr Asn Ala Phe Asp Ile
            100   105   110
Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
        115   120

<210> 466
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 466
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Pro Tyr
            20   25   30
Lys Met Val Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45
Ser Gly Ile Ser Pro Ser Gly Gly Tyr Thr Tyr Tyr Ala Asp Ser Val
    50   55   60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65   70   75   80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95
Ala Arg Gly Gly Tyr Gly Trp Ser Tyr Tyr Tyr Tyr Gly Met Asp Val
            100   105   110
Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
        115   120

<210> 467
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 467
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Tyr
            20   25   30
Trp Met Tyr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45
Ser Val Ile Ser Ser Ser Gly Gly His Thr Phe 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 Tyr Glu Gly Gly Ser Asn Asp Tyr Trp Gly Gln Gly Thr
            100   105   110
Leu Val Thr Val Ser Ser

115

<210> 468
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 468
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Tyr
            20   25   30
Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45
Ser Ser Ile Tyr Ser Ser Gly Gly Tyr Thr Ala 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 Met Tyr Tyr Cys
                85   90   95
Ala Arg Val Pro His Val Phe Arg Gly Glu Leu Asp Tyr Trp Gly Gln
            100   105   110
Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 469
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 469
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Phe Tyr
            20   25   30
Thr Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45
Ser Ser Ile Tyr Pro Ser Gly Gly Gln Thr Leu 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 Pro Asp Ser Tyr Gly Tyr Leu Tyr Tyr Gly Met Asp Val Trp
            100   105   110
Gly Gln Gly Thr Thr Val Thr Val Ser Ser
        115   120

<210> 470
<211> 115
<212> PRT

<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 470
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Trp Tyr
            20   25   30
Pro Met Glu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45
Ser Gly Ile Gly Pro Ser Gly Gly Gln Thr Thr 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 Ser Phe Ile Trp Gly Gln Gly Thr Met Val Thr
            100   105   110
Val Ser Ser
        115

<210> 471
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 471
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Leu Tyr
            20   25   30
Lys Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45
Ser Val Ile Gly Ser Ser Gly Gly Arg Thr Pro Tyr Ala Asp Ser Val
    50   55   60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65   70   75   80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95
Ala Arg Ala Pro Leu Ser Gly Trp Phe Gly Gln Ala His Asp Ala Phe
            100   105   110
Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
        115   120   125

<210> 472
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 472
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr
            20   25   30
Glu Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45
Ser Gly Ile Val Pro Ser Gly Gly Val Thr Tyr Tyr Ala Asp Ser Val
    50   55   60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65   70   75   80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95
Ala Arg Gly Pro Tyr Ser Tyr Gly His Asp Tyr Gly Met Asp Val Trp
            100   105   110
Gly Gln Gly Thr Thr Val Thr Val Ser Ser
        115   120

<210> 473
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 473
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Val Tyr
            20   25   30
Pro Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45
Ser Ser Ile Tyr Ser Ser Gly Gly Phe Thr Met 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 Glu Gly Val Ala
                85   90   95
Asp Ala Phe Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
            100   105   110

<210> 474
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 474
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20   25   30
Thr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45

```
Ser Ser Ile Ser Pro Ser Gly Gly Met Thr Phe 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 Thr Tyr Asp Phe Trp Ser Gly Tyr Phe Asp Tyr Trp Gly Gln
            100                 105                 110
Gly Thr Leu Val Thr Val Ser Ser
        115                 120
```

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

<220>
<223> Made in a lab

<400> 475

```
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1               5                  10                  15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr
            20                  25                  30
Glu Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
Ser Val Ile Trp Ser Ser Gly Gly His Thr Trp Tyr Ala Asp Ser Val
    50                  55                  60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
Ala Arg Ser Asn Gln Gly Asp Phe Trp Ser Gly Tyr Pro Phe Ala Phe
            100                 105                 110
Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
        115                 120                 125
```

<210> 476
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 476

```
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1               5                  10                  15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Tyr
            20                  25                  30
Asn Met Tyr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
Ser Tyr Ile Ser Pro Ser Gly Gly Met Thr Lys 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 Gly Val Leu Gly Tyr Tyr Gly Met Asp Val Trp Gly Gln
            100                 105                 110
Gly Thr Thr Val Thr Val Ser Ser
        115                 120

<210> 477
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 477
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1               5                  10                  15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Leu Tyr
            20                  25                  30
Ser Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
Ser Ser Ile Ser Ser Ser Gly Gly Ala Thr Leu 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 Leu Ile Ser Ser Gly Tyr Tyr Pro Asp Ala Phe Asp Ile
            100                 105                 110
Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
        115                 120

<210> 478
<211> 128
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 478
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1               5                  10                  15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Gln Tyr
            20                  25                  30
Met Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
Ser Ser Ile Ser Ser Ser Gly Gly Trp Thr Ser Tyr Ala Asp Ser Val
    50                  55                  60
Lys Gly Ser 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 Pro Leu Ala Leu Gly Tyr Asp Phe Trp Ser Gly Tyr Gln Ala
            100                 105                 110
Ala Gly Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120                 125
```

<210> 479
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 479
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Trp Tyr
            20   25   30
Ser Met Val Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45
Ser Ser Ile Val Pro Ser Gly Gly Leu Thr Trp 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 Val Tyr Gly Asp Tyr Tyr Phe Asp Asn Trp Gly Gln Gly
            100   105   110
Thr Leu Val Thr Val Ser Ser
        115

<210> 480
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 480
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Tyr Tyr
            20   25   30
Asn Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45
Ser Ser Ile Ser Pro Ser Gly Gly Arg Thr Gly 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 Val Ser Gly Phe Tyr Ala Ala Phe Asp Tyr Trp Gly Gln Gly
            100   105   110
Thr Leu Val Thr Val Ser Ser
        115

<210> 481
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 481
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Trp Tyr
            20   25   30
Trp Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45
Ser Ser Ile Ser Pro Ser Gly Gly His Thr Ser Tyr Ala Asp Ser Val
    50   55   60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65   70   75   80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95
Ala Lys Ser Ser Gly Trp Tyr Glu Asp Tyr Phe Asp Tyr Trp Gly Gln
            100   105   110
Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 482
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 482
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Pro Tyr
            20   25   30
Glu Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45
Ser Val Ile Gly Pro Ser Gly Gly Tyr Thr Glu 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 Tyr Asp Phe Trp Ser Gly Tyr Tyr Asp Ala Phe Asp Ile
            100   105   110
Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
        115   120

<210> 483
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 483

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Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1               5                  10                  15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30
Phe Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
Ser Ser Ile Trp Pro Ser Gly Gly Asn Thr Thr 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 His Val Gly Trp Gly Arg Tyr Phe Asp Tyr Trp Gly Gln Gly
            100                 105                 110
Thr Leu Val Thr Val Ser Ser
        115
```

<210> 484
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 484

```
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1               5                  10                  15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ala Tyr
            20                  25                  30
Arg Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
Ser Tyr Ile Ser Ser Ser Gly Gly Arg Thr Asp 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
Thr Thr Gly Gly Leu Arg Tyr Phe Asp Trp Leu Ala Pro Ser Met Asp
            100                 105                 110
Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120
```

<210> 485
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 485

```
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1               5                  10                  15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ala Tyr
            20                  25                  30
Ser Met Val Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
```

```
        35                  40                  45
Ser Tyr Ile Tyr Pro Ser Gly Gly Ile Thr Thr 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 Gly Gln Val Phe Asp Ile Trp Gly Gln Gly Thr Thr Val
            100                 105                 110
Thr Val Ser Ser
        115

<210> 486
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 486
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1               5                  10                  15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Tyr
            20                  25                  30
Ala Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
Ser Arg Ile Val Pro Ser Gly Gly Met Thr Ser 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
Thr Thr Asp Asp Phe Trp Ser Gly Met Asp Val Trp Gly Gln Gly Thr
            100                 105                 110
Thr Val Thr Val Ser Ser
        115

<210> 487
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 487
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1               5                  10                  15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Leu Tyr
            20                  25                  30
Asn Met Gln Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
Ser Gly Ile Ser Leu Ser Gly Gly Lys Thr Phe 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 Tyr Gly Val Ala Thr Leu Asp Ala Phe Asp Ile Trp Gly
100 105 110
Gln Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 488
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 488
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ala Tyr
20 25 30
Thr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
Ser Ser Ile Tyr Pro Ser Gly Gly Thr Thr Pro 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 Thr Tyr Tyr Cys
85 90 95
Ala Arg Val Val Asn Ile Asp Phe Trp Ser Gly Tyr Asn Met Arg Ser
100 105 110
Ala Phe Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
115 120 125

<210> 489
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 489
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
20 25 30
Leu Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
Ser Val Ile Ser Ser Ser Gly Gly Pro Thr Ala 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 Val Gly Leu Asp Tyr Gly Ile Leu Gly Ala Phe Asp Ile Trp
100 105 110
Gly Gln Gly Thr Met Val Thr Val Ser Ser

115 120

<210> 490
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 490
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Glu Tyr
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 Arg Ser Ser Gly Gly Trp Thr Lys Tyr Ala Asp Ser Val
50 55 60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Lys Gly Leu Gly Ala Thr Ser Gly Glu Phe Asp Tyr Trp Gly Gln
100 105 110
Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 491
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 491
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Lys Tyr
20 25 30
Asp Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
Ser Ser Ile Trp Pro Ser Gly Gly Trp Thr Ser Tyr Ala Asp Ser Val
50 55 60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Lys Ser Arg Gly Ser Pro Trp Tyr Gly Asp Phe Asp His Trp Gly
100 105 110
Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 492
<211> 118
<212> PRT

<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 492
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Met Tyr
            20   25   30
Thr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45
Ser Trp Ile Ser Pro Ser Gly Gly Trp Thr Lys 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 Val Ser Pro Trp Gly Gly Pro Phe Asp Tyr Trp Gly Gln Gly Thr
            100   105   110
Leu Val Thr Val Ser Ser
        115

<210> 493
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 493
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Gln Tyr
            20   25   30
Phe Met Met Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45
Ser Ser Ile Ser Pro Ser Gly Gly Tyr Thr Gln Tyr Ala Asp Ser Val
    50   55   60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65   70   75   80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95
Ala Lys Thr Gly Asp Tyr Thr Arg Tyr Tyr Ser Tyr Gly Met Asp Val
            100   105   110
Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 494
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 494
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Gly Tyr
            20   25   30
Ser Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45
Ser Gly Ile Tyr Ser Ser Gly Gly Trp Thr Trp 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
Thr Arg Asp Gln Ser Phe Ser Tyr Asp Ser Ser Leu Asp Ala Phe Asp
            100   105   110
Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
        115   120

<210> 495
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 495
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Leu Tyr
            20   25   30
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45
Ser Ser Ile Val Pro Ser Gly Gly Leu Thr Arg 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 Thr Tyr Tyr Cys
                85   90   95
Ala Arg Leu Ala Tyr Tyr Asp Phe Trp Ser Gly Arg Asp Ala Phe Asp
            100   105   110
Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
        115   120

<210> 496
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 496
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser His Tyr
            20   25   30

```
Gly Met Asp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
Ser Ser Ile Tyr Ser Ser Gly Gly Tyr Thr Leu 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 Thr Tyr Tyr Cys
                85                  90                  95
Ala Thr Arg Thr Trp Ala Asp Ala Phe Asp Val Trp Gly Gln Gly Thr
            100                 105                 110
Thr Val Thr Val Ser Ser
        115

<210> 497
<211> 2
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 497
Asn Ser
 1

<210> 498
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 498
Ser Cys Pro Pro Cys Pro
 1               5

<210> 499
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 499
Gly Gly Gly Gly Ser Gly Asn Ser
 1               5

<210> 500
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab
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<400> 500
Gly Cys Pro Pro Cys Pro Asn Ser
 1   5

<210> 501
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 501
Gly Ser Pro Pro Ser Pro Asn Ser
 1   5

<210> 502
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 502
Gly Ser Pro Pro Ser Pro Asn Ser
 1   5

<210> 503
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 503
Gly Cys Pro Pro Cys Pro Asn Ser
 1   5

<210> 504
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 504
Gly Cys Pro Pro Cys Pro Asn Ser
 1   5

<210> 505
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 505
Gly Cys Pro Pro Cys Pro Gly Asn Ser
 1   5

<210> 506
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 506
Gly Cys Pro Pro Cys Pro Ala Asn Ser
 1   5

<210> 507
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 507
Gly Cys Pro Pro Cys Pro Ala Asn Ser
 1   5

<210> 508
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 508
Glu Glu Glu Glu Asp Glu Gly Asn Ser
 1   5

<210> 509
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 509
Asn Tyr Gly Gly Gly Gly Ser Gly Asn Ser
 1   5   10

<210> 510
<211> 10

<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 510
Val Ser Glu Arg Pro Phe Pro Pro Asn Ser
 1   5   10

<210> 511
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 511
Glu Pro Lys Ser Cys Asp Lys Thr Cys Cys Pro
 1   5   10

<210> 512
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 512
Ser Gln Pro Glu Ile Val Pro Ile Ser Asn Ser
 1   5   10

<210> 513
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 513
Gly Gly Gly Gly Ser Cys Pro Pro Cys Pro Asn Ser
 1   5   10

<210> 514
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 514
Lys Ala Asp Phe Leu Thr Pro Ser Ile Gly Asn Ser
 1   5   10

<210> 515
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 515
Gln Met Asn Ser Glu Leu Ser Val Leu Ala Asn Ser
 1   5   10

<210> 516
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 516
Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Cys Pro
 1   5   10

<210> 517
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 517
Glu Pro Lys Ser Cys Asp Lys Thr Cys Pro Pro Cys Pro
 1   5   10

<210> 518
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 518
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Asn Ser
 1   5   10

<210> 519
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 519
Gly Cys Pro Pro Cys Pro Gly Gly Gly Gly Ser Asn Ser
 1   5   10

<210> 520
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 520
Gly Gly Gly Gly Ser Cys Pro Pro Cys Pro Gly Asn Ser
 1   5   10

<210> 521
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 521
Gly Cys Pro Pro Cys Pro Gly Gly Gly Gly Ser Asn Ser
 1   5   10

<210> 522
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 522
Gly Gly Gly Ala Ser Cys Pro Pro Cys Pro Gly Asn Ser
 1   5   10

<210> 523
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 523
Gly Gly Gly Ala Ser Cys Pro Pro Cys Ala Gly Asn Ser
 1   5   10

<210> 524
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 524
Gly Gly Gly Ala Ser Cys Pro Pro Cys Ala Gly Asn Ser
 1   5   10

<210> 525
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 525
Asn Tyr Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Asn Ser
 1   5   10   15

<210> 526
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 526
Leu Ser Val Lys Ala Asp Phe Leu Thr Pro Ser Ile Gly Asn Ser
 1   5   10   15

<210> 527
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 527
Leu Ser Val Leu Ala Asn Phe Ser Gln Pro Glu Ile Gly Asn Ser
 1   5   10   15

<210> 528
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 528
Leu Lys Ile Gln Glu Arg Val Ser Lys Pro Lys Ile Ser Asn Ser
 1   5   10   15

<210> 529
<211> 15

<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 529
Leu Asp Val Ser Glu Arg Pro Phe Pro Pro His Ile Gln Asn Ser
 1   5   10   15

<210> 530
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 530
Arg Glu Gln Leu Ala Glu Val Thr Leu Ser Leu Lys Ala Asn Ser
 1   5   10   15

<210> 531
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 531
Arg Ile His Gln Met Asn Ser Glu Leu Ser Val Leu Ala Asn Ser
 1   5   10   15

<210> 532
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 532
Asp Thr Lys Gly Lys Asn Val Leu Glu Lys Ile Phe Ser Asn Ser
 1   5   10   15

<210> 533
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 533
Leu Pro Pro Glu Thr Gln Glu Ser Gln Glu Val Thr Leu Asn Ser
 1   5   10   15

<210> 534
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 534
Arg Ile His Leu Asn Val Ser Glu Arg Pro Phe Pro Pro Asn Ser
 1   5   10   15

<210> 535
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 535
Leu Ser Val Lys Ala Asp Phe Leu Thr Pro Ser Ile Gly Asn Ser
 1   5   10   15

<210> 536
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 536
Leu Ser Val Leu Ala Asn Phe Ser Gln Pro Glu Ile Gly Asn Ser
 1   5   10   15

<210> 537
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 537
Leu Ser Val Leu Ala Asn Phe Ser Gln Pro Glu Ile Gly Asn Ser
 1   5   10   15

<210> 538
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 538
Arg Ile His Gln Met Asn Ser Glu Leu Ser Val Leu Ala Asn Ser
 1   5   10   15

<210> 539
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 539
Lys Pro Phe Phe Thr Cys Gly Ser Ala Asp Thr Cys Pro Asn Ser
 1   5   10   15

<210> 540
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 540
Lys Pro Phe Phe Thr Cys Gly Ser Ala Asp Thr Cys Pro Asn Ser
 1   5   10   15

<210> 541
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 541
Gln Tyr Asn Cys Pro Gly Gln Tyr Thr Phe Ser Met Pro Asn Ser
 1   5   10   15

<210> 542
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 542
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 1   5   10   15

<210> 543
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 543
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro
 1   5   10   15

<210> 544
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 544
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Ser
 1   5   10   15

<210> 545
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 545
Glu Pro Lys Ser Cys Asp Lys Thr His Thr Ser Pro Pro Cys Ser
 1   5   10   15

<210> 546
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 546
Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
 1   5   10   15

<210> 547
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 547
Glu Pro Lys Ser Cys Asp Lys Thr His Thr Ser Pro Pro Ser Ser
 1   5   10   15

<210> 548
<211> 15

<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 548
Pro Arg Gly Pro Thr Ile Lys Pro Cys Pro Pro Cys Lys Cys Pro
 1   5   10   15

<210> 549
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 549
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser Pro Pro Ser Ser
 1   5   10   15

<210> 550
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 550
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser Pro Pro Cys Ser
 1   5   10   15

<210> 551
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 551
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Ser Ser
 1   5   10   15

<210> 552
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 552
Glu Pro Lys Ser Cys Asp Lys Thr His Thr Ser Pro Pro Cys Pro
 1   5   10   15

<210> 553
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 553
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser Pro Pro Ser Pro
 1   5   10   15

<210> 554
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 554
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser Pro Pro Cys Pro
 1   5   10   15

<210> 555
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 555
Glu Pro Lys Ser Cys Asp Lys Thr His Thr Ser Pro Pro Ser Pro
 1   5   10   15

<210> 556
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 556
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Ser Pro
 1   5   10   15

<210> 557
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 557
Gly Gly Gly Gly Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
 1   5   10   15

<210> 558
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 558
Glu Pro Lys Ser Cys Gly Gly Gly Gly Gly Cys Pro Pro Cys Pro
 1   5   10   15

<210> 559
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 559
Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Gly Gly Cys Pro
 1   5   10   15

<210> 560
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 560
Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Gly
 1   5   10   15

<210> 561
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 561
Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Ser Pro
 1   5   10   15

<210> 562
<211> 15
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<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 562
Glu Pro Lys Ser Cys Asp Lys Cys His Thr Cys Pro Pro Cys Pro
 1   5   10   15

<210> 563
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 563
Glu Pro Lys Ser Cys Asp Lys Thr Cys Cys Cys Pro Pro Cys Pro
 1   5   10   15

<210> 564
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 564
Glu Pro Lys Ser Cys Pro Pro Pro Pro Pro Cys Pro Pro Cys Pro
 1   5   10   15

<210> 565
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 565
Pro Pro Pro Pro Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
 1   5   10   15

<210> 566
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 566
Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Trp Trp Cys Pro
 1   5   10   15

<210> 567
<211> 15

<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 567
Glu Pro Lys Ser Cys Asp Trp Trp His Thr Cys Pro Pro Cys Pro
 1   5   10   15

<210> 568
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 568
Glu Pro Lys Cys Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro
 1   5   10   15

<210> 569
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 569
Glu Pro Lys Ser Asp Cys Lys Thr His Thr Cys Pro Pro Cys Pro
 1   5   10   15

<210> 570
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 570
Glu Pro Lys Ser Asp Cys Trp Trp His Thr Cys Pro Pro Cys Pro
 1   5   10   15

<210> 571
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 571
Glu Pro Lys Ser Cys Asp Phe Phe His Thr Cys Pro Pro Cys Pro
 1   5   10   15

<210> 572
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 572
Glu Pro Lys Ser Cys Asp Trp Trp Trp Thr Cys Pro Pro Cys Pro
 1   5   10   15

<210> 573
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 573
Glu Pro Lys Ser Cys Trp Trp Thr His Thr Cys Pro Pro Cys Pro
 1   5   10   15

<210> 574
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 574
Glu Pro Trp Trp Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
 1   5   10   15

<210> 575
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 575
Ser Gln Pro Glu Ile Val Pro Ile Ser Cys Pro Pro Cys Pro Asn Ser
 1   5   10   15

<210> 576
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 576
Thr Gly Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys
 1   5   10   15
Pro

<210> 577
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 577
Glu Pro Lys Ser Thr Asp Lys Thr His Thr Cys Pro Pro Cys Pro Asn
 1   5   10   15
Ser

<210> 578
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 578
Glu Pro Lys Ser Thr Asp Lys Thr His Thr Ser Pro Pro Ser Pro Asn
 1   5   10   15
Ser

<210> 579
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 579
Glu Pro Lys Ser Thr Asp Lys Thr His Thr Cys Pro Pro Cys Pro Asn
 1   5   10   15
Ser

<210> 580
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 580

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Asn
 1   5   10   15
Ser

<210> 581
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 581
Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Gly Gly Gly Pro
 1   5   10   15
Cys Pro

<210> 582
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 582
Glu Pro Lys Ser Cys Asp Gly Gly Gly Lys Thr His Thr Cys Pro Pro
 1   5   10   15
Cys Pro

<210> 583
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 583
Glu Pro Lys Ser Cys Asp Pro Pro Pro Lys Thr His Thr Cys Pro Pro
 1   5   10   15
Cys Pro

<210> 584
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 584
Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Pro Pro Pro

1 5 10 15
Cys Pro

<210> 585
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 585
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
1 5 10 15
Asn Ser

<210> 586
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 586
Asn Tyr Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
1 5 10 15
Ser Asn Ser

<210> 587
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 587
Leu Ser Val Lys Ala Asp Phe Leu Thr Pro Ser Ile Ser Pro Pro Cys
1 5 10 15
Pro Asn Ser

<210> 588
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 588
Ser Val Leu Ala Asn Phe Ser Gln Pro Glu Ile Ser Cys Pro Pro Cys
1 5 10 15

Pro Asn Ser

<210> 589
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 589
Gly Gln Arg His Asn Asn Ser Ser Leu Asn Thr Arg Thr Gln Lys Ala
 1   5   10   15
Arg His Ser Pro
            20

<210> 590
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 590
Leu Ser Val Leu Ala Asn Phe Ser Gln Pro Glu Ile Ser Cys Pro Pro
 1   5   10   15
Cys Pro Asn Ser
            20

<210> 591
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 591
Leu Lys Ile Gln Glu Arg Val Ser Lys Pro Lys Ile Ser Cys Pro Pro
 1   5   10   15
Cys Pro Asn Ser
            20

<210> 592
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 592
Arg Glu Gln Leu Ala Glu Val Thr Leu Ser Leu Lys Ala Cys Pro Pro
 1   5   10   15
Cys Pro Asn Ser

20

<210> 593
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 593
Arg Ile His Gln Met Asn Ser Glu Leu Ser Val Leu Ala Cys Pro Pro
 1   5   10   15
Cys Pro Asn Ser
            20

<210> 594
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 594
Arg Ile His Leu Asn Val Ser Glu Arg Pro Phe Pro Pro Cys Pro Pro
 1   5   10   15
Cys Pro Asn Ser
            20

<210> 595
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 595
Asn Ser Leu Phe Asn Gln Glu Val Gln Ile Pro Leu Thr Glu Ser Tyr
 1   5   10   15
Cys Pro Asn Ser
            20

<210> 596
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 596
Glu Glu Glu Glu Asp Glu Glu Asp Glu Glu Asp Glu Glu Glu Glu Glu
 1   5   10   15
Asp Gly Asn Ser
            20

<210> 597
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 597
Leu Asp Val Ser Glu Arg Pro Phe Pro Pro His Ile Gln Ser Cys Pro
 1   5   10   15
Pro Cys Pro Asn Ser
            20

<210> 598
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 598
Asp Thr Lys Gly Lys Asn Val Leu Glu Lys Ile Phe Asp Ser Cys Pro
 1   5   10   15
Pro Cys Pro Asn Ser
            20

<210> 599
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 599
Leu Pro Pro Glu Thr Gln Glu Ser Gln Glu Val Thr Leu Ser Cys Pro
 1   5   10   15
Pro Cys Pro Asn Ser
            20

<210> 600
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 600
Glu Pro Ala Phe Thr Pro Gly Pro Asn Ile Glu Leu Gln Lys Asp Ser
 1   5   10   15
Asp Cys Pro Asn Ser
            20

<210> 601
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 601
Gln Arg His Asn Asn Ser Ser Leu Asn Thr Arg Thr Gln Lys Ala Arg
 1   5   10   15
His Cys Pro Asn Ser
            20

<210> 602
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 602
Gln Arg His Asn Asn Ser Ser Leu Asn Thr Arg Thr Gln Lys Ala Arg
 1   5   10   15
His Ser Pro Asn Ser
            20

<210> 603
<211> 36
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 603
Asn Tyr Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 1   5   10   15
Ser Asn Tyr Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
            20   25   30
Gly Ser Asn Ser
        35

<210> 604
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 604
Arg Thr Arg Tyr Leu Gln Val Ser Gln Gln Leu Gln Gln Thr Asn Arg
 1   5   10   15
Val Leu Glu Val Thr Asn Ser Ser Leu Arg Gln Gln Leu Arg Leu Lys
            20   25   30

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Ile Thr Gln Leu Gly Gln Ser Ala Glu Asp Leu Gln Gly Ser Arg Arg
        35                  40                  45
Glu Leu Ala Gln Ser Gln Glu Ala Leu Gln Val Glu Gln Arg Ala His
    50                  55                  60
Gln Ala Ala Glu Gly Gln Leu Gln Ala Cys Gln Ala Asp Arg Gln Lys
65                  70                  75                  80
Thr Lys Glu Thr Leu Gln Ser Glu Glu Gln Gln Arg Arg Ala Leu Glu
                85                  90                  95
Gln Lys Leu Ser Asn Met Glu Asn Arg Leu Lys Pro Phe Phe Thr Cys
            100                 105                 110
Gly Ser Ala Asp Thr Cys Cys Pro Asn Ser
        115                 120
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<210> 605
<211> 1971
<212> DNA
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 605

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cccctcagca atgttgtttg tgagtggggt cctcggagca ccccatccct gacgacaaag     180
gctgtgctct tggtgaggaa gtttcagaac agtccggccg aagacttcca ggagccgtgc     240
cagtattccc aggagtccca gaagttctcc tgccagttag cagtcccgga gggagacagc     300
tctttctaca tagtgtccat gtgcgtcgcc agtagtgtcg ggagcaagtt cagcaaaact     360
caaacctttc agggttgtgg aatcttgcag cctgatccgc ctgccaacat cacagtcact     420
gccgtggcca gaaacccccg ctggctcagt gtcacctggc aagaccccca ctcctggaac     480
tcatctttct acagactacg gtttgagctc agatatcggg ctgaacggtc aaagacattc     540
acaacatgga tggtcaagga cctccagcat cactgtgtca tccacgacgc ctggagcggc     600
ctgaggcacg tggtgcagct tcgtgcccag gaggagttcg ggcaaggcga gtggagcgag     660
tggagcccgg aggccatggg cacgccttgg acagaatcca ggagtcctcc agctggaggc     720
ggatctgatg tagccgcccc acacagacag ccactcacct cttcagaacg aattgacaaa     780
caaattcggt acatcctcga cggcatctca gccctgagaa aggagacatg taacaagagt     840
aacatgtgtg aaagcagcaa agaggcactg gcagaaaaca acctgaacct tccaaagatg     900
gctgaaaaag atggatgctt ccaatctgga ttcaatgagg agacttgcct ggtgaaaatc     960
atcactggtc ttttggagtt tgaggtatac ctagagtacc tccagaacag atttgagagt    1020
agtgaggaac aagccagagc tgtgcagatg agtacaaaag tcctgatcca gttcctgcag    1080
aaaaaggcaa agaatctaga tgcaataacc acccctgacc caaccacaaa tgccagcctg    1140
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cgcagcttta aggagttcct gcagtccagc ctgagggctc ttcggcaaat ggatcagccc    1260
agagggccca caatcaagcc ctgtcctcca tgcaaatgcc cggctccaaa tcttcttggt    1320
ggttcatccg tcttcatctt ccctccaaag atcaaggatg tactcatgat ctccctgagc    1380
cccatagtca catgtgtggt ggtggatgtg agcgaggacg acccagatgt ccagatcagc    1440
tggtttgtga acaacgtgga agtacacaca gctcagacac aaacccatag agaggattac    1500
aacagtactc tccgggtggt cagtgccctc cccatccagc accaggactg gatgagtggc    1560
aaggagttca aatgcaaggt caacaacaaa gacctcccag cgcccatcga gagaaccatc    1620
tcaaaaccca aagggtcagt aagagctcca caggtatatg tcttgcctcc accagaagaa    1680
gagatgacta agaaacaggt cactctgacc tgcatggtca cagacttcat gcctgaagac    1740
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gtcctggact ctgatggttc ttacttcatg tacagcaagc tgagagtgga aaagaagaac    1860
tgggtggaaa gaaatagcta ctcctgttca gtggtccacg agggtctgca caatcaccac    1920
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<210> 606

<211> 647
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 606
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1   5   10   15
Val Ile Ile Ala Arg Gly Val Asp Pro Glu Glu Pro Gln Leu Ser Cys
            20   25   30
Phe Arg Lys Ser Pro Leu Ser Asn Val Val Cys Glu Trp Gly Pro Arg
        35   40   45
Ser Thr Pro Ser Leu Thr Thr Lys Ala Val Leu Leu Val Arg Lys Phe
    50   55   60
Gln Asn Ser Pro Ala Glu Asp Phe Gln Glu Pro Cys Gln Tyr Ser Gln
65   70   75   80
Glu Ser Gln Lys Phe Ser Cys Gln Leu Ala Val Pro Glu Gly Asp Ser
                85   90   95
Ser Phe Tyr Ile Val Ser Met Cys Val Ala Ser Ser Val Gly Ser Lys
            100   105   110
Phe Ser Lys Thr Gln Thr Phe Gln Gly Cys Gly Ile Leu Gln Pro Asp
        115   120   125
Pro Pro Ala Asn Ile Thr Val Thr Ala Val Ala Arg Asn Pro Arg Trp
    130   135   140
Leu Ser Val Thr Trp Gln Asp Pro His Ser Trp Asn Ser Ser Phe Tyr
145   150   155   160
Arg Leu Arg Phe Glu Leu Arg Tyr Arg Ala Glu Arg Ser Lys Thr Phe
                165   170   175
Thr Thr Trp Met Val Lys Asp Leu Gln His His Cys Val Ile His Asp
            180   185   190
Ala Trp Ser Gly Leu Arg His Val Val Gln Leu Arg Ala Gln Glu Glu
        195   200   205
Phe Gly Gln Gly Glu Trp Ser Glu Trp Ser Pro Glu Ala Met Gly Thr
    210   215   220
Pro Trp Thr Glu Ser Arg Ser Pro Pro Ala Gly Gly Gly Ser Asp Val
225   230   235   240
Ala Ala Pro His Arg Gln Pro Leu Thr Ser Ser Glu Arg Ile Asp Lys
                245   250   255
Gln Ile Arg Tyr Ile Leu Asp Gly Ile Ser Ala Leu Arg Lys Glu Thr
            260   265   270
Cys Asn Lys Ser Asn Met Cys Glu Ser Ser Lys Glu Ala Leu Ala Glu
        275   280   285
Asn Asn Leu Asn Leu Pro Lys Met Ala Glu Lys Asp Gly Cys Phe Gln
    290   295   300
Ser Gly Phe Asn Glu Glu Thr Cys Leu Val Lys Ile Ile Thr Gly Leu
305   310   315   320
Leu Glu Phe Glu Val Tyr Leu Glu Tyr Leu Gln Asn Arg Phe Glu Ser
                325   330   335
Ser Glu Glu Gln Ala Arg Ala Val Gln Met Ser Thr Lys Val Leu Ile
            340   345   350
Gln Phe Leu Gln Lys Lys Ala Lys Asn Leu Asp Ala Ile Thr Thr Pro
        355   360   365
Asp Pro Thr Thr Asn Ala Ser Leu Leu Thr Lys Leu Gln Ala Gln Asn
    370   375   380
Gln Trp Leu Gln Asp Met Thr Thr His Leu Ile Leu Arg Ser Phe Lys

385 390 395 400
Glu Phe Leu Gln Ser Ser Leu Arg Ala Leu Arg Gln Met Asp Gln Pro
405 410 415
Arg Gly Pro Thr Ile Lys Pro Cys Pro Pro Cys Lys Cys Pro Ala Pro
420 425 430
Asn Leu Leu Gly Gly Ser Ser Val Phe Ile Phe Pro Pro Lys Ile Lys
435 440 445
Asp Val Leu Met Ile Ser Leu Ser Pro Ile Val Thr Cys Val Val Val
450 455 460
Asp Val Ser Glu Asp Asp Pro Asp Val Gln Ile Ser Trp Phe Val Asn
465 470 475 480
Asn Val Glu Val His Thr Ala Gln Thr Gln Thr His Arg Glu Asp Tyr
485 490 495
Asn Ser Thr Leu Arg Val Val Ser Ala Leu Pro Ile Gln His Gln Asp
500 505 510
Trp Met Ser Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys Asp Leu
515 520 525
Pro Ala Pro Ile Glu Arg Thr Ile Ser Lys Pro Lys Gly Ser Val Arg
530 535 540
Ala Pro Gln Val Tyr Val Leu Pro Pro Pro Glu Glu Glu Met Thr Lys
545 550 555 560
Lys Gln Val Thr Leu Thr Cys Met Val Thr Asp Phe Met Pro Glu Asp
565 570 575
Ile Tyr Val Glu Trp Thr Asn Asn Gly Lys Thr Glu Leu Asn Tyr Lys
580 585 590
Asn Thr Glu Pro Val Leu Asp Ser Asp Gly Ser Tyr Phe Met Tyr Ser
595 600 605
Lys Leu Arg Val Glu Lys Lys Asn Trp Val Glu Arg Asn Ser Tyr Ser
610 615 620
Cys Ser Val Val His Glu Gly Leu His Asn His His Thr Thr Lys Ser
625 630 635 640
Phe Ser Arg Thr Pro Gly Lys
645

<210> 607
<211> 749
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 607
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1 5 10 15
Val Ile Met Ser Arg Gly Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr
20 25 30
Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln
35 40 45
Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys
50 55 60
Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp
65 70 75 80
Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys
85 90 95
Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
100 105 110

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Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu
        115                 120                 125
Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg
    130                 135                 140
Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val
145                 150                 155                 160
Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr
                165                 170                 175
Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly
            180                 185                 190
Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser
        195                 200                 205
Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser
    210                 215                 220
Gln His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser
225                 230                 235                 240
Phe Leu Leu Pro Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly
                245                 250                 255
Asp Thr Gly Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro
            260                 265                 270
Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro
        275                 280                 285
Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
    290                 295                 300
Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
305                 310                 315                 320
Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
                325                 330                 335
Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
            340                 345                 350
Leu His Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser
        355                 360                 365
Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
    370                 375                 380
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
385                 390                 395                 400
Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
                405                 410                 415
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
            420                 425                 430
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
        435                 440                 445
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
    450                 455                 460
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
465                 470                 475                 480
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser
                485                 490                 495
Ser Leu Asn Thr Arg Thr Gln Lys Ala Arg His Ser Pro Asn Ser Glu
            500                 505                 510
Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
        515                 520                 525
Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Lys Tyr Ser
    530                 535                 540
Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
545                 550                 555                 560
Ser Ile Trp Pro Ser Gly Gly Trp Thr Thr Tyr Ala Asp Ser Val Lys
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Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
            580                 585                 590
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
        595                 600                 605
Arg Gly Gly Tyr Tyr Tyr Ala Leu Asp Tyr Trp Gly Gln Gly Thr Leu
    610                 615                 620
Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
625                 630                 635                 640
Gly Gly Gly Ser Gln Ser Glu Leu Thr Gln Pro Pro Ser Val Ser Val
                645                 650                 655
Ser Pro Gly Gln Thr Ala Thr Ile Thr Cys Ser Gly Glu Lys Leu Gly
            660                 665                 670
Asp Ile Tyr Ala Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Val
        675                 680                 685
Leu Val Ile Tyr Gln Asp Thr Lys Arg Pro Ser Gly Ile Pro Val Arg
    690                 695                 700
Phe Ser Gly Ser Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly
705                 710                 715                 720
Thr Gln Ala Met Asp Glu Ala Asp Tyr Tyr Cys Gln Ala Trp Asp Ser
                725                 730                 735
Ser Thr Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            740                 745

<210> 608
<211> 758
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 608
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1               5                  10                  15
Val Ile Met Ser Arg Gly Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr
            20                  25                  30
Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln
        35                  40                  45
Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys
    50                  55                  60
Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp
65                  70                  75                  80
Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys
                85                  90                  95
Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
            100                 105                 110
Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu
        115                 120                 125
Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg
    130                 135                 140
Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val
145                 150                 155                 160
Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr
                165                 170                 175
Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly
            180                 185                 190
```

```
Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser
        195                 200                 205
Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser
    210                 215                 220
Gln His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser
225                 230                 235                 240
Phe Leu Leu Pro Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly
                245                 250                 255
Asp Thr Gly Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro
            260                 265                 270
Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro
        275                 280                 285
Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
    290                 295                 300
Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
305                 310                 315                 320
Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
                325                 330                 335
Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
            340                 345                 350
Leu His Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser
        355                 360                 365
Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
    370                 375                 380
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
385                 390                 395                 400
Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
                405                 410                 415
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
            420                 425                 430
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
        435                 440                 445
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
    450                 455                 460
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
465                 470                 475                 480
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser
                485                 490                 495
Ser Leu Asn Thr Arg Thr Gln Lys Ala Arg His Ser Pro Asn Ser Glu
            500                 505                 510
Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
        515                 520                 525
Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Phe Tyr Gln
    530                 535                 540
Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
545                 550                 555                 560
Gly Ile Tyr Pro Ser Gly Gly Tyr Thr Lys Tyr Ala Asp Ser Val Lys
                565                 570                 575
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
            580                 585                 590
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
        595                 600                 605
Arg Asp Leu Gly Tyr Gly Ser Ser Trp Tyr Tyr Phe Asp Tyr Trp Gly
    610                 615                 620
Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
625                 630                 635                 640
Gly Gly Ser Gly Gly Gly Gly Ser Gln Ser Ala Leu Thr Gln Pro Ala
```

```
                645                 650                 655
Ser Val Ser Gly Ser Pro Gly Gln Ser Ile Thr Ile Ser Cys Ser Gly
            660                 665                 670
Thr Asp Ser Asp Val Gly Gly Tyr Asn His Val Ser Trp Tyr Gln Gln
        675                 680                 685
His Pro Gly Lys Ala Pro Lys Leu Ile Ile Tyr Asp Val Asp His Arg
    690                 695                 700
Pro Ser Gly Ile Ser Asn Arg Phe Ser Gly Ser Lys Ser Gly Asn Thr
705                 710                 715                 720
Ala Ser Leu Thr Ile Ser Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr
                725                 730                 735
Tyr Cys Ser Ser Tyr Arg Ser Gly Ser Thr Tyr Val Phe Gly Thr Gly
            740                 745                 750
Thr Lys Val Thr Val Leu
        755

<210> 609
<211> 751
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 609
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1               5                  10                  15
Val Ile Met Ser Arg Gly Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr
            20                  25                  30
Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln
        35                  40                  45
Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys
    50                  55                  60
Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp
65                  70                  75                  80
Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys
                85                  90                  95
Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
            100                 105                 110
Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu
        115                 120                 125
Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg
    130                 135                 140
Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val
145                 150                 155                 160
Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr
                165                 170                 175
Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly
            180                 185                 190
Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser
        195                 200                 205
Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser
    210                 215                 220
Gln His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser
225                 230                 235                 240
Phe Leu Leu Pro Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly
                245                 250                 255
```

```
Asp Thr Gly Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro
            260                 265                 270
Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro
        275                 280                 285
Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
    290                 295                 300
Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
305                 310                 315                 320
Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
                325                 330                 335
Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
            340                 345                 350
Leu His Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser
        355                 360                 365
Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
    370                 375                 380
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
385                 390                 395                 400
Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
                405                 410                 415
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
            420                 425                 430
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
        435                 440                 445
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
    450                 455                 460
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
465                 470                 475                 480
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser
                485                 490                 495
Ser Leu Asn Thr Arg Thr Gln Lys Ala Arg His Ser Pro Asn Ser Glu
            500                 505                 510
Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
        515                 520                 525
Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Lys Tyr Ser
    530                 535                 540
Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
545                 550                 555                 560
Gly Ile Ser Pro Ser Gly Tyr Thr Arg Tyr Ala Asp Ser Val Lys Gly
                565                 570                 575
Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln
            580                 585                 590
Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
        595                 600                 605
Asp Gln Leu Leu Glu Ala Phe Asp Ile Trp Gly Gln Gly Thr Thr Val
    610                 615                 620
Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
625                 630                 635                 640
Gly Gly Ser Gln Asp Ile Gln Met Thr Gln Ser Pro Leu Ser Leu Ser
                645                 650                 655
Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser
            660                 665                 670
Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Glu Ala Pro
        675                 680                 685
Lys Leu Leu Ile Tyr Ala Ala Ser Ala Leu Gln Ser Gly Val Pro Ser
    690                 695                 700
Arg Phe Ser Gly Ser Gly Leu Gly Thr Val Phe Thr Leu Thr Ile Thr
```

705 710 715 720
Ser Leu Gln Pro Glu Asp Ser Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr
725 730 735
Ser Pro Pro Val Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
740 745 750

<210> 610
<211> 752
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 610
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1 5 10 15
Val Ile Met Ser Arg Gly Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr
20 25 30
Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln
35 40 45
Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys
50 55 60
Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp
65 70 75 80
Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys
85 90 95
Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
100 105 110
Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu
115 120 125
Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg
130 135 140
Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val
145 150 155 160
Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr
165 170 175
Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly
180 185 190
Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser
195 200 205
Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser
210 215 220
Gln His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser
225 230 235 240
Phe Leu Leu Pro Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly
245 250 255
Asp Thr Gly Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro
260 265 270
Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro
275 280 285
Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
290 295 300
Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
305 310 315 320
Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
325 330 335

```
Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
            340                 345                 350
Leu His Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser
        355                 360                 365
Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
    370                 375                 380
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
385                 390                 395                 400
Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
                405                 410                 415
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
            420                 425                 430
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
        435                 440                 445
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
    450                 455                 460
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
465                 470                 475                 480
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser
                485                 490                 495
Ser Leu Asn Thr Arg Thr Gln Lys Ala Arg His Ser Pro Asn Ser Glu
            500                 505                 510
Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
        515                 520                 525
Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Glu Tyr Pro
    530                 535                 540
Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
545                 550                 555                 560
Gly Ile Tyr Ser Ser Gly Gly Leu Thr Lys Tyr Ala Asp Ser Val Lys
                565                 570                 575
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
            580                 585                 590
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
        595                 600                 605
Arg Asp His Tyr Gly Asp Tyr Ala Phe Asp Tyr Trp Gly Gln Gly Thr
    610                 615                 620
Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
625                 630                 635                 640
Gly Gly Gly Gly Ser Gln Asp Ile Gln Met Thr Gln Ser Pro Ser Thr
                645                 650                 655
Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
            660                 665                 670
Gln Ser Ile Ser Ser Trp Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys
        675                 680                 685
Ala Pro Lys Leu Leu Ile Tyr Lys Ala Ser Ser Leu Glu Ser Gly Val
    690                 695                 700
Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr
705                 710                 715                 720
Ile Ser Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
                725                 730                 735
Tyr Asn Ser Tyr Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
            740                 745                 750

<210> 611
<211> 761
<212> PRT
<213> Artificial Sequence
```

<220>
<223> Made in a lab

<400> 611
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1   5   10   15
Val Ile Met Ser Arg Gly Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr
            20   25   30
Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln
        35   40   45
Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys
    50   55   60
Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp
65   70   75   80
Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys
                85   90   95
Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
            100   105   110
Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu
        115   120   125
Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg
    130   135   140
Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val
145   150   155   160
Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr
                165   170   175
Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly
            180   185   190
Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser
        195   200   205
Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser
    210   215   220
Gln His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser
225   230   235   240
Phe Leu Leu Pro Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly
                245   250   255
Asp Thr Gly Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro
            260   265   270
Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro
        275   280   285
Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
    290   295   300
Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
305   310   315   320
Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
                325   330   335
Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
            340   345   350
Leu His Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser
        355   360   365
Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
    370   375   380
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
385   390   395   400
Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
                405   410   415

```
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
            420                 425                 430
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
        435                 440                 445
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
    450                 455                 460
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
465                 470                 475                 480
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser
                485                 490                 495
Ser Leu Asn Thr Arg Thr Gln Lys Ala Arg His Ser Pro Asn Ser Glu
            500                 505                 510
Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
        515                 520                 525
Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Leu Tyr Glu
    530                 535                 540
Met Val Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
545                 550                 555                 560
Gly Ile Trp Pro Ser Gly Gly Trp Thr Gln Tyr Ala Asp Ser Val Lys
                565                 570                 575
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
            580                 585                 590
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
        595                 600                 605
Arg Asp Leu Ala Val Ala Gly Trp Asp Tyr Tyr Tyr Tyr Tyr Gly Met
    610                 615                 620
Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly
625                 630                 635                 640
Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Asp Ile Gln
                645                 650                 655
Met Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala
            660                 665                 670
Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Tyr Leu Ala Trp
        675                 680                 685
Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Asp Ala
    690                 695                 700
Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser
705                 710                 715                 720
Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp Ser
                725                 730                 735
Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asn Trp Pro Pro Phe Thr Phe
            740                 745                 750
Gly Gly Gly Thr Lys Val Glu Ile Lys
        755                 760

<210> 612
<211> 759
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 612
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1               5                  10                  15
Val Ile Met Ser Arg Gly Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr
```

```
            20                  25                  30
Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln
        35                  40                  45
Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys
    50                  55                  60
Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp
65                  70                  75                  80
Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys
                85                  90                  95
Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
            100                 105                 110
Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu
        115                 120                 125
Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg
    130                 135                 140
Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val
145                 150                 155                 160
Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr
                165                 170                 175
Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly
            180                 185                 190
Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser
        195                 200                 205
Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser
    210                 215                 220
Gln His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser
225                 230                 235                 240
Phe Leu Leu Pro Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly
                245                 250                 255
Asp Thr Gly Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro
            260                 265                 270
Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro
        275                 280                 285
Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
    290                 295                 300
Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
305                 310                 315                 320
Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
                325                 330                 335
Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
            340                 345                 350
Leu His Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser
        355                 360                 365
Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
    370                 375                 380
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
385                 390                 395                 400
Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
                405                 410                 415
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
            420                 425                 430
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
        435                 440                 445
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
    450                 455                 460
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
465                 470                 475                 480
```

```
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser
                485                 490                 495
Ser Leu Asn Thr Arg Thr Gln Lys Ala Arg His Ser Pro Asn Ser Glu
            500                 505                 510
Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
        515                 520                 525
Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Gln Tyr Asn
    530                 535                 540
Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
545                 550                 555                 560
Trp Ile Ser Ser Ser Gly Gly Thr Glu Tyr Ala Asp Ser Val Lys Gly
                565                 570                 575
Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln
            580                 585                 590
Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys
        595                 600                 605
Asp Arg Gly Tyr Gly Ser Gly Ser Tyr Gly Ala Tyr Asp Ala Phe Asp
    610                 615                 620
Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly
625                 630                 635                 640
Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Asp Ile Gln Met
                645                 650                 655
Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr
            660                 665                 670
Ile Thr Cys Gln Thr Ser Gln Ser Ile Asp Arg Tyr Leu Asn Trp Tyr
        675                 680                 685
Gln Gln Lys Ala Gly Glu Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser
    690                 695                 700
Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
705                 710                 715                 720
Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala
                725                 730                 735
Ser Tyr Tyr Cys Gln Gln Ser Tyr Arg Thr Pro Arg Thr Phe Gly Gln
            740                 745                 750
Gly Thr Lys Val Glu Ile Lys
        755

<210> 613
<211> 754
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 613
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1               5                  10                  15
Val Ile Met Ser Arg Gly Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr
            20                  25                  30
Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln
        35                  40                  45
Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys
    50                  55                  60
Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp
65                  70                  75                  80
Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys
```

```
                85                  90                  95
Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
            100                 105                 110
Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu
        115                 120                 125
Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg
    130                 135                 140
Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val
145                 150                 155                 160
Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr
                165                 170                 175
Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly
            180                 185                 190
Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser
        195                 200                 205
Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser
    210                 215                 220
Gln His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser
225                 230                 235                 240
Phe Leu Leu Pro Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly
                245                 250                 255
Asp Thr Gly Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro
            260                 265                 270
Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro
        275                 280                 285
Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
    290                 295                 300
Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
305                 310                 315                 320
Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
                325                 330                 335
Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
            340                 345                 350
Leu His Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser
        355                 360                 365
Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
    370                 375                 380
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
385                 390                 395                 400
Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
                405                 410                 415
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
            420                 425                 430
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
        435                 440                 445
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
    450                 455                 460
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
465                 470                 475                 480
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser
                485                 490                 495
Ser Leu Asn Thr Arg Thr Gln Lys Ala Arg His Ser Pro Asn Ser Glu
            500                 505                 510
Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
        515                 520                 525
Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser His Tyr Ser
    530                 535                 540
```

```
Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
545                 550                 555                 560
Ser Ile Tyr Pro Ser Gly Gly Ser Thr Leu Tyr Ala Asp Ser Val Lys
                565                 570                 575
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
            580                 585                 590
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
        595                 600                 605
Arg Trp Gly Val Gly Ala Thr Phe Asp Tyr Trp Gly Gln Gly Thr Leu
    610                 615                 620
Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
625                 630                 635                 640
Gly Gly Gly Ser Gln Asp Ile Gln Met Thr Gln Ser Pro Gly Thr Leu
                645                 650                 655
Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln
            660                 665                 670
Ser Val Ser Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
        675                 680                 685
Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile
    690                 695                 700
Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
705                 710                 715                 720
Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln
                725                 730                 735
Tyr Gly Ser Ser Pro Leu Trp Thr Phe Gly Gln Gly Thr Lys Val Glu
            740                 745                 750
Ile Lys


<210> 614
<211> 752
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 614
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1               5                  10                  15
Val Ile Met Ser Arg Gly Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr
            20                  25                  30
Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln
        35                  40                  45
Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys
    50                  55                  60
Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp
65                  70                  75                  80
Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys
                85                  90                  95
Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
            100                 105                 110
Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu
        115                 120                 125
Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg
    130                 135                 140
Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val
```

```
145                 150                 155                 160
Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr
                165                 170                 175
Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly
            180                 185                 190
Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser
        195                 200                 205
Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser
    210                 215                 220
Gln His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser
225                 230                 235                 240
Phe Leu Leu Pro Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly
                245                 250                 255
Asp Thr Gly Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro
            260                 265                 270
Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro
        275                 280                 285
Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
    290                 295                 300
Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
305                 310                 315                 320
Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
                325                 330                 335
Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
            340                 345                 350
Leu His Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser
        355                 360                 365
Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
    370                 375                 380
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
385                 390                 395                 400
Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
                405                 410                 415
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
            420                 425                 430
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
        435                 440                 445
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
    450                 455                 460
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
465                 470                 475                 480
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser
                485                 490                 495
Ser Leu Asn Thr Arg Thr Gln Lys Ala Arg His Ser Pro Asn Ser Glu
            500                 505                 510
Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
        515                 520                 525
Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser His Tyr Met
    530                 535                 540
Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
545                 550                 555                 560
Tyr Ile Tyr Pro Ser Gly Gly Trp Thr Ser Tyr Ala Asp Ser Val Lys
                565                 570                 575
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
            580                 585                 590
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
        595                 600                 605
```

```
Arg Phe Asp Tyr Thr Ile Gly Phe Asp Phe Trp Gly Gln Gly Thr Leu
    610                 615                 620
Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
625                 630                 635                 640
Gly Gly Gly Ser Gln Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu
                645                 650                 655
Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln
            660                 665                 670
Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala
        675                 680                 685
Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro
    690                 695                 700
Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
705                 710                 715                 720
Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser
                725                 730                 735
Tyr Ser Thr Pro Arg Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
            740                 745                 750

<210> 615
<211> 756
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 615
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1               5                  10                  15
Val Ile Met Ser Arg Gly Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr
            20                  25                  30
Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln
        35                  40                  45
Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys
    50                  55                  60
Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp
65                  70                  75                  80
Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys
                85                  90                  95
Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
            100                 105                 110
Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu
        115                 120                 125
Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg
    130                 135                 140
Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val
145                 150                 155                 160
Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr
                165                 170                 175
Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly
            180                 185                 190
Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser
        195                 200                 205
Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser
    210                 215                 220
Gln His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser
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225                 230                 235                 240
Phe Leu Leu Pro Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly
                245                 250                 255
Asp Thr Gly Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro
            260                 265                 270
Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro
        275                 280                 285
Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
    290                 295                 300
Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
305                 310                 315                 320
Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
                325                 330                 335
Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
            340                 345                 350
Leu His Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser
        355                 360                 365
Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
    370                 375                 380
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
385                 390                 395                 400
Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
                405                 410                 415
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
            420                 425                 430
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
        435                 440                 445
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
    450                 455                 460
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
465                 470                 475                 480
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser
                485                 490                 495
Ser Leu Asn Thr Arg Thr Gln Lys Ala Arg His Ser Pro Asn Ser Glu
            500                 505                 510
Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
        515                 520                 525
Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser His Tyr Gly
    530                 535                 540
Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
545                 550                 555                 560
Gly Ile Arg Ser Ser Gly Gly Val Thr Asn Tyr Ala Asp Ser Val Lys
                565                 570                 575
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
            580                 585                 590
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
        595                 600                 605
Arg Glu Gly Ser Gly Trp Ser Lys Ala Phe Asp Ile Trp Gly Gln Gly
    610                 615                 620
Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
625                 630                 635                 640
Ser Gly Gly Gly Gly Ser Gln Asp Ile Gln Met Thr Gln Ser Pro Ala
                645                 650                 655
Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala
            660                 665                 670
Ser Gln Ser Ile Ser Thr Ser Leu Ala Trp Tyr Gln Gln Ile Pro Gly
        675                 680                 685
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Gln Ala Pro Arg Leu Leu Met Tyr Asp Ala Ser Lys Arg Ala Ser Gly
    690                 695                 700
Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Leu Thr Leu
705                 710                 715                 720
Thr Ile Ser Ser Leu Glu Pro Glu Asp Ser Ala Val Tyr Tyr Cys Gln
                725                 730                 735
Leu Arg Ile Asn Trp Pro Pro Glu Phe Thr Phe Gly Pro Gly Thr Lys
            740                 745                 750
Val Asp Ile Lys
        755

<210> 616
<211> 761
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 616
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1               5                  10                  15
Val Ile Met Ser Arg Gly Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr
            20                  25                  30
Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln
        35                  40                  45
Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys
    50                  55                  60
Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp
65                  70                  75                  80
Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys
                85                  90                  95
Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
            100                 105                 110
Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu
        115                 120                 125
Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg
    130                 135                 140
Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val
145                 150                 155                 160
Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr
                165                 170                 175
Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly
            180                 185                 190
Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser
        195                 200                 205
Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser
    210                 215                 220
Gln His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser
225                 230                 235                 240
Phe Leu Leu Pro Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly
                245                 250                 255
Asp Thr Gly Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro
            260                 265                 270
Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro
        275                 280                 285
Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
```

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    290                 295                 300
Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
305                 310                 315                 320
Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
                325                 330                 335
Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
            340                 345                 350
Leu His Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser
        355                 360                 365
Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
    370                 375                 380
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
385                 390                 395                 400
Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
                405                 410                 415
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
            420                 425                 430
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
        435                 440                 445
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
    450                 455                 460
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
465                 470                 475                 480
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser
                485                 490                 495
Ser Leu Asn Thr Arg Thr Gln Lys Ala Arg His Ser Pro Asn Ser Glu
            500                 505                 510
Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
        515                 520                 525
Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser His Tyr Asn
    530                 535                 540
Met Arg Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
545                 550                 555                 560
Ser Ile Ser Pro Ser Gly Gly Phe Thr Gly Tyr Ala Asp Ser Val Lys
                565                 570                 575
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
            580                 585                 590
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
        595                 600                 605
Arg Gly Ile Asn Tyr Tyr Asp Ser Ser Gly Tyr Tyr Pro Pro Val Gly
    610                 615                 620
Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly
625                 630                 635                 640
Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Asp Ile
                645                 650                 655
Gln Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly Asp Arg
            660                 665                 670
Val Thr Ile Thr Cys Arg Ala Ser Arg Gly Val Ile Thr Trp Leu Asn
        675                 680                 685
Trp Tyr Gln Gln Lys Pro Gly Arg Val Pro Ser Pro Leu Ile Phe Gly
    690                 695                 700
Ala Ser Thr Leu Gln Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
705                 710                 715                 720
Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Asp Leu Gln Pro Glu Asp
                725                 730                 735
Phe Ala Thr Tyr Tyr Cys Gln Gln Thr His Ser Phe Pro Leu Thr Phe
            740                 745                 750
```

```
Gly Gly Gly Thr Lys Val Glu Ile Lys
        755                 760

<210> 617
<211> 755
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 617
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1               5                  10                  15
Val Ile Met Ser Arg Gly Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr
            20                  25                  30
Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln
        35                  40                  45
Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys
    50                  55                  60
Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp
65                  70                  75                  80
Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys
                85                  90                  95
Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
            100                 105                 110
Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu
        115                 120                 125
Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg
    130                 135                 140
Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val
145                 150                 155                 160
Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr
                165                 170                 175
Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly
            180                 185                 190
Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser
        195                 200                 205
Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser
    210                 215                 220
Gln His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser
225                 230                 235                 240
Phe Leu Leu Pro Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly
                245                 250                 255
Asp Thr Gly Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro
            260                 265                 270
Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro
        275                 280                 285
Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
    290                 295                 300
Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
305                 310                 315                 320
Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
                325                 330                 335
Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
            340                 345                 350
Leu His Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser
```

```
        355                 360                 365
Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
    370                 375                 380
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
385                 390                 395                 400
Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
                405                 410                 415
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
            420                 425                 430
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
        435                 440                 445
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
    450                 455                 460
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
465                 470                 475                 480
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser
                485                 490                 495
Ser Leu Asn Thr Arg Thr Gln Lys Ala Arg His Ser Pro Asn Ser Glu
            500                 505                 510
Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
        515                 520                 525
Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Trp Tyr Asn
    530                 535                 540
Met Leu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
545                 550                 555                 560
Ser Ile Ser Pro Ser Gly Gly Tyr Thr Val Tyr Ala Asp Ser Val Lys
                565                 570                 575
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
            580                 585                 590
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
        595                 600                 605
Arg Asp Arg Gly Gly Ser Pro Phe Arg Pro Asp Ala Phe Asp Ile Trp
    610                 615                 620
Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
625                 630                 635                 640
Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Ser Ala Leu Thr Gln Pro
                645                 650                 655
Pro Ser Val Ser Val Ser Pro Gly Gln Thr Ala Arg Ile Thr Cys Ser
            660                 665                 670
Gly Asp Lys Leu Gly Glu Lys Tyr Val Ser Trp Tyr Gln Gln Arg Ser
        675                 680                 685
Gly Gln Ser Pro Leu Leu Val Ile Ser Gln Asp Thr Lys Arg Pro Ser
    690                 695                 700
Gly Ile Pro Glu Arg Phe Ser Gly Ser Asn Ser Gly Asn Thr Ala Thr
705                 710                 715                 720
Leu Thr Ile Ser Gly Ala Gln Ala Ala Asp Glu Ala Asp Tyr Tyr Cys
                725                 730                 735
Gln Thr Trp Asp Ser Asp Thr Tyr Val Phe Gly Ser Gly Ser Thr Val
            740                 745                 750
Thr Val Leu
        755

<210> 618
<211> 759
<212> PRT
<213> Artificial Sequence
```

<220>
<223> Made in a lab

<400> 618
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1   5   10   15
Val Ile Met Ser Arg Gly Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr
            20   25   30
Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln
        35   40   45
Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys
    50   55   60
Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp
65   70   75   80
Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys
                85   90   95
Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
            100   105   110
Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu
        115   120   125
Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg
    130   135   140
Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val
145   150   155   160
Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr
                165   170   175
Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly
            180   185   190
Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser
        195   200   205
Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser
    210   215   220
Gln His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser
225   230   235   240
Phe Leu Leu Pro Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly
                245   250   255
Asp Thr Gly Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro
            260   265   270
Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro
        275   280   285
Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
    290   295   300
Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
305   310   315   320
Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
                325   330   335
Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
            340   345   350
Leu His Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser
        355   360   365
Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
    370   375   380
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
385   390   395   400
Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
                405   410   415
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu

```
            420                 425                 430
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
        435                 440                 445
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
    450                 455                 460
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
465                 470                 475                 480
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser
                485                 490                 495
Ser Leu Asn Thr Arg Thr Gln Lys Ala Arg His Ser Pro Asn Ser Glu
            500                 505                 510
Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
        515                 520                 525
Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Glu Tyr Asp
    530                 535                 540
Met Leu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
545                 550                 555                 560
Ser Ile Trp Pro Ser Gly Gly Phe Thr Gln Tyr Ala Asp Ser Val Lys
                565                 570                 575
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
            580                 585                 590
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
        595                 600                 605
Arg Asn Tyr Tyr Asp Phe Trp Ser Gly Pro Tyr Tyr Tyr Gly Met Asp
    610                 615                 620
Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly
625                 630                 635                 640
Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Asp Ile Gln Met
                645                 650                 655
Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr
            660                 665                 670
Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr
        675                 680                 685
Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser
    690                 695                 700
Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
705                 710                 715                 720
Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala
                725                 730                 735
Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Leu Trp Thr Phe Gly Gln
            740                 745                 750
Gly Thr Lys Val Glu Ile Lys
        755

<210> 619
<211> 756
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 619
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1               5                  10                  15
Val Ile Met Ser Arg Gly Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr
            20                  25                  30
```

```
Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln
        35                  40                  45
Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys
    50                  55                  60
Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp
65                  70                  75                  80
Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys
                85                  90                  95
Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
            100                 105                 110
Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu
        115                 120                 125
Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg
    130                 135                 140
Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val
145                 150                 155                 160
Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr
                165                 170                 175
Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly
            180                 185                 190
Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser
        195                 200                 205
Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser
    210                 215                 220
Gln His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser
225                 230                 235                 240
Phe Leu Leu Pro Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly
                245                 250                 255
Asp Thr Gly Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro
            260                 265                 270
Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro
        275                 280                 285
Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
    290                 295                 300
Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
305                 310                 315                 320
Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
                325                 330                 335
Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
            340                 345                 350
Leu His Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser
        355                 360                 365
Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
    370                 375                 380
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
385                 390                 395                 400
Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
                405                 410                 415
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
            420                 425                 430
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
        435                 440                 445
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
    450                 455                 460
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
465                 470                 475                 480
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser
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                485                 490                 495
Ser Leu Asn Thr Arg Thr Gln Lys Ala Arg His Ser Pro Asn Ser Glu
            500                 505                 510
Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
        515                 520                 525
Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Gly Tyr Val
    530                 535                 540
Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
545                 550                 555                 560
Ser Ile Ser Pro Ser Gly Gly Tyr Thr Leu Tyr Ala Asp Ser Val Lys
                565                 570                 575
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
            580                 585                 590
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
        595                 600                 605
Arg Ala Phe Ser Thr Arg Trp Tyr Trp Gly Ala Phe Asp Ile Trp Gly
    610                 615                 620
Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
625                 630                 635                 640
Gly Gly Ser Gly Gly Gly Gly Ser Gln Asp Ile Gln Met Thr Gln Ser
                645                 650                 655
Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys
            660                 665                 670
Arg Ala Ser Gln Ser Val Arg Ser Tyr Leu Ala Trp Tyr Gln Gln Lys
        675                 680                 685
Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Asp Ala Ser Asn Arg Ala
    690                 695                 700
Thr Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
705                 710                 715                 720
Thr Leu Thr Ile Thr Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr
                725                 730                 735
Cys Gln Gln Tyr Asp Asn Leu Pro Leu Thr Phe Gly Gly Gly Thr Lys
            740                 745                 750
Val Glu Ile Lys
        755

<210> 620
<211> 759
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 620
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1                5                  10                  15
Val Ile Met Ser Arg Gly Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr
            20                  25                  30
Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln
        35                  40                  45
Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys
    50                  55                  60
Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp
65                  70                  75                  80
Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys
                85                  90                  95
```

```
Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
            100                 105                 110
Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu
        115                 120                 125
Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg
    130                 135                 140
Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val
145                 150                 155                 160
Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr
                165                 170                 175
Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly
            180                 185                 190
Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser
        195                 200                 205
Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser
    210                 215                 220
Gln His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser
225                 230                 235                 240
Phe Leu Leu Pro Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly
                245                 250                 255
Asp Thr Gly Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro
            260                 265                 270
Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro
        275                 280                 285
Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
    290                 295                 300
Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
305                 310                 315                 320
Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
                325                 330                 335
Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
            340                 345                 350
Leu His Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser
        355                 360                 365
Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
    370                 375                 380
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
385                 390                 395                 400
Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
                405                 410                 415
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
            420                 425                 430
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
        435                 440                 445
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
    450                 455                 460
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
465                 470                 475                 480
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser
                485                 490                 495
Ser Leu Asn Thr Arg Thr Gln Lys Ala Arg His Ser Pro Asn Ser Glu
            500                 505                 510
Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
        515                 520                 525
Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ile Tyr His
    530                 535                 540
Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
```

```
545                 550                 555                 560
Gly Ile Ser Ser Ser Gly Gly Arg Thr Asn Tyr Ala Asp Ser Val Lys
                565                 570                 575
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
            580                 585                 590
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
        595                 600                 605
Ser Ser Tyr Arg Ala Ala Gly Trp Val Asp Tyr Tyr Tyr Gly Met Asp
    610                 615                 620
Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly
625                 630                 635                 640
Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Asp Ile Gln Met
                645                 650                 655
Thr Gln Ser Pro Ser Ser Leu Ser Ala Phe Val Gly Asp Arg Val Thr
            660                 665                 670
Ile Thr Cys Arg Thr Ser Gln Ser Val Ala Thr Tyr Val Asn Trp Tyr
        675                 680                 685
Gln Gln Lys Pro Gly Glu Gly Pro Lys Leu Leu Ile Tyr Ala Ala Ser
    690                 695                 700
Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Arg Gly Ser Gly Ser Gly
705                 710                 715                 720
Thr Asp Phe Thr Leu Thr Ile Gly Ser Leu Gln Pro Glu Asp Phe Ala
                725                 730                 735
Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Val Pro Ile Thr Phe Gly Gln
            740                 745                 750
Gly Thr Arg Leu Asp Ile Lys
        755
```

<210> 621
<211> 756
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 621

```
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1               5                  10                  15
Val Ile Met Ser Arg Gly Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr
            20                  25                  30
Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln
        35                  40                  45
Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys
    50                  55                  60
Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp
65                  70                  75                  80
Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys
                85                  90                  95
Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
            100                 105                 110
Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu
        115                 120                 125
Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg
    130                 135                 140
Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val
145                 150                 155                 160
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```
Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr
                165                 170                 175
Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly
            180                 185                 190
Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser
        195                 200                 205
Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser
    210                 215                 220
Gln His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser
225                 230                 235                 240
Phe Leu Leu Pro Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly
                245                 250                 255
Asp Thr Gly Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro
            260                 265                 270
Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro
        275                 280                 285
Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
    290                 295                 300
Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
305                 310                 315                 320
Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
                325                 330                 335
Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
            340                 345                 350
Leu His Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser
        355                 360                 365
Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
    370                 375                 380
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
385                 390                 395                 400
Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
                405                 410                 415
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
            420                 425                 430
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
        435                 440                 445
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
    450                 455                 460
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
465                 470                 475                 480
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser
                485                 490                 495
Ser Leu Asn Thr Arg Thr Gln Lys Ala Arg His Ser Pro Asn Ser Glu
            500                 505                 510
Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
        515                 520                 525
Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Leu Tyr Asp
    530                 535                 540
Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
545                 550                 555                 560
Arg Ile Tyr Ser Ser Gly Gly Thr Thr Gln Tyr Ala Asp Ser Val Lys
                565                 570                 575
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
            580                 585                 590
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Met Tyr Tyr Cys Ala
        595                 600                 605
Arg Asp Pro Gly Tyr Gly Ser His His Ser Phe Asp Tyr Trp Gly Gln
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    610                 615                 620
Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
625                 630                 635                 640
Gly Ser Gly Gly Gly Gly Ser Gln Asp Ile Gln Met Thr Gln Ser Pro
                645                 650                 655
Ser Thr Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg
            660                 665                 670
Ala Ser Gln Ser Met Ser Asn Trp Leu Ala Trp Tyr Gln Gln Lys Pro
        675                 680                 685
Gly Lys Ala Pro Lys Leu Leu Ile Tyr Asp Val Phe Thr Leu Lys Ser
    690                 695                 700
Gly Val Pro Ser Arg Phe Ser Gly Ser Arg Ser Gly Thr Glu Phe Thr
705                 710                 715                 720
Leu Thr Ile Ser Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys
                725                 730                 735
Gln Gln Tyr Ser Asp Tyr Ser Gly Ile Thr Phe Gly Pro Gly Thr Glu
            740                 745                 750
Val Asp Ile Arg
        755

<210> 622
<211> 754
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 622
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1               5                  10                  15
Val Ile Met Ser Arg Gly Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr
            20                  25                  30
Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln
        35                  40                  45
Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys
    50                  55                  60
Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp
65                  70                  75                  80
Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys
                85                  90                  95
Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
            100                 105                 110
Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu
        115                 120                 125
Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg
    130                 135                 140
Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val
145                 150                 155                 160
Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr
                165                 170                 175
Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly
            180                 185                 190
Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser
        195                 200                 205
Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser
    210                 215                 220
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```
Gln His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser
225                 230                 235                 240
Phe Leu Leu Pro Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly
                245                 250                 255
Asp Thr Gly Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro
            260                 265                 270
Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro
        275                 280                 285
Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
    290                 295                 300
Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
305                 310                 315                 320
Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
                325                 330                 335
Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
            340                 345                 350
Leu His Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser
        355                 360                 365
Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
    370                 375                 380
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
385                 390                 395                 400
Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
                405                 410                 415
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
            420                 425                 430
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
        435                 440                 445
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
    450                 455                 460
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
465                 470                 475                 480
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser
                485                 490                 495
Ser Leu Asn Thr Arg Thr Gln Lys Ala Arg His Ser Pro Asn Ser Glu
            500                 505                 510
Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
        515                 520                 525
Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Tyr
    530                 535                 540
Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
545                 550                 555                 560
Gly Ile Tyr Ser Ser Gly Gly Pro Thr Gln Tyr Ala Asp Ser Val Lys
                565                 570                 575
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
            580                 585                 590
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
        595                 600                 605
Arg Ala Gly Gly Asp Ala Phe Asp Ile Trp Gly Gln Gly Thr Met Val
    610                 615                 620
Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
625                 630                 635                 640
Gly Gly Ser Gln Ser Val Leu Thr Gln Pro Pro Ser Ala Ser Gly Thr
                645                 650                 655
Pro Gly Gln Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile
            660                 665                 670
Gly Ser Lys Val Val Tyr Trp Tyr Gln Gln Val Pro Gly Thr Ala Pro
```

```
        675                 680                 685
Lys Leu Leu Ile Tyr Arg Asn Asp Gln Arg Pro Ser Gly Val Pro Asp
    690                 695                 700
Arg Phe Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser
705                 710                 715                 720
Gly Leu Arg Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp
                725                 730                 735
Asp Ser Leu Ser Gly Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
            740                 745                 750
Val Leu


<210> 623
<211> 752
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 623
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1               5                  10                  15
Val Ile Met Ser Arg Gly Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr
            20                  25                  30
Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln
        35                  40                  45
Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys
    50                  55                  60
Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp
65                  70                  75                  80
Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys
                85                  90                  95
Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
            100                 105                 110
Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu
        115                 120                 125
Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg
    130                 135                 140
Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val
145                 150                 155                 160
Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr
                165                 170                 175
Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly
            180                 185                 190
Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser
        195                 200                 205
Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser
    210                 215                 220
Gln His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser
225                 230                 235                 240
Phe Leu Leu Pro Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly
                245                 250                 255
Asp Thr Gly Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro
            260                 265                 270
Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro
        275                 280                 285
```

```
Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
    290                 295                 300
Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
305                 310                 315                 320
Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
                325                 330                 335
Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
            340                 345                 350
Leu His Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser
        355                 360                 365
Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
    370                 375                 380
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
385                 390                 395                 400
Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
                405                 410                 415
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
            420                 425                 430
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
        435                 440                 445
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
    450                 455                 460
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
465                 470                 475                 480
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser
                485                 490                 495
Ser Leu Asn Thr Arg Thr Gln Lys Ala Arg His Ser Pro Asn Ser Glu
            500                 505                 510
Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
        515                 520                 525
Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Glu
    530                 535                 540
Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
545                 550                 555                 560
Ser Ile Ser Pro Ser Gly Gly Tyr Thr Tyr Tyr Ala Asp Ser Val Lys
                565                 570                 575
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
            580                 585                 590
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
        595                 600                 605
Thr Met Thr Thr Ser Gly Phe His Leu Ile Trp Gly Gln Gly Thr Met
    610                 615                 620
Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
625                 630                 635                 640
Gly Gly Gly Ser Gln Asp Ile Gln Met Thr Gln Ser Pro Ala Thr Leu
                645                 650                 655
Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln
            660                 665                 670
Ser Ile Ser Ser Trp Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala
        675                 680                 685
Pro Lys Leu Leu Ile Tyr Lys Ala Ser Gly Leu Glu Ser Gly Val Pro
    690                 695                 700
Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile
705                 710                 715                 720
Ser Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr
                725                 730                 735
Asn Ser Tyr Pro Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
```

740 745 750

<210> 624
<211> 751
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 624
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1 5 10 15
Val Ile Met Ser Arg Gly Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr
20 25 30
Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln
35 40 45
Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys
50 55 60
Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp
65 70 75 80
Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys
85 90 95
Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
100 105 110
Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu
115 120 125
Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg
130 135 140
Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val
145 150 155 160
Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr
165 170 175
Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly
180 185 190
Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser
195 200 205
Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser
210 215 220
Gln His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser
225 230 235 240
Phe Leu Leu Pro Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly
245 250 255
Asp Thr Gly Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro
260 265 270
Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro
275 280 285
Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
290 295 300
Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
305 310 315 320
Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
325 330 335
Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
340 345 350
Leu His Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser
355 360 365

```
Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
    370                 375                 380
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
385                 390                 395                 400
Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
                405                 410                 415
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
            420                 425                 430
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
        435                 440                 445
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
    450                 455                 460
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
465                 470                 475                 480
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser
                485                 490                 495
Ser Leu Asn Thr Arg Thr Gln Lys Ala Arg His Ser Pro Asn Ser Glu
            500                 505                 510
Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
        515                 520                 525
Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr Pro
    530                 535                 540
Met Gln Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
545                 550                 555                 560
Trp Ile Gly Pro Ser Gly Gly Trp Thr Val Tyr Ala Asp Ser Val Lys
                565                 570                 575
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
            580                 585                 590
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
        595                 600                 605
Arg Asp Asp Gly Ile Ala Gly Phe Leu Trp Gly Gln Gly Thr Leu Val
    610                 615                 620
Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
625                 630                 635                 640
Gly Gly Ser Gln Asp Ile Gln Met Thr Gln Ser Pro Leu Ser Leu Ser
                645                 650                 655
Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Arg Asp
            660                 665                 670
Ile Ser Ile Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Val Pro
        675                 680                 685
Lys Leu Leu Ile Phe Gly Ala Ser Thr Leu Arg Ser Gly Val Pro Ser
    690                 695                 700
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Thr
705                 710                 715                 720
Ser Leu Gln Pro Glu Asp Val Ala Thr Tyr Tyr Cys Gln Lys Tyr Asn
                725                 730                 735
Ser Ala Pro Tyr Thr Phe Gly Pro Gly Thr Lys Val Glu Ile Arg
            740                 745                 750

<210> 625
<211> 759
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab
```

<400> 625
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1   5   10   15
Val Ile Met Ser Arg Gly Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr
            20   25   30
Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln
        35   40   45
Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys
    50   55   60
Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp
65   70   75   80
Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys
                85   90   95
Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
            100   105   110
Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu
        115   120   125
Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg
    130   135   140
Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val
145   150   155   160
Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr
                165   170   175
Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly
            180   185   190
Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser
        195   200   205
Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser
    210   215   220
Gln His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser
225   230   235   240
Phe Leu Leu Pro Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly
                245   250   255
Asp Thr Gly Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro
            260   265   270
Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro
        275   280   285
Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
    290   295   300
Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
305   310   315   320
Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
                325   330   335
Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
            340   345   350
Leu His Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser
        355   360   365
Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
    370   375   380
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
385   390   395   400
Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
                405   410   415
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
            420   425   430
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
        435   440   445

```
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
    450                 455                 460
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
465                 470                 475                 480
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser
                485                 490                 495
Ser Leu Asn Thr Arg Thr Gln Lys Ala Arg His Ser Pro Asn Ser Glu
            500                 505                 510
Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
        515                 520                 525
Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Trp Tyr Leu
    530                 535                 540
Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
545                 550                 555                 560
Gly Ile Trp Pro Ser Gly Gly His Thr Leu Tyr Ala Asp Ser Val Lys
                565                 570                 575
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
            580                 585                 590
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
        595                 600                 605
Arg Glu Pro Leu Leu Trp Phe Gly Glu Leu Ser Tyr Asn Trp Phe Asp
    610                 615                 620
Pro Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly
625                 630                 635                 640
Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Asp Ile Gln Met
                645                 650                 655
Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly Asp Arg Val Thr
            660                 665                 670
Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Ser Trp Leu Ala Trp Tyr
        675                 680                 685
Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser
    690                 695                 700
Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
705                 710                 715                 720
Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala
                725                 730                 735
Thr Tyr Tyr Cys Gln Gln Ala Asn Ser Phe Pro Leu Thr Phe Gly Gly
            740                 745                 750
Gly Thr Lys Val Glu Ile Lys
        755

<210> 626
<211> 757
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 626
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1               5                  10                  15
Val Ile Met Ser Arg Gly Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr
            20                  25                  30
Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln
        35                  40                  45
Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys
```

```
    50                  55                  60
Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp
65                  70                  75                  80
Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys
                85                  90                  95
Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
            100                 105                 110
Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu
        115                 120                 125
Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg
    130                 135                 140
Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val
145                 150                 155                 160
Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr
                165                 170                 175
Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly
            180                 185                 190
Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser
        195                 200                 205
Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser
    210                 215                 220
Gln His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser
225                 230                 235                 240
Phe Leu Leu Pro Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly
                245                 250                 255
Asp Thr Gly Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro
            260                 265                 270
Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro
        275                 280                 285
Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
    290                 295                 300
Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
305                 310                 315                 320
Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
                325                 330                 335
Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
            340                 345                 350
Leu His Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser
        355                 360                 365
Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
    370                 375                 380
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
385                 390                 395                 400
Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
                405                 410                 415
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
            420                 425                 430
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
        435                 440                 445
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
    450                 455                 460
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
465                 470                 475                 480
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser
                485                 490                 495
Ser Leu Asn Thr Arg Thr Gln Lys Ala Arg His Ser Pro Asn Ser Glu
            500                 505                 510
```

```
Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
        515                 520                 525
Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Tyr Tyr Glu
    530                 535                 540
Asn Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
545                 550                 555                 560
Ser Gly Ile Tyr Pro Ser Gly Gly Leu Thr Tyr Tyr Ala Asp Ser Val
                565                 570                 575
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
            580                 585                 590
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
        595                 600                 605
Ala Arg Ser Arg Arg Tyr Tyr Asp Ser Ser Asp Ala Phe Asp Ile Trp
    610                 615                 620
Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
625                 630                 635                 640
Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Asp Ile Gln Met Thr Gln
                645                 650                 655
Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser
            660                 665                 670
Cys Arg Ala Ser Gln Ser Ile Asn Thr Tyr Leu Ala Trp Tyr Gln Gln
        675                 680                 685
Lys Pro Gly His Pro Pro Arg Leu Leu Ile Tyr Asp Ala Ser Asn Arg
    690                 695                 700
Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
705                 710                 715                 720
Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Val Val Tyr
                725                 730                 735
Tyr Cys Gln Gln Tyr Gly Arg Ser Arg Tyr Thr Phe Gly Gln Gly Thr
            740                 745                 750
Lys Leu Glu Ile Lys
        755

<210> 627
<211> 757
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 627
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1               5                  10                  15
Val Ile Met Ser Arg Gly Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr
            20                  25                  30
Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln
        35                  40                  45
Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys
    50                  55                  60
Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp
65                  70                  75                  80
Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys
                85                  90                  95
Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
            100                 105                 110
Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu
```

```
        115                 120                 125
Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg
    130                 135                 140
Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val
145                 150                 155                 160
Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr
                165                 170                 175
Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly
            180                 185                 190
Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser
        195                 200                 205
Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser
    210                 215                 220
Gln His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser
225                 230                 235                 240
Phe Leu Leu Pro Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly
                245                 250                 255
Asp Thr Gly Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro
            260                 265                 270
Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro
        275                 280                 285
Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
    290                 295                 300
Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
305                 310                 315                 320
Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
                325                 330                 335
Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
            340                 345                 350
Leu His Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser
        355                 360                 365
Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
    370                 375                 380
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
385                 390                 395                 400
Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
                405                 410                 415
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
            420                 425                 430
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
        435                 440                 445
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
    450                 455                 460
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
465                 470                 475                 480
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser
                485                 490                 495
Ser Leu Asn Thr Arg Thr Gln Lys Ala Arg His Ser Pro Asn Ser Glu
            500                 505                 510
Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
        515                 520                 525
Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr Val
    530                 535                 540
Met Tyr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
545                 550                 555                 560
Gly Ile Gly Pro Ser Gly Gly Asn Thr Phe Tyr Ala Asp Ser Val Lys
                565                 570                 575
```

```
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
            580                 585                 590
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Cys Tyr Cys Ala
        595                 600                 605
Arg Asp Pro Gly Asp Phe Trp Ser Gly Tyr Tyr Gly Met Asp Val Trp
    610                 615                 620
Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
625                 630                 635                 640
Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Asp Ile Gln Met Thr Gln
                645                 650                 655
Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr
            660                 665                 670
Cys Arg Ala Ser Gln Gly Ile Ser Asn Tyr Leu Ala Trp Tyr Gln Gln
        675                 680                 685
Lys Pro Gly Lys Val Pro Lys Leu Leu Ile Asn Ala Ala Ser Thr Leu
    690                 695                 700
Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu
705                 710                 715                 720
Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr
                725                 730                 735
Tyr Cys Gln Gln Ser Asp Asn Ile Pro Tyr Thr Phe Gly Leu Gly Thr
            740                 745                 750
Lys Leu Glu Ile Lys
        755

<210> 628
<211> 758
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 628
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1               5                  10                  15
Val Ile Met Ser Arg Gly Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr
            20                  25                  30
Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln
        35                  40                  45
Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys
    50                  55                  60
Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp
65                  70                  75                  80
Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys
                85                  90                  95
Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
            100                 105                 110
Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu
        115                 120                 125
Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg
    130                 135                 140
Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val
145                 150                 155                 160
Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr
                165                 170                 175
Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly
```

```
            180                 185                 190
Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser
        195                 200                 205
Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser
    210                 215                 220
Gln His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser
225                 230                 235                 240
Phe Leu Leu Pro Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly
                245                 250                 255
Asp Thr Gly Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro
            260                 265                 270
Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro
        275                 280                 285
Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
    290                 295                 300
Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
305                 310                 315                 320
Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
                325                 330                 335
Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
            340                 345                 350
Leu His Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser
        355                 360                 365
Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
    370                 375                 380
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
385                 390                 395                 400
Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
                405                 410                 415
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
            420                 425                 430
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
        435                 440                 445
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
    450                 455                 460
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
465                 470                 475                 480
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser
                485                 490                 495
Ser Leu Asn Thr Arg Thr Gln Lys Ala Arg His Ser Pro Asn Ser Glu
            500                 505                 510
Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
        515                 520                 525
Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Phe Tyr Gly
    530                 535                 540
Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
545                 550                 555                 560
Ser Ile Tyr Pro Ser Gly Gly Tyr Thr Asp Tyr Ala Asp Ser Val Lys
                565                 570                 575
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
            580                 585                 590
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
        595                 600                 605
Arg Ser Ala Gly Gly Trp Ile Gly Gly Gly Ala Phe Asp Ile Trp Gly
    610                 615                 620
Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
625                 630                 635                 640
```

```
Gly Gly Ser Gly Gly Gly Gly Ser Gln Ser Glu Leu Thr Gln Pro Pro
                645                 650                 655
Ser Ala Ser Gly Thr Pro Gly Gln Arg Val Thr Ile Ser Cys Ser Gly
            660                 665                 670
Ser Ser Ser Asn Ile Gly Ser Asn Thr Val Asn Trp Tyr Gln Gln Leu
        675                 680                 685
Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr Ser Asn Asn Gln Arg Pro
    690                 695                 700
Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ser Ala
705                 710                 715                 720
Ser Leu Ala Ile Ser Gly Leu Gln Ser Glu Asp Glu Ala Asp Tyr Tyr
                725                 730                 735
Cys Ala Ala Trp Asp Asp Ser Leu Asn Gly Tyr Val Phe Gly Ile Gly
            740                 745                 750
Thr Lys Val Thr Val Leu
        755

<210> 629
<211> 760
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 629
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1                5                  10                  15
Val Ile Met Ser Arg Gly Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr
            20                  25                  30
Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln
        35                  40                  45
Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys
    50                  55                  60
Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp
65                  70                  75                  80
Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys
                85                  90                  95
Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
            100                 105                 110
Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu
        115                 120                 125
Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg
    130                 135                 140
Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val
145                 150                 155                 160
Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr
                165                 170                 175
Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly
            180                 185                 190
Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser
        195                 200                 205
Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser
    210                 215                 220
Gln His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser
225                 230                 235                 240
Phe Leu Leu Pro Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly
```

```
                245                 250                 255
Asp Thr Gly Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro
            260                 265                 270
Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro
        275                 280                 285
Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
    290                 295                 300
Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
305                 310                 315                 320
Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
                325                 330                 335
Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
            340                 345                 350
Leu His Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser
        355                 360                 365
Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
    370                 375                 380
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
385                 390                 395                 400
Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
                405                 410                 415
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
            420                 425                 430
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
        435                 440                 445
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
    450                 455                 460
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
465                 470                 475                 480
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser
                485                 490                 495
Ser Leu Asn Thr Arg Thr Gln Lys Ala Arg His Ser Pro Asn Ser Glu
            500                 505                 510
Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
        515                 520                 525
Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Lys Tyr Pro
    530                 535                 540
Met Met Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
545                 550                 555                 560
Tyr Ile Tyr Pro Ser Gly Gly Lys Thr Ala Tyr Ala Asp Ser Val Lys
                565                 570                 575
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
            580                 585                 590
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
        595                 600                 605
Thr Tyr Gly Ser Gly Ser Tyr Tyr Leu Tyr Tyr Tyr Tyr Tyr Tyr Met
    610                 615                 620
Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly
625                 630                 635                 640
Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Asp Ile Gln
                645                 650                 655
Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Ser Val
            660                 665                 670
Thr Ile Ala Cys Arg Ala Ser Gln Ser Ile Ser Thr Tyr Leu Asn Trp
        675                 680                 685
Tyr Gln Gln Lys Pro Gly Gln Ala Pro Lys Leu Leu Ile Tyr Glu Ala
    690                 695                 700
```

```
Thr Asn Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser
705                 710                 715                 720
Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Val
                725                 730                 735
Ala Thr Tyr Tyr Cys Gln Gln Ala Asn Asn Phe Pro Phe Thr Phe Gly
            740                 745                 750
Pro Gly Thr Lys Val Asp Ile Lys
        755                 760

<210> 630
<211> 761
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 630
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1               5                  10                  15
Val Ile Met Ser Arg Gly Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr
            20                  25                  30
Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln
        35                  40                  45
Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys
    50                  55                  60
Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp
65                  70                  75                  80
Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys
                85                  90                  95
Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
            100                 105                 110
Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu
        115                 120                 125
Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg
    130                 135                 140
Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val
145                 150                 155                 160
Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr
                165                 170                 175
Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly
            180                 185                 190
Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser
        195                 200                 205
Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser
    210                 215                 220
Gln His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser
225                 230                 235                 240
Phe Leu Leu Pro Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly
                245                 250                 255
Asp Thr Gly Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro
            260                 265                 270
Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro
        275                 280                 285
Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
    290                 295                 300
Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
```

```
305                 310                 315                 320
Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
                325                 330                 335
Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
            340                 345                 350
Leu His Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser
        355                 360                 365
Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
    370                 375                 380
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
385                 390                 395                 400
Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
                405                 410                 415
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
            420                 425                 430
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
        435                 440                 445
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
    450                 455                 460
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
465                 470                 475                 480
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser
                485                 490                 495
Ser Leu Asn Thr Arg Thr Gln Lys Ala Arg His Ser Pro Asn Ser Glu
            500                 505                 510
Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
        515                 520                 525
Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Trp Tyr Ser
    530                 535                 540
Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
545                 550                 555                 560
Tyr Ile Val Pro Ser Gly Gly Glu Thr Ile Tyr Ala Asp Ser Val Lys
                565                 570                 575
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
            580                 585                 590
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
        595                 600                 605
Lys Asn Leu Gly Glu Gly Phe Trp Ser Asp Tyr Tyr Pro Pro Leu Asp
    610                 615                 620
Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly
625                 630                 635                 640
Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Ser Val Leu Thr
                645                 650                 655
Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln Arg Val Thr Ile Ser
            660                 665                 670
Cys Ser Gly Ser Ser Ser Asn Ile Gly Gly Asn Ala Val Asn Trp Tyr
        675                 680                 685
Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Val Leu Tyr Ser Ser Asn
    690                 695                 700
His Arg Pro Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Arg Ser Gly
705                 710                 715                 720
Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln Ser Gln Asp Glu Ala
                725                 730                 735
Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu Asn Gly Pro Leu Phe
            740                 745                 750
Gly Gly Gly Thr Lys Leu Thr Val Leu
        755                 760
```

<210> 631
<211> 752
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 631
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1   5   10   15
Val Ile Met Ser Arg Gly Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr
            20   25   30
Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln
        35   40   45
Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys
    50   55   60
Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp
65   70   75   80
Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys
                85   90   95
Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
            100   105   110
Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu
        115   120   125
Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg
    130   135   140
Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val
145   150   155   160
Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr
                165   170   175
Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly
            180   185   190
Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser
        195   200   205
Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser
    210   215   220
Gln His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser
225   230   235   240
Phe Leu Leu Pro Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly
                245   250   255
Asp Thr Gly Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro
            260   265   270
Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro
        275   280   285
Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
    290   295   300
Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
305   310   315   320
Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
                325   330   335
Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
            340   345   350
Leu His Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser
        355   360   365
Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys

```
    370                 375                 380
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
385                 390                 395                 400
Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
                405                 410                 415
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
            420                 425                 430
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
        435                 440                 445
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
    450                 455                 460
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
465                 470                 475                 480
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser
                485                 490                 495
Ser Leu Asn Thr Arg Thr Gln Lys Ala Arg His Ser Pro Asn Ser Glu
            500                 505                 510
Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
        515                 520                 525
Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser His Tyr Gly
    530                 535                 540
Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
545                 550                 555                 560
Ser Ile Tyr Pro Gly Met Thr Gln Tyr Ala Asp Ser Val Lys Gly Arg
                565                 570                 575
Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met
            580                 585                 590
Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp
        595                 600                 605
Arg Gly Ser Gly Ile Asp Ala Phe Asp Ile Trp Gly Gln Gly Thr Met
    610                 615                 620
Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
625                 630                 635                 640
Gly Gly Gly Ser Gln Ser Glu Leu Thr Gln Pro Pro Ser Val Ser Val
                645                 650                 655
Ser Pro Gly Gln Thr Ala Thr Val Ser Cys Ser Gly Glu Lys Leu Gly
            660                 665                 670
Asp Arg Tyr Ala Trp Trp Tyr Gln Gln Lys Ala Gly Gln Ser Pro Val
        675                 680                 685
Leu Val Ile Tyr Gln Asp Thr Lys Arg Pro Ser Gly Val Pro Asp Arg
    690                 695                 700
Phe Ser Gly Ser Asn Ser Gly Thr Ser Ala Ser Leu Val Ile Ser Gly
705                 710                 715                 720
Pro Gln Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp
                725                 730                 735
Ser Leu Lys Gly Val Val Phe Gly Gly Gly Ser Lys Leu Thr Val Leu
            740                 745                 750

<210> 632
<211> 761
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 632
```

```
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1               5                  10                  15
Val Ile Met Ser Arg Gly Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr
            20                  25                  30
Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln
        35                  40                  45
Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys
    50                  55                  60
Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp
65                  70                  75                  80
Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys
                85                  90                  95
Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
            100                 105                 110
Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu
        115                 120                 125
Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg
    130                 135                 140
Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val
145                 150                 155                 160
Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr
                165                 170                 175
Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly
            180                 185                 190
Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser
        195                 200                 205
Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser
    210                 215                 220
Gln His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser
225                 230                 235                 240
Phe Leu Leu Pro Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly
                245                 250                 255
Asp Thr Gly Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro
            260                 265                 270
Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro
        275                 280                 285
Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
    290                 295                 300
Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
305                 310                 315                 320
Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
                325                 330                 335
Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
            340                 345                 350
Leu His Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser
        355                 360                 365
Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
    370                 375                 380
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
385                 390                 395                 400
Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
                405                 410                 415
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
            420                 425                 430
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
        435                 440                 445
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
```

```
    450                 455                 460
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
465                 470                 475                 480
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser
                485                 490                 495
Ser Leu Asn Thr Arg Thr Gln Lys Ala Arg His Ser Pro Asn Ser Glu
            500                 505                 510
Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
        515                 520                 525
Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Trp Tyr Asp
    530                 535                 540
Met Leu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
545                 550                 555                 560
Val Ile Ser Pro Ser Gly Gly Arg Thr Phe Tyr Ala Asp Ser Val Lys
                565                 570                 575
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
            580                 585                 590
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
        595                 600                 605
Val Thr Arg Ser Met Tyr Ser Ser Ser Trp Tyr Gly Ala Pro Pro Thr
    610                 615                 620
His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly
625                 630                 635                 640
Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Ser Glu Leu Thr
                645                 650                 655
Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln Arg Val Thr Ile Ser
            660                 665                 670
Cys Ser Gly Arg Ser Ser Asn Ile Gly Ser Asn Ser Val Asn Trp Tyr
        675                 680                 685
Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr Ser Asn Asn
    690                 695                 700
His Arg Pro Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly
705                 710                 715                 720
Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln Ser Glu Asp Glu Ala
                725                 730                 735
Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu Tyr Gln Gly Val Phe
            740                 745                 750
Gly Gly Gly Thr Lys Leu Thr Val Leu
        755                 760

<210> 633
<211> 754
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 633
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1               5                  10                  15
Val Ile Met Ser Arg Gly Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr
            20                  25                  30
Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln
        35                  40                  45
Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys
    50                  55                  60
```

```
Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp
65                  70                  75                  80
Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys
                85                  90                  95
Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
            100                 105                 110
Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu
        115                 120                 125
Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg
    130                 135                 140
Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val
145                 150                 155                 160
Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr
                165                 170                 175
Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly
            180                 185                 190
Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser
        195                 200                 205
Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser
    210                 215                 220
Gln His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser
225                 230                 235                 240
Phe Leu Leu Pro Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly
                245                 250                 255
Asp Thr Gly Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro
            260                 265                 270
Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro
        275                 280                 285
Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
    290                 295                 300
Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
305                 310                 315                 320
Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
                325                 330                 335
Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
            340                 345                 350
Leu His Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser
        355                 360                 365
Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
    370                 375                 380
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
385                 390                 395                 400
Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
                405                 410                 415
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
            420                 425                 430
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
        435                 440                 445
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
    450                 455                 460
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
465                 470                 475                 480
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser
                485                 490                 495
Ser Leu Asn Thr Arg Thr Gln Lys Ala Arg His Ser Pro Asn Ser Glu
            500                 505                 510
Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
```

```
        515                 520                 525
Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Trp Tyr Lys
    530                 535                 540
Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
545                 550                 555                 560
Gly Ile Ser Ser Ser Gly Gly Leu Thr Lys Tyr Ala Asp Ser Val Lys
                565                 570                 575
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
            580                 585                 590
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Thr
        595                 600                 605
Thr Glu Arg Arg Gly Asp Gly Gly Ala Phe Asp Ile Trp Gly Gln Gly
    610                 615                 620
Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
625                 630                 635                 640
Ser Gly Gly Gly Gly Ser Gln Asp Ile Gln Met Thr Gln Ser Pro Ser
                645                 650                 655
Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala
            660                 665                 670
Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly
        675                 680                 685
Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly
    690                 695                 700
Val Pro Ser Lys Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
705                 710                 715                 720
Thr Ile Ser Ser Leu Leu Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln
                725                 730                 735
Gln Tyr Glu Tyr Phe Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu
            740                 745                 750
Ile Lys


<210> 634
<211> 757
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 634
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1               5                  10                  15
Val Ile Met Ser Arg Gly Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr
            20                  25                  30
Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln
        35                  40                  45
Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys
    50                  55                  60
Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp
65                  70                  75                  80
Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys
                85                  90                  95
Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
            100                 105                 110
Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu
        115                 120                 125
```

```
Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg
    130                 135                 140
Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val
145                 150                 155                 160
Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr
                165                 170                 175
Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly
            180                 185                 190
Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser
        195                 200                 205
Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser
    210                 215                 220
Gln His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser
225                 230                 235                 240
Phe Leu Leu Pro Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly
                245                 250                 255
Asp Thr Gly Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro
            260                 265                 270
Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro
        275                 280                 285
Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
    290                 295                 300
Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
305                 310                 315                 320
Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
                325                 330                 335
Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
            340                 345                 350
Leu His Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser
        355                 360                 365
Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
    370                 375                 380
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
385                 390                 395                 400
Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
                405                 410                 415
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
            420                 425                 430
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
        435                 440                 445
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
    450                 455                 460
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
465                 470                 475                 480
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser
                485                 490                 495
Ser Leu Asn Thr Arg Thr Gln Lys Ala Arg His Ser Pro Asn Ser Glu
            500                 505                 510
Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
        515                 520                 525
Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Glu Tyr Thr
    530                 535                 540
Met Tyr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
545                 550                 555                 560
Tyr Ile Ser Pro Ser Gly Gly Thr Thr Asn Tyr Ala Gly Ser Val Lys
                565                 570                 575
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
```

```
            580                 585                 590
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
        595                 600                 605
Lys Gly Ala Trp Gly Asp Ile Tyr Tyr Tyr Gly Met Asp Val Trp Gly
    610                 615                 620
Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
625                 630                 635                 640
Gly Gly Ser Gly Gly Gly Gly Ser Gln Asp Ile Gln Met Thr Gln Ser
                645                 650                 655
Pro Asp Ser Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys
            660                 665                 670
Arg Ala Ser Gln Ser Val Ser Ser Ser Tyr Ser Ala Trp Tyr Gln Gln
        675                 680                 685
Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg
    690                 695                 700
Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
705                 710                 715                 720
Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr
                725                 730                 735
Tyr Cys Gln Gln Tyr Gly Ser Ser Ser Leu Thr Phe Gly Gly Gly Thr
            740                 745                 750
Glu Val Glu Ile Lys
        755

<210> 635
<211> 749
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 635
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1               5                  10                  15
Val Ile Met Ser Arg Gly Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr
            20                  25                  30
Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln
        35                  40                  45
Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys
    50                  55                  60
Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp
65                  70                  75                  80
Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys
                85                  90                  95
Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
            100                 105                 110
Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu
        115                 120                 125
Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg
    130                 135                 140
Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val
145                 150                 155                 160
Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr
                165                 170                 175
Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly
            180                 185                 190
```

```
Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser
        195                 200                 205
Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser
    210                 215                 220
Gln His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser
225                 230                 235                 240
Phe Leu Leu Pro Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly
                245                 250                 255
Asp Thr Gly Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro
            260                 265                 270
Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro
        275                 280                 285
Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
    290                 295                 300
Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
305                 310                 315                 320
Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
                325                 330                 335
Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
            340                 345                 350
Leu His Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser
        355                 360                 365
Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
    370                 375                 380
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
385                 390                 395                 400
Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
                405                 410                 415
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
            420                 425                 430
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
        435                 440                 445
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
    450                 455                 460
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
465                 470                 475                 480
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser
                485                 490                 495
Ser Leu Asn Thr Arg Thr Gln Lys Ala Arg His Ser Pro Asn Ser Glu
            500                 505                 510
Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
        515                 520                 525
Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Trp
    530                 535                 540
Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
545                 550                 555                 560
Ser Ile Tyr Pro Ser Gly Gly Ser Thr Glu Tyr Ala Asp Ser Val Lys
                565                 570                 575
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
            580                 585                 590
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
        595                 600                 605
Lys Gly Ile Trp Phe Asp Pro Trp Gly Gln Gly Thr Leu Val Thr Val
    610                 615                 620
Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
625                 630                 635                 640
Ser Gln Asp Ile Gln Met Thr Gln Ser Pro Ala Thr Leu Ser Ala Ser
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                645                 650                 655
Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ser Ser Gln Arg Ile Ser
            660                 665                 670
Gly Tyr Leu Asn Trp Tyr Gln Gln Gln Pro Gly Lys Ala Pro Lys Leu
        675                 680                 685
Leu Ile Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Ile
    690                 695                 700
Ser Gly Ser Gly Ser Gly Thr Asp Phe Ser Leu Ile Ile Ser Ser Leu
705                 710                 715                 720
Gln Pro Glu Asp Val Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Pro
                725                 730                 735
Pro Phe Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
            740                 745

<210> 636
<211> 755
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 636
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1               5                  10                  15
Val Ile Met Ser Arg Gly Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr
            20                  25                  30
Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln
        35                  40                  45
Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys
    50                  55                  60
Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp
65                  70                  75                  80
Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys
                85                  90                  95
Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
            100                 105                 110
Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu
        115                 120                 125
Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg
    130                 135                 140
Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val
145                 150                 155                 160
Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr
                165                 170                 175
Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly
            180                 185                 190
Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser
        195                 200                 205
Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser
    210                 215                 220
Gln His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser
225                 230                 235                 240
Phe Leu Leu Pro Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly
                245                 250                 255
Asp Thr Gly Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro
            260                 265                 270
```

```
Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro
        275                 280                 285
Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
    290                 295                 300
Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
305                 310                 315                 320
Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
                325                 330                 335
Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
            340                 345                 350
Leu His Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser
        355                 360                 365
Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
    370                 375                 380
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
385                 390                 395                 400
Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
                405                 410                 415
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
            420                 425                 430
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
        435                 440                 445
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
    450                 455                 460
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
465                 470                 475                 480
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser
                485                 490                 495
Ser Leu Asn Thr Arg Thr Gln Lys Ala Arg His Ser Pro Asn Ser Glu
            500                 505                 510
Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Pro
        515                 520                 525
Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Tyr Gly
    530                 535                 540
Met Met Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
545                 550                 555                 560
Tyr Ile Ser Ser Ser Gly Gly Phe Thr Arg Tyr Ala Asp Ser Val Lys
                565                 570                 575
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
            580                 585                 590
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
        595                 600                 605
Arg Val Gly Gly Tyr Ser Tyr Gly Pro His Phe Asp Phe Trp Gly Gln
    610                 615                 620
Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
625                 630                 635                 640
Gly Ser Gly Gly Gly Gly Ser Gln Asp Ile Gln Met Thr Gln Ser Pro
                645                 650                 655
Ser Thr Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg
            660                 665                 670
Ala Ser Gln Ser Ile Ser Thr Trp Leu Ala Trp Phe Gln Gln Lys Pro
        675                 680                 685
Gly Lys Ala Pro Lys Leu Leu Ile Tyr Lys Ala Ser Ser Leu Gln Ser
    690                 695                 700
Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
705                 710                 715                 720
Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
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                725                 730                 735
Gln Gln Tyr Lys Ser Tyr Pro Phe Thr Phe Gly Gly Gly Thr Lys Val
            740                 745                 750
Glu Ile Lys
        755

<210> 637
<211> 757
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 637
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1               5                  10                  15
Val Ile Met Ser Arg Gly Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr
            20                  25                  30
Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln
        35                  40                  45
Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys
    50                  55                  60
Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp
65                  70                  75                  80
Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys
                85                  90                  95
Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
            100                 105                 110
Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu
        115                 120                 125
Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg
    130                 135                 140
Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val
145                 150                 155                 160
Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr
                165                 170                 175
Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly
            180                 185                 190
Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser
        195                 200                 205
Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser
    210                 215                 220
Gln His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser
225                 230                 235                 240
Phe Leu Leu Pro Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly
                245                 250                 255
Asp Thr Gly Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro
            260                 265                 270
Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro
        275                 280                 285
Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
    290                 295                 300
Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
305                 310                 315                 320
Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
                325                 330                 335
```

```
Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
            340                 345                 350
Leu His Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser
        355                 360                 365
Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
    370                 375                 380
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
385                 390                 395                 400
Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
                405                 410                 415
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
            420                 425                 430
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
        435                 440                 445
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
    450                 455                 460
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
465                 470                 475                 480
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser
                485                 490                 495
Ser Leu Asn Thr Arg Thr Gln Lys Ala Arg His Ser Pro Asn Ser Glu
            500                 505                 510
Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
        515                 520                 525
Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Trp Tyr His
    530                 535                 540
Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
545                 550                 555                 560
Trp Ile Ser Pro Ser Gly Gly Phe Thr Lys Tyr Ala Asp Ser Val Lys
                565                 570                 575
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
            580                 585                 590
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
        595                 600                 605
Arg Tyr Asp Ser Arg Ala Ala Ala Gly Thr Asn Ala Phe Asp Ile Trp
    610                 615                 620
Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
625                 630                 635                 640
Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Asp Ile Gln Met Thr Gln
                645                 650                 655
Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Ser Val Thr Ile Thr
            660                 665                 670
Cys Gln Ala Ser Gln Asp Ile Arg Ser Tyr Leu Asn Trp Phe Gln Gln
        675                 680                 685
Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Asp Thr Val Asn Leu
    690                 695                 700
Gln Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
705                 710                 715                 720
Tyr Ser Phe Thr Ile Asn Asn Leu Gln Pro Glu Asp Phe Ala Thr Tyr
                725                 730                 735
Cys Cys Gln Gln Tyr Glu Tyr Leu Pro Ile Thr Phe Gly Gln Gly Thr
            740                 745                 750
Arg Leu Glu Ile Lys
        755
```

<210> 638
<211> 757

<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 638
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1   5   10   15
Val Ile Met Ser Arg Gly Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr
            20   25   30
Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln
        35   40   45
Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys
    50   55   60
Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp
65   70   75   80
Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys
                85   90   95
Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
            100   105   110
Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu
        115   120   125
Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg
    130   135   140
Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val
145   150   155   160
Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr
                165   170   175
Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly
            180   185   190
Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser
        195   200   205
Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser
    210   215   220
Gln His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser
225   230   235   240
Phe Leu Leu Pro Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly
                245   250   255
Asp Thr Gly Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro
            260   265   270
Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro
        275   280   285
Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
    290   295   300
Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
305   310   315   320
Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
                325   330   335
Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
            340   345   350
Leu His Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser
        355   360   365
Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
    370   375   380
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
385   390   395   400

```
Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
                405                 410                 415
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
            420                 425                 430
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
        435                 440                 445
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
    450                 455                 460
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
465                 470                 475                 480
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser
                485                 490                 495
Ser Leu Asn Thr Arg Thr Gln Lys Ala Arg His Ser Pro Asn Ser Glu
            500                 505                 510
Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
        515                 520                 525
Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Pro Tyr Lys
    530                 535                 540
Met Val Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
545                 550                 555                 560
Gly Ile Ser Pro Ser Gly Gly Tyr Thr Tyr Tyr Ala Asp Ser Val Lys
                565                 570                 575
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
            580                 585                 590
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
        595                 600                 605
Arg Gly Gly Tyr Gly Trp Ser Tyr Tyr Tyr Tyr Gly Met Asp Val Trp
    610                 615                 620
Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
625                 630                 635                 640
Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Asp Ile Gln Met Thr Gln
                645                 650                 655
Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr
            660                 665                 670
Cys Arg Ala Ser Gln Ser Ile Ser Asn Tyr Leu Asn Trp Tyr Gln Gln
        675                 680                 685
Lys Ser Gly Lys Ala Pro Asn Leu Leu Met Tyr Ala Ala Ser Ser Leu
    690                 695                 700
His Ser Gly Val Ser Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu
705                 710                 715                 720
Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Tyr Ala Thr Tyr
                725                 730                 735
Tyr Cys Gln Gln Ser Tyr Ser Thr Ser Gly Thr Phe Gly Gln Gly Thr
            740                 745                 750
Lys Val Glu Ile Lys
        755

<210> 639
<211> 752
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 639
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
```

```
 1               5                  10                  15
Val Ile Met Ser Arg Gly Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr
            20                  25                  30
Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln
        35                  40                  45
Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys
    50                  55                  60
Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp
65                  70                  75                  80
Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys
                85                  90                  95
Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
            100                 105                 110
Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu
        115                 120                 125
Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg
    130                 135                 140
Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val
145                 150                 155                 160
Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr
                165                 170                 175
Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly
            180                 185                 190
Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser
        195                 200                 205
Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser
    210                 215                 220
Gln His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser
225                 230                 235                 240
Phe Leu Leu Pro Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly
                245                 250                 255
Asp Thr Gly Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro
            260                 265                 270
Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro
        275                 280                 285
Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
    290                 295                 300
Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
305                 310                 315                 320
Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
                325                 330                 335
Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
            340                 345                 350
Leu His Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser
        355                 360                 365
Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
    370                 375                 380
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
385                 390                 395                 400
Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
                405                 410                 415
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
            420                 425                 430
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
        435                 440                 445
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
    450                 455                 460
```

```
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
465                 470                 475                 480
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser
                485                 490                 495
Ser Leu Asn Thr Arg Thr Gln Lys Ala Arg His Ser Pro Asn Ser Glu
            500                 505                 510
Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
        515                 520                 525
Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Tyr Trp
    530                 535                 540
Met Tyr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
545                 550                 555                 560
Val Ile Ser Ser Ser Gly Gly His Thr Phe Tyr Ala Asp Ser Val Lys
                565                 570                 575
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
            580                 585                 590
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
        595                 600                 605
Arg Asp Tyr Glu Gly Gly Ser Asn Asp Tyr Trp Gly Gln Gly Thr Leu
    610                 615                 620
Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
625                 630                 635                 640
Gly Gly Gly Ser Gln Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu
                645                 650                 655
Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln
            660                 665                 670
Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala
        675                 680                 685
Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro
    690                 695                 700
Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
705                 710                 715                 720
Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser
                725                 730                 735
Tyr Ser Thr Pro Val Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            740                 745                 750

<210> 640
<211> 755
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 640
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1               5                  10                  15
Val Ile Met Ser Arg Gly Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr
            20                  25                  30
Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln
        35                  40                  45
Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys
    50                  55                  60
Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp
65                  70                  75                  80
Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys
```

```
                85                  90                  95
Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
            100                 105                 110
Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu
        115                 120                 125
Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg
    130                 135                 140
Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val
145                 150                 155                 160
Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr
                165                 170                 175
Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly
            180                 185                 190
Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser
        195                 200                 205
Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser
    210                 215                 220
Gln His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser
225                 230                 235                 240
Phe Leu Leu Pro Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly
                245                 250                 255
Asp Thr Gly Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro
            260                 265                 270
Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro
        275                 280                 285
Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
    290                 295                 300
Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
305                 310                 315                 320
Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
                325                 330                 335
Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
            340                 345                 350
Leu His Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser
        355                 360                 365
Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
    370                 375                 380
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
385                 390                 395                 400
Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
                405                 410                 415
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
            420                 425                 430
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
        435                 440                 445
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
    450                 455                 460
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
465                 470                 475                 480
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser
                485                 490                 495
Ser Leu Asn Thr Arg Thr Gln Lys Ala Arg His Ser Pro Asn Ser Glu
            500                 505                 510
Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
        515                 520                 525
Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Tyr Ala
    530                 535                 540
```

```
Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
545                 550                 555                 560
Ser Ile Tyr Ser Ser Gly Gly Tyr Thr Ala Tyr Ala Asp Ser Val Lys
                565                 570                 575
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
            580                 585                 590
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Met Tyr Tyr Cys Ala
        595                 600                 605
Arg Val Pro His Val Phe Arg Gly Glu Leu Asp Tyr Trp Gly Gln Gly
    610                 615                 620
Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
625                 630                 635                 640
Ser Gly Gly Gly Gly Ser Gln Asp Ile Gln Met Thr Gln Ser Pro Ser
                645                 650                 655
Ser Leu Ser Ala Ser Val Gly Asp Arg Val Ala Ile Thr Cys Arg Ala
            660                 665                 670
Ser Gln Ser Ile Asp Thr Tyr Leu Asn Trp Tyr Gln His Lys Pro Gly
        675                 680                 685
Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly
    690                 695                 700
Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
705                 710                 715                 720
Thr Ile Ser Gly Leu Gln Pro Glu Asp Phe Ala Ser Tyr Phe Cys Gln
                725                 730                 735
Gln Ser Tyr Ser Ser Pro Gly Ile Thr Phe Gly Gly Gly Thr Arg Val
            740                 745                 750
Glu Ile Lys
        755

<210> 641
<211> 756
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 641
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1               5                  10                  15
Val Ile Met Ser Arg Gly Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr
            20                  25                  30
Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln
        35                  40                  45
Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys
    50                  55                  60
Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp
65                  70                  75                  80
Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys
                85                  90                  95
Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
            100                 105                 110
Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu
        115                 120                 125
Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg
    130                 135                 140
Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val
```

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145                 150                 155                 160
Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr
                165                 170                 175
Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly
            180                 185                 190
Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser
        195                 200                 205
Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser
    210                 215                 220
Gln His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser
225                 230                 235                 240
Phe Leu Leu Pro Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly
                245                 250                 255
Asp Thr Gly Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro
            260                 265                 270
Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro
        275                 280                 285
Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
    290                 295                 300
Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
305                 310                 315                 320
Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
                325                 330                 335
Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
            340                 345                 350
Leu His Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser
        355                 360                 365
Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
    370                 375                 380
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
385                 390                 395                 400
Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
                405                 410                 415
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
            420                 425                 430
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
        435                 440                 445
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
    450                 455                 460
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
465                 470                 475                 480
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser
                485                 490                 495
Ser Leu Asn Thr Arg Thr Gln Lys Ala Arg His Ser Pro Asn Ser Glu
            500                 505                 510
Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
        515                 520                 525
Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Phe Tyr Thr
    530                 535                 540
Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
545                 550                 555                 560
Ser Ile Tyr Pro Ser Gly Gly Gln Thr Leu Tyr Ala Asp Ser Val Lys
                565                 570                 575
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
            580                 585                 590
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
        595                 600                 605
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Arg Pro Asp Ser Tyr Gly Tyr Leu Tyr Tyr Gly Met Asp Val Trp Gly
    610                 615                 620
Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
625                 630                 635                 640
Gly Gly Ser Gly Gly Gly Gly Ser Gln Asp Ile Gln Met Thr Gln Ser
                645                 650                 655
Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
            660                 665                 670
Arg Ala Ser Gln Ser Ile Gly Thr Tyr Leu Asn Trp Tyr Gln Gln Lys
        675                 680                 685
Pro Gly Lys Ala Pro Asn Leu Leu Ile Tyr Gly Thr Ser Ser Leu Gln
    690                 695                 700
Arg Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
705                 710                 715                 720
Thr Leu Thr Ile Ser Thr Leu Gln Pro Glu Asp Phe Val His Tyr Tyr
                725                 730                 735
Cys Gln Gln Ser Tyr Thr Ser Pro Pro Thr Phe Gly Gln Gly Thr Lys
            740                 745                 750
Val Glu Val Lys
        755

<210> 642
<211> 747
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 642
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1               5                  10                  15
Val Ile Met Ser Arg Gly Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr
            20                  25                  30
Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln
        35                  40                  45
Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys
    50                  55                  60
Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp
65                  70                  75                  80
Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys
                85                  90                  95
Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
            100                 105                 110
Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu
        115                 120                 125
Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg
    130                 135                 140
Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val
145                 150                 155                 160
Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr
                165                 170                 175
Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly
            180                 185                 190
Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser
        195                 200                 205
Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser
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    210                 215                 220
Gln His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser
225                 230                 235                 240
Phe Leu Leu Pro Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly
                245                 250                 255
Asp Thr Gly Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro
            260                 265                 270
Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro
        275                 280                 285
Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
    290                 295                 300
Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
305                 310                 315                 320
Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
                325                 330                 335
Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
            340                 345                 350
Leu His Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser
        355                 360                 365
Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
    370                 375                 380
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
385                 390                 395                 400
Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
                405                 410                 415
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
            420                 425                 430
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
        435                 440                 445
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
    450                 455                 460
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
465                 470                 475                 480
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser
                485                 490                 495
Ser Leu Asn Thr Arg Thr Gln Lys Ala Arg His Ser Pro Asn Ser Glu
            500                 505                 510
Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
        515                 520                 525
Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Trp Tyr Pro
    530                 535                 540
Met Glu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
545                 550                 555                 560
Gly Ile Gly Pro Ser Gly Gly Gln Thr Thr Tyr Ala Asp Ser Val Lys
                565                 570                 575
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
            580                 585                 590
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
        595                 600                 605
Arg Gly Ser Tyr Ser Phe Ile Trp Gly Gln Gly Thr Met Val Thr Val
    610                 615                 620
Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
625                 630                 635                 640
Ser Gln Tyr Glu Leu Thr Gln Ser Pro Ser Val Ser Val Ser Pro Gly
                645                 650                 655
Gln Thr Ala Ser Ile Pro Cys Ser Gly Asp Gln Leu Gly Gly Lys Phe
            660                 665                 670
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Thr Ser Trp Tyr Gln Gln Lys Ala Gly Gln Ser Pro Leu Leu Val Ile
        675                 680                 685
Tyr Gln Asp Thr Lys Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly
    690                 695                 700
Ser Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Thr Gly Thr Gln Ala
705                 710                 715                 720
Met Asp Glu Ala Asp Tyr Tyr Cys Leu Val Trp Asp Ser Asn Thr Tyr
                725                 730                 735
Val Phe Gly Pro Gly Thr Lys Val Thr Val Leu
            740                 745

<210> 643
<211> 759
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 643
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1                5                  10                  15
Val Ile Met Ser Arg Gly Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr
            20                  25                  30
Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln
        35                  40                  45
Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys
    50                  55                  60
Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp
65                  70                  75                  80
Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys
                85                  90                  95
Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
            100                 105                 110
Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu
        115                 120                 125
Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg
    130                 135                 140
Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val
145                 150                 155                 160
Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr
                165                 170                 175
Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly
            180                 185                 190
Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser
        195                 200                 205
Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser
    210                 215                 220
Gln His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser
225                 230                 235                 240
Phe Leu Leu Pro Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly
                245                 250                 255
Asp Thr Gly Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro
            260                 265                 270
Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro
        275                 280                 285
Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
```

```
    290                 295                 300
Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
305                 310                 315                 320
Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
                325                 330                 335
Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
            340                 345                 350
Leu His Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser
        355                 360                 365
Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
    370                 375                 380
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
385                 390                 395                 400
Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
                405                 410                 415
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
            420                 425                 430
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
        435                 440                 445
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
    450                 455                 460
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
465                 470                 475                 480
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser
                485                 490                 495
Ser Leu Asn Thr Arg Thr Gln Lys Ala Arg His Ser Pro Asn Ser Glu
            500                 505                 510
Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
        515                 520                 525
Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Leu Tyr Lys
    530                 535                 540
Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
545                 550                 555                 560
Val Ile Gly Ser Ser Gly Gly Arg Thr Pro Tyr Ala Asp Ser Val Lys
                565                 570                 575
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
            580                 585                 590
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
        595                 600                 605
Arg Ala Pro Leu Ser Gly Trp Phe Gly Gln Ala His Asp Ala Phe Asp
    610                 615                 620
Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly
625                 630                 635                 640
Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Tyr Glu Leu Thr
                645                 650                 655
Gln Ser Pro Ser Val Ser Val Ala Pro Gly Gln Thr Ala Arg Ile Thr
            660                 665                 670
Cys Gly Gly Asn Asn Ile Gly Ser Lys Ser Val His Trp Tyr Gln Gln
        675                 680                 685
Lys Pro Gly Gln Ala Pro Val Leu Val Val Tyr Asp Asp Ser Asp Arg
    690                 695                 700
Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser Asn Ser Gly Asn Thr
705                 710                 715                 720
Ala Thr Leu Thr Val Ser Arg Val Glu Ala Gly Asp Glu Ala Asp Tyr
                725                 730                 735
Tyr Cys Gln Val Trp Asp Ser Ser Gly Gly Leu Gln Val Phe Gly Thr
            740                 745                 750
```

Gly Thr Lys Val Thr Val Leu
755

<210> 644
<211> 756
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 644
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1 5 10 15
Val Ile Met Ser Arg Gly Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr
20 25 30
Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln
35 40 45
Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys
50 55 60
Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp
65 70 75 80
Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys
85 90 95
Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
100 105 110
Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu
115 120 125
Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg
130 135 140
Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val
145 150 155 160
Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr
165 170 175
Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly
180 185 190
Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser
195 200 205
Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser
210 215 220
Gln His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser
225 230 235 240
Phe Leu Leu Pro Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly
245 250 255
Asp Thr Gly Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro
260 265 270
Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro
275 280 285
Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
290 295 300
Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
305 310 315 320
Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
325 330 335
Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
340 345 350
Leu His Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser

```
        355                 360                 365
Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
    370                 375                 380
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
385                 390                 395                 400
Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
                405                 410                 415
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
            420                 425                 430
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
        435                 440                 445
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
    450                 455                 460
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
465                 470                 475                 480
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser
                485                 490                 495
Ser Leu Asn Thr Arg Thr Gln Lys Ala Arg His Ser Pro Asn Ser Glu
            500                 505                 510
Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
        515                 520                 525
Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr Glu
    530                 535                 540
Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
545                 550                 555                 560
Gly Ile Val Pro Ser Gly Gly Val Thr Tyr Tyr Ala Asp Ser Val Lys
                565                 570                 575
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
            580                 585                 590
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
        595                 600                 605
Arg Gly Pro Tyr Ser Tyr Gly His Asp Tyr Gly Met Asp Val Trp Gly
    610                 615                 620
Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
625                 630                 635                 640
Gly Gly Ser Gly Gly Gly Gly Ser Gln Asp Ile Gln Met Thr Gln Ser
                645                 650                 655
Pro Ser Thr Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
            660                 665                 670
Arg Ala Ser Gln Ser Ile Ser Ser Trp Leu Ala Trp Tyr Gln Gln Lys
        675                 680                 685
Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Lys Ala Ser Asn Leu Glu
    690                 695                 700
Ser Glu Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe
705                 710                 715                 720
Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr
                725                 730                 735
Cys Gln Gln Tyr Asn Ala Tyr Pro Phe Ile Phe Gly Pro Gly Thr Lys
            740                 745                 750
Val Asp Ile Lys
        755

<210> 645
<211> 751
<212> PRT
<213> Artificial Sequence
```

<220>
<223> Made in a lab

<400> 645
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1   5   10   15
Val Ile Met Ser Arg Gly Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr
            20   25   30
Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln
        35   40   45
Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys
    50   55   60
Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp
65   70   75   80
Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys
                85   90   95
Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
            100   105   110
Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu
        115   120   125
Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg
    130   135   140
Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val
145   150   155   160
Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr
                165   170   175
Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly
            180   185   190
Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser
        195   200   205
Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser
    210   215   220
Gln His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser
225   230   235   240
Phe Leu Leu Pro Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly
                245   250   255
Asp Thr Gly Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro
            260   265   270
Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro
        275   280   285
Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
    290   295   300
Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
305   310   315   320
Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
                325   330   335
Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
            340   345   350
Leu His Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser
        355   360   365
Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
    370   375   380
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
385   390   395   400
Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
                405   410   415
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu

```
            420                 425                 430
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
        435                 440                 445
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
    450                 455                 460
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
465                 470                 475                 480
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser
                485                 490                 495
Ser Leu Asn Thr Arg Thr Gln Lys Ala Arg His Ser Pro Asn Ser Glu
            500                 505                 510
Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
        515                 520                 525
Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Val Tyr Pro
    530                 535                 540
Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
545                 550                 555                 560
Ser Ile Tyr Ser Ser Gly Gly Phe Thr Met Tyr Ala Asp Ser Val Lys
                565                 570                 575
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
            580                 585                 590
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Val
        595                 600                 605
Arg Glu Gly Val Ala Asp Ala Phe Asp Ile Trp Gly Gln Gly Thr Met
    610                 615                 620
Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
625                 630                 635                 640
Gly Gly Gly Ser Gln Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu
                645                 650                 655
Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln
            660                 665                 670
Ser Ile Ser Ser Trp Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala
        675                 680                 685
Pro Lys Leu Leu Ile Tyr Lys Ala Ser Ser Leu Glu Ser Gly Val Pro
    690                 695                 700
Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile
705                 710                 715                 720
Ser Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr His Cys Gln Gln Tyr
                725                 730                 735
Lys Ser Tyr Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
            740                 745                 750

<210> 646
<211> 756
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 646
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1               5                  10                  15
Val Ile Met Ser Arg Gly Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr
            20                  25                  30
Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln
        35                  40                  45
```

```
Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys
    50                  55                  60
Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp
65                  70                  75                  80
Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys
                85                  90                  95
Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
            100                 105                 110
Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu
        115                 120                 125
Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg
    130                 135                 140
Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val
145                 150                 155                 160
Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr
                165                 170                 175
Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly
            180                 185                 190
Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser
        195                 200                 205
Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser
    210                 215                 220
Gln His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser
225                 230                 235                 240
Phe Leu Leu Pro Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly
                245                 250                 255
Asp Thr Gly Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro
            260                 265                 270
Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro
        275                 280                 285
Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
    290                 295                 300
Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
305                 310                 315                 320
Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
                325                 330                 335
Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
            340                 345                 350
Leu His Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser
        355                 360                 365
Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
    370                 375                 380
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
385                 390                 395                 400
Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
                405                 410                 415
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
            420                 425                 430
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
        435                 440                 445
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
    450                 455                 460
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
465                 470                 475                 480
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser
                485                 490                 495
Ser Leu Asn Thr Arg Thr Gln Lys Ala Arg His Ser Pro Asn Ser Glu
```

```
            500                 505                 510
Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
        515                 520                 525
Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Thr
    530                 535                 540
Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
545                 550                 555                 560
Ser Ile Ser Pro Ser Gly Gly Met Thr Phe Tyr Ala Asp Ser Val Lys
                565                 570                 575
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
            580                 585                 590
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
        595                 600                 605
Arg Thr Tyr Asp Phe Trp Ser Gly Tyr Phe Asp Tyr Trp Gly Gln Gly
    610                 615                 620
Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
625                 630                 635                 640
Ser Gly Gly Gly Gly Ser Gln Ser Glu Leu Thr Gln Pro Pro Ser Val
                645                 650                 655
Ser Glu Ala Pro Arg Gln Arg Val Thr Val Ser Cys Ser Gly Ser Pro
            660                 665                 670
Ser Asn Ile Gly Ser Asn Ser Val Asn Trp Tyr Gln Gln Leu Pro Gly
        675                 680                 685
Lys Ala Pro Lys Val Val Ile Tyr Tyr Asp Asp Leu Val Pro Ser Gly
    690                 695                 700
Val Ser Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu
705                 710                 715                 720
Ala Ile Ser Gly Leu Gln Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala
                725                 730                 735
Ala Trp Asp Asp Arg Leu Asn Gly Trp Val Phe Gly Gly Gly Thr Lys
            740                 745                 750
Leu Thr Val Leu
        755
```

<210> 647
<211> 759
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 647

```
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1               5                  10                  15
Val Ile Met Ser Arg Gly Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr
            20                  25                  30
Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln
        35                  40                  45
Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys
    50                  55                  60
Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp
65                  70                  75                  80
Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys
                85                  90                  95
Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
            100                 105                 110
```

```
Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu
        115                 120                 125
Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg
    130                 135                 140
Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val
145                 150                 155                 160
Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr
                165                 170                 175
Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly
            180                 185                 190
Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser
        195                 200                 205
Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser
    210                 215                 220
Gln His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser
225                 230                 235                 240
Phe Leu Leu Pro Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly
                245                 250                 255
Asp Thr Gly Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro
            260                 265                 270
Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro
        275                 280                 285
Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
    290                 295                 300
Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
305                 310                 315                 320
Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
                325                 330                 335
Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
            340                 345                 350
Leu His Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser
        355                 360                 365
Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
    370                 375                 380
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
385                 390                 395                 400
Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
                405                 410                 415
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
            420                 425                 430
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
        435                 440                 445
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
    450                 455                 460
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
465                 470                 475                 480
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser
                485                 490                 495
Ser Leu Asn Thr Arg Thr Gln Lys Ala Arg His Ser Pro Asn Ser Glu
            500                 505                 510
Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
        515                 520                 525
Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr Glu
    530                 535                 540
Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
545                 550                 555                 560
Val Ile Trp Ser Ser Gly Gly His Thr Trp Tyr Ala Asp Ser Val Lys
```

```
                565                 570                 575
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
            580                 585                 590
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
        595                 600                 605
Arg Ser Asn Gln Gly Asp Phe Trp Ser Gly Tyr Pro Phe Ala Phe Asp
    610                 615                 620
Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly
625                 630                 635                 640
Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Asp Ile Gln Met
                645                 650                 655
Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly Asp Arg Val Thr
            660                 665                 670
Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Ser Trp Leu Ala Trp Tyr
        675                 680                 685
Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser
    690                 695                 700
Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
705                 710                 715                 720
Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala
                725                 730                 735
Thr Tyr Tyr Cys Gln Gln Ala Asn Ser Phe Pro Leu Thr Phe Gly Gly
            740                 745                 750
Gly Thr Lys Val Glu Ile Lys
        755

<210> 648
<211> 754
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 648
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1               5                  10                  15
Val Ile Met Ser Arg Gly Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr
            20                  25                  30
Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln
        35                  40                  45
Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys
    50                  55                  60
Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp
65                  70                  75                  80
Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys
                85                  90                  95
Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
            100                 105                 110
Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu
        115                 120                 125
Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg
    130                 135                 140
Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val
145                 150                 155                 160
Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr
                165                 170                 175
```

```
Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly
            180                 185                 190
Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser
        195                 200                 205
Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser
    210                 215                 220
Gln His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser
225                 230                 235                 240
Phe Leu Leu Pro Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly
                245                 250                 255
Asp Thr Gly Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro
            260                 265                 270
Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro
        275                 280                 285
Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
    290                 295                 300
Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
305                 310                 315                 320
Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
                325                 330                 335
Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
            340                 345                 350
Leu His Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser
        355                 360                 365
Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
    370                 375                 380
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
385                 390                 395                 400
Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
                405                 410                 415
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
            420                 425                 430
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
        435                 440                 445
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
    450                 455                 460
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
465                 470                 475                 480
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser
                485                 490                 495
Ser Leu Asn Thr Arg Thr Gln Lys Ala Arg His Ser Pro Asn Ser Glu
            500                 505                 510
Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
        515                 520                 525
Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Tyr Asn
    530                 535                 540
Met Tyr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
545                 550                 555                 560
Tyr Ile Ser Pro Ser Gly Gly Met Thr Lys Tyr Ala Asp Ser Val Lys
                565                 570                 575
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
            580                 585                 590
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
        595                 600                 605
Arg Arg Gly Val Leu Gly Tyr Tyr Gly Met Asp Val Trp Gly Gln Gly
    610                 615                 620
Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
```

625 630 635 640
Ser Gly Gly Gly Gly Ser Gln Asp Ile Gln Met Thr Gln Ser Pro Ser
645 650 655
Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala
660 665 670
Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly
675 680 685
Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly
690 695 700
Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
705 710 715 720
Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln
725 730 735
Gln Ser Tyr Ser Thr Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu
740 745 750
Ile Lys

<210> 649
<211> 757
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 649
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1 5 10 15
Val Ile Met Ser Arg Gly Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr
20 25 30
Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln
35 40 45
Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys
50 55 60
Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp
65 70 75 80
Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys
85 90 95
Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
100 105 110
Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu
115 120 125
Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg
130 135 140
Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val
145 150 155 160
Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr
165 170 175
Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly
180 185 190
Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser
195 200 205
Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser
210 215 220
Gln His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser
225 230 235 240

```
Phe Leu Leu Pro Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly
                245                 250                 255
Asp Thr Gly Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro
            260                 265                 270
Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro
        275                 280                 285
Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
    290                 295                 300
Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
305                 310                 315                 320
Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
                325                 330                 335
Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
            340                 345                 350
Leu His Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser
        355                 360                 365
Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
    370                 375                 380
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
385                 390                 395                 400
Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
                405                 410                 415
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
            420                 425                 430
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
        435                 440                 445
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
    450                 455                 460
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
465                 470                 475                 480
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser
                485                 490                 495
Ser Leu Asn Thr Arg Thr Gln Lys Ala Arg His Ser Pro Asn Ser Glu
            500                 505                 510
Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
        515                 520                 525
Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Leu Tyr Ser
    530                 535                 540
Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
545                 550                 555                 560
Ser Ile Ser Ser Ser Gly Gly Ala Thr Leu Tyr Ala Asp Ser Val Lys
                565                 570                 575
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
            580                 585                 590
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
        595                 600                 605
Arg Asp Leu Ile Ser Ser Gly Tyr Tyr Pro Asp Ala Phe Asp Ile Trp
    610                 615                 620
Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
625                 630                 635                 640
Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Asp Ile Gln Met Thr Gln
                645                 650                 655
Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser
            660                 665                 670
Cys Arg Ala Ser Gln Ser Val Ser Ser Ser Tyr Leu Ala Trp Tyr Gln
        675                 680                 685
Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Asn
```

```
    690                 695                 700
Arg Val Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr
705                 710                 715                 720
Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Ser Ala Val
                725                 730                 735
Tyr Tyr Cys His Gln Tyr Gly Ser Gln Tyr Thr Phe Gly Pro Gly Thr
            740                 745                 750
Lys Leu Glu Ile Lys
        755
```

<210> 650
<211> 762
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 650

```
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1               5                  10                  15
Val Ile Met Ser Arg Gly Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr
            20                  25                  30
Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln
        35                  40                  45
Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys
    50                  55                  60
Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp
65                  70                  75                  80
Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys
                85                  90                  95
Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
            100                 105                 110
Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu
        115                 120                 125
Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg
    130                 135                 140
Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val
145                 150                 155                 160
Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr
                165                 170                 175
Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly
            180                 185                 190
Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser
        195                 200                 205
Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser
    210                 215                 220
Gln His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser
225                 230                 235                 240
Phe Leu Leu Pro Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly
                245                 250                 255
Asp Thr Gly Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro
            260                 265                 270
Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro
        275                 280                 285
Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
    290                 295                 300
```

```
Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
305                 310                 315                 320
Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
                325                 330                 335
Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
            340                 345                 350
Leu His Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser
        355                 360                 365
Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
    370                 375                 380
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
385                 390                 395                 400
Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
                405                 410                 415
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
            420                 425                 430
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
        435                 440                 445
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
    450                 455                 460
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
465                 470                 475                 480
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser
                485                 490                 495
Ser Leu Asn Thr Arg Thr Gln Lys Ala Arg His Ser Pro Asn Ser Glu
            500                 505                 510
Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
        515                 520                 525
Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Gln Tyr Met
    530                 535                 540
Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
545                 550                 555                 560
Ser Ile Ser Ser Ser Gly Gly Trp Thr Ser Tyr Ala Asp Ser Val Lys
                565                 570                 575
Gly Ser Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
            580                 585                 590
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
        595                 600                 605
Arg Pro Leu Ala Leu Gly Tyr Asp Phe Trp Ser Gly Tyr Gln Ala Ala
    610                 615                 620
Gly Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly
625                 630                 635                 640
Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Asp
                645                 650                 655
Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp
            660                 665                 670
Arg Val Thr Ile Ser Cys Gln Ala Ser Gln His Ile Ser Asn Phe Leu
        675                 680                 685
Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
    690                 695                 700
Asp Thr Ser Asn Leu Arg Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
705                 710                 715                 720
Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu
                725                 730                 735
Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asp Asn Phe Pro Leu Thr
            740                 745                 750
Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
```

```
        755                 760

<210> 651
<211> 755
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 651
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1               5                  10                  15
Val Ile Met Ser Arg Gly Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr
            20                  25                  30
Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln
        35                  40                  45
Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys
    50                  55                  60
Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp
65                  70                  75                  80
Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys
                85                  90                  95
Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
            100                 105                 110
Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu
        115                 120                 125
Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg
    130                 135                 140
Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val
145                 150                 155                 160
Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr
                165                 170                 175
Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly
            180                 185                 190
Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser
        195                 200                 205
Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser
    210                 215                 220
Gln His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser
225                 230                 235                 240
Phe Leu Leu Pro Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly
                245                 250                 255
Asp Thr Gly Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro
            260                 265                 270
Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro
        275                 280                 285
Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
    290                 295                 300
Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
305                 310                 315                 320
Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
                325                 330                 335
Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
            340                 345                 350
Leu His Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser
        355                 360                 365
```

```
Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
    370                 375                 380
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
385                 390                 395                 400
Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
                405                 410                 415
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
            420                 425                 430
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
        435                 440                 445
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
    450                 455                 460
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
465                 470                 475                 480
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser
                485                 490                 495
Ser Leu Asn Thr Arg Thr Gln Lys Ala Arg His Ser Pro Asn Ser Glu
            500                 505                 510
Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
        515                 520                 525
Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Trp Tyr Ser
    530                 535                 540
Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
545                 550                 555                 560
Ser Ile Val Pro Ser Gly Gly Leu Thr Trp Tyr Ala Asp Ser Val Lys
                565                 570                 575
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
            580                 585                 590
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
        595                 600                 605
Arg Asp Val Tyr Gly Asp Tyr Tyr Phe Asp Asn Trp Gly Gln Gly Thr
    610                 615                 620
Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
625                 630                 635                 640
Gly Gly Gly Gly Ser Gln Ser Glu Leu Thr Gln Pro Pro Ser Val Ser
                645                 650                 655
Glu Ala Pro Gly Gln Arg Val Thr Ile Ser Cys Ser Gly Ser Thr Ser
            660                 665                 670
Asn Ile Gly Asn Asn Ala Val Ile Trp Tyr Gln Gln Leu Pro Gly Lys
        675                 680                 685
Ala Pro Lys Leu Leu Ile Tyr Tyr Asp Asp Leu Leu Pro Ser Gly Val
    690                 695                 700
Ser Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ser Gly Ser Leu Ala
705                 710                 715                 720
Ile Ser Gly Leu Gln Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ser
                725                 730                 735
Trp Asp Asp Asn Leu Asn Gly Pro Leu Phe Gly Gly Gly Thr Lys Leu
            740                 745                 750
Thr Val Leu
        755

<210> 652
<211> 753
<212> PRT
<213> Artificial Sequence

<220>
```

<223> Made in a lab

<400> 652

```
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1               5                  10                  15
Val Ile Met Ser Arg Gly Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr
            20                  25                  30
Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln
        35                  40                  45
Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys
    50                  55                  60
Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp
65                  70                  75                  80
Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys
                85                  90                  95
Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
            100                 105                 110
Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu
        115                 120                 125
Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg
    130                 135                 140
Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val
145                 150                 155                 160
Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr
                165                 170                 175
Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly
            180                 185                 190
Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser
        195                 200                 205
Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser
    210                 215                 220
Gln His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser
225                 230                 235                 240
Phe Leu Leu Pro Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly
                245                 250                 255
Asp Thr Gly Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro
            260                 265                 270
Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro
        275                 280                 285
Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
    290                 295                 300
Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
305                 310                 315                 320
Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
                325                 330                 335
Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
            340                 345                 350
Leu His Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser
        355                 360                 365
Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
    370                 375                 380
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
385                 390                 395                 400
Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
                405                 410                 415
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
            420                 425                 430
```

```
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
        435                 440                 445
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
    450                 455                 460
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
465                 470                 475                 480
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser
                485                 490                 495
Ser Leu Asn Thr Arg Thr Gln Lys Ala Arg His Ser Pro Asn Ser Glu
            500                 505                 510
Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
        515                 520                 525
Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Tyr Tyr Asn
    530                 535                 540
Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
545                 550                 555                 560
Ser Ile Ser Pro Ser Gly Gly Arg Thr Gly Tyr Ala Asp Ser Val Lys
                565                 570                 575
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
            580                 585                 590
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
        595                 600                 605
Arg Val Ser Gly Phe Tyr Ala Ala Phe Asp Tyr Trp Gly Gln Gly Thr
    610                 615                 620
Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
625                 630                 635                 640
Gly Gly Gly Gly Ser Gln Asp Ile Gln Met Thr Gln Ser Pro Ser Thr
                645                 650                 655
Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
            660                 665                 670
Gln Ser Ile Ser Ser Trp Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys
        675                 680                 685
Ala Pro Lys Leu Leu Ile Tyr Gln Ala Ser Thr Leu Glu Ser Gly Val
    690                 695                 700
Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
705                 710                 715                 720
Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
                725                 730                 735
Ala Asn Ser Phe Pro Ile Thr Phe Gly Gly Gly Thr Lys Val Glu Ile
            740                 745                 750
Asn


<210> 653
<211> 754
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 653
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1               5                  10                  15
Val Ile Met Ser Arg Gly Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr
            20                  25                  30
Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln
```

```
        35                  40                  45
Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys
    50                  55                  60
Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp
65                  70                  75                  80
Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys
                85                  90                  95
Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
            100                 105                 110
Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu
        115                 120                 125
Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg
    130                 135                 140
Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val
145                 150                 155                 160
Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr
                165                 170                 175
Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly
            180                 185                 190
Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser
        195                 200                 205
Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser
    210                 215                 220
Gln His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser
225                 230                 235                 240
Phe Leu Leu Pro Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly
                245                 250                 255
Asp Thr Gly Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro
            260                 265                 270
Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro
        275                 280                 285
Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
    290                 295                 300
Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
305                 310                 315                 320
Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
                325                 330                 335
Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
            340                 345                 350
Leu His Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser
        355                 360                 365
Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
    370                 375                 380
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
385                 390                 395                 400
Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
                405                 410                 415
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
            420                 425                 430
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
        435                 440                 445
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
    450                 455                 460
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
465                 470                 475                 480
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser
                485                 490                 495
```

```
Ser Leu Asn Thr Arg Thr Gln Lys Ala Arg His Ser Pro Asn Ser Glu
            500                 505                 510
Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
        515                 520                 525
Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Trp Tyr Trp
    530                 535                 540
Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
545                 550                 555                 560
Ser Ile Pro Pro Ser Gly Gly His Thr Ser Tyr Ala Asp Ser Val Lys
                565                 570                 575
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
            580                 585                 590
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
        595                 600                 605
Lys Ser Ser Gly Trp Tyr Glu Asp Tyr Phe Asp Tyr Trp Gly Gln Gly
    610                 615                 620
Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
625                 630                 635                 640
Ser Gly Gly Gly Gly Ser Gln Asp Ile Gln Met Thr Gln Ser Pro Ser
                645                 650                 655
Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Gln Ala
            660                 665                 670
Ser Gln Asp Ile Thr Asn Tyr Leu Asn Trp Tyr Leu His Lys Pro Gly
        675                 680                 685
Lys Ala Pro Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Gln Thr Gly
    690                 695                 700
Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe
705                 710                 715                 720
Thr Ile Thr Ser Leu Gln Pro Glu Asp Phe Gly Thr Tyr Tyr Cys Gln
                725                 730                 735
Gln Tyr Asp Thr Leu His Pro Ser Phe Gly Pro Gly Thr Thr Val Asp
            740                 745                 750
Ile Lys


<210> 654
<211> 759
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 654
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1               5                  10                  15
Val Ile Met Ser Arg Gly Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr
            20                  25                  30
Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln
        35                  40                  45
Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys
    50                  55                  60
Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp
65                  70                  75                  80
Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys
                85                  90                  95
Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
```

```
            100                 105                 110
Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu
        115                 120                 125
Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg
    130                 135                 140
Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val
145                 150                 155                 160
Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr
                165                 170                 175
Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly
            180                 185                 190
Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser
        195                 200                 205
Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser
    210                 215                 220
Gln His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser
225                 230                 235                 240
Phe Leu Leu Pro Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly
                245                 250                 255
Asp Thr Gly Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro
            260                 265                 270
Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro
        275                 280                 285
Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
    290                 295                 300
Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
305                 310                 315                 320
Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
                325                 330                 335
Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
            340                 345                 350
Leu His Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser
        355                 360                 365
Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
    370                 375                 380
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
385                 390                 395                 400
Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
                405                 410                 415
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
            420                 425                 430
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
        435                 440                 445
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
    450                 455                 460
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
465                 470                 475                 480
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser
                485                 490                 495
Ser Leu Asn Thr Arg Thr Gln Lys Ala Arg His Ser Pro Asn Ser Glu
            500                 505                 510
Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
        515                 520                 525
Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Pro Tyr Glu
    530                 535                 540
Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
545                 550                 555                 560
```

```
Val Ile Gly Pro Ser Gly Gly Tyr Thr Glu Tyr Ala Asp Ser Val Lys
                565                 570                 575
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
            580                 585                 590
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
        595                 600                 605
Arg Gly Tyr Asp Phe Trp Ser Gly Tyr Tyr Asp Ala Phe Asp Ile Trp
    610                 615                 620
Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
625                 630                 635                 640
Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Ser Ala Leu Thr Gln Pro
                645                 650                 655
Pro Ser Ala Ser Gly Ser Pro Gly Gln Ser Val Thr Ile Ser Cys Thr
            660                 665                 670
Gly Thr Ser Ser Asp Val Gly Val Tyr Asp Ser Val Ser Trp Tyr Gln
        675                 680                 685
Gln His Pro Gly Lys Ala Pro Lys Leu Met Ile Tyr Asp Val Ser Asp
    690                 695                 700
Arg Pro Ser Gly Val Ser Asn Arg Phe Ser Gly Ser Lys Ser Gly Tyr
705                 710                 715                 720
Thr Ala Ser Leu Thr Ile Ser Ala Leu Gln Ala Glu Asp Glu Ala Asp
                725                 730                 735
Tyr Tyr Cys Gly Ser Tyr Arg Ala Ser Ser Ser Tyr Val Phe Gly Thr
            740                 745                 750
Gly Thr Lys Val Thr Val Leu
        755
```

<210> 655
<211> 753
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 655

```
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1               5                  10                  15
Val Ile Met Ser Arg Gly Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr
            20                  25                  30
Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln
        35                  40                  45
Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys
    50                  55                  60
Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp
65                  70                  75                  80
Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys
                85                  90                  95
Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
            100                 105                 110
Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu
        115                 120                 125
Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg
    130                 135                 140
Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val
145                 150                 155                 160
Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr
```

```
                165                 170                 175
Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly
            180                 185                 190
Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser
        195                 200                 205
Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser
    210                 215                 220
Gln His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser
225                 230                 235                 240
Phe Leu Leu Pro Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly
                245                 250                 255
Asp Thr Gly Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro
            260                 265                 270
Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro
        275                 280                 285
Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
    290                 295                 300
Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
305                 310                 315                 320
Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
                325                 330                 335
Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
            340                 345                 350
Leu His Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser
        355                 360                 365
Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
    370                 375                 380
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
385                 390                 395                 400
Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
                405                 410                 415
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
            420                 425                 430
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
        435                 440                 445
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
    450                 455                 460
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
465                 470                 475                 480
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser
                485                 490                 495
Ser Leu Asn Thr Arg Thr Gln Lys Ala Arg His Ser Pro Asn Ser Glu
            500                 505                 510
Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
        515                 520                 525
Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Phe
    530                 535                 540
Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
545                 550                 555                 560
Ser Ile Trp Pro Ser Gly Gly Asn Thr Thr Tyr Ala Asp Ser Val Lys
                565                 570                 575
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
            580                 585                 590
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
        595                 600                 605
Arg His Val Gly Trp Gly Arg Tyr Phe Asp Tyr Trp Gly Gln Gly Thr
    610                 615                 620
```

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
625 630 635 640
Gly Gly Gly Gly Ser Gln Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
645 650 655
Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
660 665 670
Gln Asn Ile Tyr His Tyr Leu His Trp Tyr Gln Gln Lys Pro Gly Lys
675 680 685
Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Thr Leu Glu Ser Gly Val
690 695 700
Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Leu Thr Leu Thr
705 710 715 720
Ile Asn Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
725 730 735
Thr Tyr Asp Thr Pro Leu Thr Phe Gly Gly Gly Ser Lys Val Glu Val
740 745 750
Lys

<210> 656
<211> 757
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 656
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1 5 10 15
Val Ile Met Ser Arg Gly Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr
20 25 30
Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln
35 40 45
Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys
50 55 60
Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp
65 70 75 80
Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys
85 90 95
Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
100 105 110
Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu
115 120 125
Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg
130 135 140
Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val
145 150 155 160
Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr
165 170 175
Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly
180 185 190
Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser
195 200 205
Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser
210 215 220
Gln His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser

```
225                 230                 235                 240
Phe Leu Leu Pro Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly
                245                 250                 255
Asp Thr Gly Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro
            260                 265                 270
Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro
        275                 280                 285
Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
    290                 295                 300
Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
305                 310                 315                 320
Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
                325                 330                 335
Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
            340                 345                 350
Leu His Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser
        355                 360                 365
Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
    370                 375                 380
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
385                 390                 395                 400
Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
                405                 410                 415
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
            420                 425                 430
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
        435                 440                 445
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
    450                 455                 460
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
465                 470                 475                 480
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser
                485                 490                 495
Ser Leu Asn Thr Arg Thr Gln Lys Ala Arg His Ser Pro Asn Ser Glu
            500                 505                 510
Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
        515                 520                 525
Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ala Tyr Arg
    530                 535                 540
Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
545                 550                 555                 560
Tyr Ile Ser Ser Ser Gly Gly Arg Thr Asp Tyr Ala Asp Ser Val Lys
                565                 570                 575
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
            580                 585                 590
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Thr
        595                 600                 605
Thr Gly Gly Leu Arg Tyr Phe Asp Trp Leu Ala Pro Ser Met Asp Tyr
    610                 615                 620
Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser
625                 630                 635                 640
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Ser Ala Leu Thr Gln
                645                 650                 655
Pro Pro Ser Val Ser Val Ser Pro Gly Gln Thr Ala Ser Ile Thr Cys
            660                 665                 670
Ser Gly Asp Lys Leu Gly Glu Lys Phe Ala Ser Trp Tyr Gln Gln Arg
        675                 680                 685
```

```
Pro Gly Gln Ser Pro Ile Leu Val Ile Tyr Gln Asp Ser Lys Arg Pro
    690                 695                 700
Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser Asn Ser Gly Asn Thr Ala
705                 710                 715                 720
Thr Leu Thr Ile Ser Gly Thr Gln Thr Met Asp Glu Ala Asp Tyr Tyr
                725                 730                 735
Cys Gln Ala Trp Gly Gly Ser Thr Ala Tyr Val Phe Gly Ser Gly Thr
            740                 745                 750
Lys Val Thr Val Leu
        755
```

<210> 657
<211> 752
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 657

```
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1               5                  10                  15
Val Ile Met Ser Arg Gly Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr
            20                  25                  30
Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln
        35                  40                  45
Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys
    50                  55                  60
Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp
65                  70                  75                  80
Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys
                85                  90                  95
Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
            100                 105                 110
Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu
        115                 120                 125
Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg
    130                 135                 140
Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val
145                 150                 155                 160
Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr
                165                 170                 175
Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly
            180                 185                 190
Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser
        195                 200                 205
Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser
    210                 215                 220
Gln His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser
225                 230                 235                 240
Phe Leu Leu Pro Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly
                245                 250                 255
Asp Thr Gly Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro
            260                 265                 270
Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro
        275                 280                 285
Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
```

```
    290                 295                 300
Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
305                 310                 315                 320
Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
                325                 330                 335
Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
            340                 345                 350
Leu His Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser
        355                 360                 365
Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
    370                 375                 380
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
385                 390                 395                 400
Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
                405                 410                 415
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
            420                 425                 430
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
        435                 440                 445
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
    450                 455                 460
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
465                 470                 475                 480
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser
                485                 490                 495
Ser Leu Asn Thr Arg Thr Gln Lys Ala Arg His Ser Pro Asn Ser Glu
            500                 505                 510
Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
        515                 520                 525
Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ala Tyr Ser
    530                 535                 540
Met Val Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
545                 550                 555                 560
Tyr Ile Tyr Pro Ser Gly Gly Ile Thr Thr Tyr Ala Asp Ser Val Lys
                565                 570                 575
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
            580                 585                 590
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
        595                 600                 605
Arg Glu Gly Gln Val Phe Asp Ile Trp Gly Gln Gly Thr Thr Val Thr
    610                 615                 620
Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
625                 630                 635                 640
Gly Ser Gln Asp Ile Gln Met Thr Gln Ser Pro Ala Thr Leu Ser Leu
                645                 650                 655
Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val
            660                 665                 670
Thr Thr Tyr Leu Ala Trp Tyr Gln Gln Arg Pro Gly Gln Ala Pro Arg
        675                 680                 685
Leu Leu Ile Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg
    690                 695                 700
Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser
705                 710                 715                 720
Val Glu Pro Glu Asp Tyr Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asn
                725                 730                 735
Trp Pro Pro Ser Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu Ser Lys
            740                 745                 750
```

<210> 658
<211> 754
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 658
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1   5   10   15
Val Ile Met Ser Arg Gly Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr
            20   25   30
Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln
        35   40   45
Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys
    50   55   60
Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp
65   70   75   80
Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys
                85   90   95
Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
            100   105   110
Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu
        115   120   125
Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg
    130   135   140
Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val
145   150   155   160
Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr
                165   170   175
Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly
            180   185   190
Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser
        195   200   205
Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser
    210   215   220
Gln His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser
225   230   235   240
Phe Leu Leu Pro Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly
                245   250   255
Asp Thr Gly Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro
            260   265   270
Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro
        275   280   285
Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
    290   295   300
Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
305   310   315   320
Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
                325   330   335
Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
            340   345   350
Leu His Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser
        355   360   365
Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys

```
    370                 375                 380
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
385                 390                 395                 400
Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
                405                 410                 415
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
            420                 425                 430
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
        435                 440                 445
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
    450                 455                 460
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
465                 470                 475                 480
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser
                485                 490                 495
Ser Leu Asn Thr Arg Thr Gln Lys Ala Arg His Ser Pro Asn Ser Glu
            500                 505                 510
Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
        515                 520                 525
Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Tyr Ala
    530                 535                 540
Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
545                 550                 555                 560
Arg Ile Val Pro Ser Gly Gly Met Thr Ser Tyr Ala Asp Ser Val Lys
                565                 570                 575
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
            580                 585                 590
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Thr
        595                 600                 605
Thr Asp Asp Phe Trp Ser Gly Met Asp Val Trp Gly Gln Gly Thr Thr
    610                 615                 620
Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
625                 630                 635                 640
Gly Gly Gly Ser Gln Ser Ala Leu Thr Gln Pro Ala Ser Val Ser Gly
                645                 650                 655
Ser Pro Gly Gln Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp
            660                 665                 670
Val Gly Ser Tyr Asn Leu Val Ser Trp Tyr Gln Gln His Pro Gly Lys
        675                 680                 685
Ala Pro Lys Val Met Ile Tyr Glu Gly Ser Lys Arg Pro Ser Gly Val
    690                 695                 700
Ser Asn Arg Phe Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr
705                 710                 715                 720
Ile Ser Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Cys Ser
                725                 730                 735
Tyr Ala Gly Arg Ser Thr Tyr Val Phe Gly Thr Gly Thr Lys Val Thr
            740                 745                 750
Val Leu
```

<210> 659
<211> 754
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 659
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1   5   10   15
Val Ile Met Ser Arg Gly Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr
            20   25   30
Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln
        35   40   45
Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys
    50   55   60
Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp
65   70   75   80
Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys
                85   90   95
Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
            100   105   110
Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu
        115   120   125
Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg
    130   135   140
Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val
145   150   155   160
Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr
                165   170   175
Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly
            180   185   190
Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser
        195   200   205
Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser
    210   215   220
Gln His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser
225   230   235   240
Phe Leu Leu Pro Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly
                245   250   255
Asp Thr Gly Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro
            260   265   270
Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro
        275   280   285
Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
    290   295   300
Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
305   310   315   320
Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
                325   330   335
Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
            340   345   350
Leu His Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser
        355   360   365
Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
    370   375   380
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
385   390   395   400
Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
                405   410   415
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
            420   425   430
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe

```
        435                 440                 445
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
    450                 455                 460
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
465                 470                 475                 480
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser
                485                 490                 495
Ser Leu Asn Thr Arg Thr Gln Lys Ala Arg His Ser Pro Asn Ser Glu
            500                 505                 510
Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
        515                 520                 525
Ser Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Leu Tyr Asn
    530                 535                 540
Met Gln Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
545                 550                 555                 560
Gly Ile Ser Leu Ser Gly Gly Lys Thr Phe Tyr Ala Asp Ser Val Lys
                565                 570                 575
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
            580                 585                 590
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
        595                 600                 605
Arg Asp Tyr Gly Val Ala Thr Leu Asp Ala Phe Asp Ile Trp Gly Gln
    610                 615                 620
Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
625                 630                 635                 640
Gly Ser Gly Gly Gly Gly Ser Gln Ser Glu Leu Thr Gln Thr Pro Ser
                645                 650                 655
Val Ser Val Ser Pro Gly Gln Thr Ala Ser Ile Thr Cys Ser Gly Asn
            660                 665                 670
Arg Leu Glu Asp Lys Tyr Val His Trp Tyr Gln Gln Lys Pro Gly Gln
        675                 680                 685
Ser Pro Val Leu Val Leu Tyr Gln Asp Asn Lys Arg Pro Ser Gly Ile
    690                 695                 700
Pro Glu Arg Phe Ser Gly Ser Asn Ser Gly Asn Thr Ala Thr Leu Thr
705                 710                 715                 720
Ile Ser Glu Thr Gln Thr Leu Asp Glu Ala Asp Tyr Tyr Cys Gln Ala
                725                 730                 735
Trp Asp Ser Ser Thr Arg Glu Val Phe Gly Gly Gly Thr Lys Leu Thr
            740                 745                 750
Val Leu


<210> 660
<211> 761
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 660
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1               5                  10                  15
Val Ile Met Ser Arg Gly Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr
            20                  25                  30
Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln
        35                  40                  45
```

```
Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys
    50                  55                  60
Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp
65                  70                  75                  80
Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys
                85                  90                  95
Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
            100                 105                 110
Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu
        115                 120                 125
Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg
    130                 135                 140
Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val
145                 150                 155                 160
Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr
                165                 170                 175
Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly
            180                 185                 190
Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser
        195                 200                 205
Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser
    210                 215                 220
Gln His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser
225                 230                 235                 240
Phe Leu Leu Pro Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly
                245                 250                 255
Asp Thr Gly Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro
            260                 265                 270
Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro
        275                 280                 285
Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
    290                 295                 300
Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
305                 310                 315                 320
Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
                325                 330                 335
Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
            340                 345                 350
Leu His Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser
        355                 360                 365
Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
    370                 375                 380
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
385                 390                 395                 400
Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
                405                 410                 415
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
            420                 425                 430
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
        435                 440                 445
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
    450                 455                 460
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
465                 470                 475                 480
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser
                485                 490                 495
Ser Leu Asn Thr Arg Thr Gln Lys Ala Arg His Ser Pro Asn Ser Glu
```

```
            500                 505                 510
Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
        515                 520                 525
Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ala Tyr Thr
    530                 535                 540
Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
545                 550                 555                 560
Ser Ile Tyr Pro Ser Gly Gly Thr Thr Pro Tyr Ala Asp Ser Val Lys
                565                 570                 575
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
            580                 585                 590
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Thr Tyr Tyr Cys Ala
        595                 600                 605
Arg Val Val Asn Ile Asp Phe Trp Ser Gly Tyr Asn Met Arg Ser Ala
    610                 615                 620
Phe Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly
625                 630                 635                 640
Gly Gly Ser Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Asp Ile
                645                 650                 655
Gln Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly Asp Thr
            660                 665                 670
Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Val Ser Asp Trp Leu Ala
        675                 680                 685
Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Asn Leu Leu Ile Tyr Gly
    690                 695                 700
Ala Ser Ser Leu Gln Thr Gly Val Pro Ser Arg Phe Ser Gly Gly Gly
705                 710                 715                 720
Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
                725                 730                 735
Phe Ala Thr Tyr Tyr Cys Gln Gln Ala His Ser Phe Pro Phe Thr Phe
            740                 745                 750
Gly Gly Gly Thr Arg Val Glu Ile Lys
        755                 760

<210> 661
<211> 757
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 661
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1               5                  10                  15
Val Ile Met Ser Arg Gly Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr
            20                  25                  30
Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln
        35                  40                  45
Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys
    50                  55                  60
Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp
65                  70                  75                  80
Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys
                85                  90                  95
Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
            100                 105                 110
```

```
Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu
        115                 120                 125
Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg
    130                 135                 140
Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val
145                 150                 155                 160
Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr
                165                 170                 175
Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly
            180                 185                 190
Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser
        195                 200                 205
Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser
    210                 215                 220
Gln His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser
225                 230                 235                 240
Phe Leu Leu Pro Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly
                245                 250                 255
Asp Thr Gly Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro
            260                 265                 270
Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro
        275                 280                 285
Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
    290                 295                 300
Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
305                 310                 315                 320
Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
                325                 330                 335
Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
            340                 345                 350
Leu His Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser
        355                 360                 365
Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
    370                 375                 380
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
385                 390                 395                 400
Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
                405                 410                 415
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
            420                 425                 430
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
        435                 440                 445
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
    450                 455                 460
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
465                 470                 475                 480
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser
                485                 490                 495
Ser Leu Asn Thr Arg Thr Gln Lys Ala Arg His Ser Pro Asn Ser Glu
            500                 505                 510
Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
        515                 520                 525
Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr Leu
    530                 535                 540
Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
545                 550                 555                 560
Val Ile Ser Ser Ser Gly Gly Pro Thr Ala Tyr Ala Asp Ser Val Lys
```

```
                565                 570                 575
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
            580                 585                 590
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
        595                 600                 605
Arg Val Gly Leu Asp Tyr Gly Ile Leu Gly Ala Phe Asp Ile Trp Gly
    610                 615                 620
Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
625                 630                 635                 640
Gly Gly Ser Gly Gly Gly Gly Ser Gln Asp Ile Gln Met Thr Gln Ser
                645                 650                 655
Pro Ala Thr Leu Ser Val Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys
            660                 665                 670
Arg Ala Ser Gln Asn Ile Asn Thr His Leu Ala Trp Tyr Gln Gln Lys
        675                 680                 685
Pro Gly Gln Ala Pro Arg Leu Leu Ile Phe Gly Ala Ser Thr Arg Ala
    690                 695                 700
Thr Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe
705                 710                 715                 720
Thr Leu Thr Ile Ser Ser Leu Gln Ser Glu Asp Phe Thr Val Tyr Tyr
                725                 730                 735
Cys Gln Gln Tyr Gly Ser Ser Leu Thr Trp Thr Phe Gly Gln Gly Thr
            740                 745                 750
Lys Val Glu Ile Lys
        755

<210> 662
<211> 755
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 662
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1               5                  10                  15
Val Ile Met Ser Arg Gly Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr
            20                  25                  30
Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln
        35                  40                  45
Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys
    50                  55                  60
Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp
65                  70                  75                  80
Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys
                85                  90                  95
Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
            100                 105                 110
Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu
        115                 120                 125
Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg
    130                 135                 140
Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val
145                 150                 155                 160
Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr
                165                 170                 175
```

```
Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly
            180                 185                 190
Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser
        195                 200                 205
Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser
    210                 215                 220
Gln His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser
225                 230                 235                 240
Phe Leu Leu Pro Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly
                245                 250                 255
Asp Thr Gly Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro
            260                 265                 270
Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro
        275                 280                 285
Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
    290                 295                 300
Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
305                 310                 315                 320
Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
                325                 330                 335
Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
            340                 345                 350
Leu His Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser
        355                 360                 365
Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
    370                 375                 380
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
385                 390                 395                 400
Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
                405                 410                 415
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
            420                 425                 430
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
        435                 440                 445
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
    450                 455                 460
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
465                 470                 475                 480
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser
                485                 490                 495
Ser Leu Asn Thr Arg Thr Gln Lys Ala Arg His Ser Pro Asn Ser Glu
            500                 505                 510
Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
        515                 520                 525
Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Glu Tyr Gly
    530                 535                 540
Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
545                 550                 555                 560
Ser Ile Arg Ser Ser Gly Gly Trp Thr Lys Tyr Ala Asp Ser Val Lys
                565                 570                 575
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
            580                 585                 590
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
        595                 600                 605
Lys Gly Leu Gly Ala Thr Ser Gly Glu Phe Asp Tyr Trp Gly Gln Gly
    610                 615                 620
Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
```

625 630 635 640
Ser Gly Gly Gly Gly Ser Gln Asp Ile Gln Met Thr Gln Ser Pro Gly
645 650 655
Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala
660 665 670
Ser Gln Ser Val Ser Gly Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Leu
675 680 685
Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr
690 695 700
Gly Thr Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr
705 710 715 720
Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
725 730 735
Leu Gln His Asn Ser Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
740 745 750
Glu Ile Lys
755

<210> 663
<211> 755
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 663
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1 5 10 15
Val Ile Met Ser Arg Gly Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr
20 25 30
Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln
35 40 45
Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys
50 55 60
Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp
65 70 75 80
Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys
85 90 95
Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
100 105 110
Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu
115 120 125
Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg
130 135 140
Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val
145 150 155 160
Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr
165 170 175
Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly
180 185 190
Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser
195 200 205
Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser
210 215 220
Gln His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser
225 230 235 240

```
Phe Leu Leu Pro Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly
                245                 250                 255
Asp Thr Gly Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro
            260                 265                 270
Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro
        275                 280                 285
Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
    290                 295                 300
Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
305                 310                 315                 320
Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
                325                 330                 335
Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
            340                 345                 350
Leu His Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser
        355                 360                 365
Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
    370                 375                 380
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
385                 390                 395                 400
Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
                405                 410                 415
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
            420                 425                 430
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
        435                 440                 445
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
    450                 455                 460
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
465                 470                 475                 480
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser
                485                 490                 495
Ser Leu Asn Thr Arg Thr Gln Lys Ala Arg His Ser Pro Asn Ser Glu
            500                 505                 510
Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
        515                 520                 525
Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Lys Tyr Asp
    530                 535                 540
Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
545                 550                 555                 560
Ser Ile Trp Pro Ser Gly Gly Trp Thr Ser Tyr Ala Asp Ser Val Lys
                565                 570                 575
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
            580                 585                 590
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
        595                 600                 605
Lys Ser Arg Gly Ser Pro Trp Tyr Gly Asp Phe Asp His Trp Gly Gln
    610                 615                 620
Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
625                 630                 635                 640
Gly Ser Gly Gly Gly Gly Ser Gln Ser Glu Leu Thr Gln Pro Pro Ser
                645                 650                 655
Val Ser Val Ala Pro Gly Glu Thr Ala Thr Val Thr Cys Gly Gly Ile
            660                 665                 670
Asn Ile Gly Ser Lys Ser Val His Trp Tyr Gln Gln Lys Pro Asp Gln
        675                 680                 685
Ala Pro Val Val Val Met Tyr Phe Asp Ser Asp Arg Pro Ser Gly Ile
```

```
    690                 695                 700
Pro Glu Arg Phe Ser Gly Ser Asn Ser Gly Asp Thr Ala Thr Leu Thr
705                 710                 715                 720
Ile Ser Arg Val Glu Ala Gly Asp Glu Ala Asp Tyr Tyr Cys Gln Val
                725                 730                 735
Trp Asp Ser Arg Ser Asp Gln Tyr Val Phe Gly Phe Gly Thr Lys Val
            740                 745                 750
Thr Val Leu
        755

<210> 664
<211> 752
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 664
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1               5                  10                  15
Val Ile Met Ser Arg Gly Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr
            20                  25                  30
Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln
        35                  40                  45
Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys
    50                  55                  60
Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp
65                  70                  75                  80
Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys
                85                  90                  95
Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
            100                 105                 110
Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu
        115                 120                 125
Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg
    130                 135                 140
Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val
145                 150                 155                 160
Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr
                165                 170                 175
Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly
            180                 185                 190
Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser
        195                 200                 205
Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser
    210                 215                 220
Gln His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser
225                 230                 235                 240
Phe Leu Leu Pro Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly
                245                 250                 255
Asp Thr Gly Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro
            260                 265                 270
Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro
        275                 280                 285
Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
    290                 295                 300
```

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Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
305                 310                 315                 320
Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
                325                 330                 335
Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
            340                 345                 350
Leu His Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser
        355                 360                 365
Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
    370                 375                 380
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
385                 390                 395                 400
Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
                405                 410                 415
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
            420                 425                 430
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
        435                 440                 445
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
    450                 455                 460
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
465                 470                 475                 480
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser
                485                 490                 495
Ser Leu Asn Thr Arg Thr Gln Lys Ala Arg His Ser Pro Asn Ser Glu
            500                 505                 510
Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
        515                 520                 525
Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Met Tyr Thr
    530                 535                 540
Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
545                 550                 555                 560
Trp Ile Ser Pro Ser Gly Gly Trp Thr Lys Tyr Ala Asp Ser Val Lys
                565                 570                 575
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
            580                 585                 590
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
        595                 600                 605
Val Ser Pro Trp Gly Gly Pro Phe Asp Tyr Trp Gly Gln Gly Thr Leu
    610                 615                 620
Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
625                 630                 635                 640
Gly Gly Gly Ser Gln Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu
                645                 650                 655
Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln
            660                 665                 670
Ser Ile Ser Ser Trp Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala
        675                 680                 685
Pro Lys Leu Leu Ile Tyr Lys Ala Ser Thr Leu Glu Ser Gly Val Pro
    690                 695                 700
Ser Arg Phe Ser Ala Gly Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile
705                 710                 715                 720
Ser Ser Leu Gln Pro Asp Asp Phe Gly Thr Tyr Tyr Cys Gln Gln Tyr
                725                 730                 735
Asn Ser Tyr Ser Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Ile
            740                 745                 750
```

<210> 665
<211> 757
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 665
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1   5   10   15
Val Ile Met Ser Arg Gly Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr
            20   25   30
Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln
        35   40   45
Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys
    50   55   60
Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp
65   70   75   80
Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys
                85   90   95
Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
            100   105   110
Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu
        115   120   125
Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg
    130   135   140
Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val
145   150   155   160
Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr
                165   170   175
Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly
            180   185   190
Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser
        195   200   205
Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser
    210   215   220
Gln His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser
225   230   235   240
Phe Leu Leu Pro Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly
                245   250   255
Asp Thr Gly Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro
            260   265   270
Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro
        275   280   285
Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
    290   295   300
Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
305   310   315   320
Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
                325   330   335
Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
            340   345   350
Leu His Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser
        355   360   365
Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
    370   375   380

```
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
385                 390                 395                 400
Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
                405                 410                 415
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
            420                 425                 430
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
        435                 440                 445
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
    450                 455                 460
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
465                 470                 475                 480
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser
                485                 490                 495
Ser Leu Asn Thr Arg Thr Gln Lys Ala Arg His Ser Pro Asn Ser Glu
            500                 505                 510
Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
        515                 520                 525
Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Gln Tyr Phe
    530                 535                 540
Met Met Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
545                 550                 555                 560
Ser Ile Ser Pro Ser Gly Gly Tyr Thr Gln Tyr Ala Asp Ser Val Lys
                565                 570                 575
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
            580                 585                 590
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
        595                 600                 605
Lys Thr Gly Asp Tyr Thr Arg Tyr Tyr Ser Tyr Gly Met Asp Val Trp
    610                 615                 620
Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
625                 630                 635                 640
Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Asp Ile Gln Met Thr Gln
                645                 650                 655
Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr
            660                 665                 670
Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln
        675                 680                 685
Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu
    690                 695                 700
Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
705                 710                 715                 720
Phe Thr Leu Ile Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr
                725                 730                 735
Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Leu Thr Phe Gly Gly Gly Thr
            740                 745                 750
Lys Val Glu Ile Lys
        755

<210> 666
<211> 758
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab
```

<400> 666
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1   5   10   15
Val Ile Met Ser Arg Gly Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr
            20   25   30
Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln
        35   40   45
Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys
    50   55   60
Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp
65   70   75   80
Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys
                85   90   95
Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
            100   105   110
Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu
        115   120   125
Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg
    130   135   140
Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val
145   150   155   160
Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr
                165   170   175
Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly
            180   185   190
Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser
        195   200   205
Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser
    210   215   220
Gln His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser
225   230   235   240
Phe Leu Leu Pro Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly
                245   250   255
Asp Thr Gly Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro
            260   265   270
Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro
        275   280   285
Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
    290   295   300
Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
305   310   315   320
Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
                325   330   335
Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
            340   345   350
Leu His Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser
        355   360   365
Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
    370   375   380
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
385   390   395   400
Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
                405   410   415
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
            420   425   430
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
        435   440   445

```
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
    450                 455                 460
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
465                 470                 475                 480
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser
                485                 490                 495
Ser Leu Asn Thr Arg Thr Gln Lys Ala Arg His Ser Pro Asn Ser Glu
            500                 505                 510
Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
        515                 520                 525
Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Gly Tyr Ser
    530                 535                 540
Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
545                 550                 555                 560
Gly Ile Tyr Ser Ser Gly Gly Trp Thr Trp Tyr Ala Asp Ser Val Lys
                565                 570                 575
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
            580                 585                 590
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Thr
        595                 600                 605
Arg Asp Gln Ser Phe Ser Tyr Asp Ser Ser Leu Asp Ala Phe Asp Ile
    610                 615                 620
Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly Ser
625                 630                 635                 640
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Asp Ile Gln Met Thr
                645                 650                 655
Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile
            660                 665                 670
Thr Cys Arg Ala Ser Gln Ser Ile Asn Asn Tyr Leu Asn Trp Tyr Gln
        675                 680                 685
Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Thr Ala Ser Thr
    690                 695                 700
Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
705                 710                 715                 720
Asp Phe Thr Leu Thr Ile Ser Asn Leu Gln Pro Glu Asp Phe Ala Thr
                725                 730                 735
Tyr Tyr Cys Gln Gln Ser Tyr Ala Thr Leu Arg Thr Phe Gly Gln Gly
            740                 745                 750
Thr Lys Val Glu Ile Lys
        755

<210> 667
<211> 760
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 667
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1               5                  10                  15
Val Ile Met Ser Arg Gly Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr
            20                  25                  30
Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln
        35                  40                  45
Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys
```

```
    50                  55                  60
Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp
65                  70                  75                  80
Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys
                85                  90                  95
Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
            100                 105                 110
Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu
        115                 120                 125
Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg
    130                 135                 140
Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val
145                 150                 155                 160
Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr
                165                 170                 175
Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly
            180                 185                 190
Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser
        195                 200                 205
Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser
    210                 215                 220
Gln His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser
225                 230                 235                 240
Phe Leu Leu Pro Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly
                245                 250                 255
Asp Thr Gly Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro
            260                 265                 270
Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro
        275                 280                 285
Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
    290                 295                 300
Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
305                 310                 315                 320
Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
                325                 330                 335
Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
            340                 345                 350
Leu His Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser
        355                 360                 365
Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
    370                 375                 380
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
385                 390                 395                 400
Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
                405                 410                 415
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
            420                 425                 430
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
        435                 440                 445
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
    450                 455                 460
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
465                 470                 475                 480
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser
                485                 490                 495
Ser Leu Asn Thr Arg Thr Gln Lys Ala Arg His Ser Pro Asn Ser Glu
            500                 505                 510
```

```
Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
        515                 520                 525
Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Leu Tyr Gly
    530                 535                 540
Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
545                 550                 555                 560
Ser Ile Val Pro Ser Gly Gly Leu Thr Arg Tyr Ala Asp Ser Val Lys
                565                 570                 575
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
            580                 585                 590
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Thr Tyr Tyr Cys Ala
        595                 600                 605
Arg Leu Ala Tyr Tyr Asp Phe Trp Ser Gly Arg Asp Ala Phe Asp Ile
    610                 615                 620
Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly Ser
625                 630                 635                 640
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Ser Val Leu Thr Gln
                645                 650                 655
Pro Ala Ser Val Ser Gly Ser Pro Gly Gln Ser Ile Thr Ile Ser Cys
            660                 665                 670
Ser Gly Ser Ser Ser Asp Val Gly His Tyr Asp Tyr Val Ser Trp Tyr
        675                 680                 685
Gln Gln His Pro Gly Lys Ala Pro Lys Leu Met Ile Tyr Asp Val Ser
    690                 695                 700
Asn Arg Pro Ser Gly Val Ser Asn Arg Phe Ser Gly Ser Lys Ser Gly
705                 710                 715                 720
Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu Gln Ala Asp Asp Glu Ala
                725                 730                 735
Glu Tyr Tyr Cys Ser Ser Tyr Thr Ser Ser Gly Thr Arg Val Phe Gly
            740                 745                 750
Thr Gly Thr Lys Val Thr Val Leu
        755                 760

<210> 668
<211> 752
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 668
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1               5                  10                  15
Val Ile Met Ser Arg Gly Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr
            20                  25                  30
Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln
        35                  40                  45
Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys
    50                  55                  60
Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp
65                  70                  75                  80
Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys
                85                  90                  95
Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
            100                 105                 110
Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu
```

```
        115                 120                 125
Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg
    130                 135                 140
Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val
145                 150                 155                 160
Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr
                165                 170                 175
Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly
            180                 185                 190
Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser
        195                 200                 205
Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser
    210                 215                 220
Gln His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser
225                 230                 235                 240
Phe Leu Leu Pro Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly
                245                 250                 255
Asp Thr Gly Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro
            260                 265                 270
Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro
        275                 280                 285
Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
    290                 295                 300
Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
305                 310                 315                 320
Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
                325                 330                 335
Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
            340                 345                 350
Leu His Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser
        355                 360                 365
Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
    370                 375                 380
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
385                 390                 395                 400
Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
                405                 410                 415
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
            420                 425                 430
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
        435                 440                 445
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
    450                 455                 460
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
465                 470                 475                 480
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser
                485                 490                 495
Ser Leu Asn Thr Arg Thr Gln Lys Ala Arg His Ser Pro Asn Ser Glu
            500                 505                 510
Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
        515                 520                 525
Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser His Tyr Gly
    530                 535                 540
Met Asp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
545                 550                 555                 560
Ser Ile Tyr Ser Ser Gly Gly Tyr Thr Leu Tyr Ala Asp Ser Val Lys
                565                 570                 575
```

```
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
            580                 585                 590
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Thr Tyr Tyr Cys Ala
        595                 600                 605
Thr Arg Thr Trp Ala Asp Ala Phe Asp Val Trp Gly Gln Gly Thr Thr
    610                 615                 620
Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
625                 630                 635                 640
Gly Gly Gly Ser Gln Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu
                645                 650                 655
Ser Ala Ser Val Gly Asp Arg Val Thr Phe Thr Cys Arg Ala Ser Gln
            660                 665                 670
Ser Val Asn Asn Trp Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala
        675                 680                 685
Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro
    690                 695                 700
Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
705                 710                 715                 720
Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser
                725                 730                 735
Tyr Ser Met Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            740                 745                 750

<210> 669
<211> 752
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 669
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1                5                  10                  15
Val Ile Met Ser Arg Gly Glu Val Gln Leu Leu Glu Ser Gly Gly Gly
            20                  25                  30
Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly
        35                  40                  45
Phe Thr Phe Ser His Tyr Met Met Ala Trp Val Arg Gln Ala Pro Gly
    50                  55                  60
Lys Gly Leu Glu Trp Val Ser Tyr Ile Tyr Pro Ser Gly Gly Trp Thr
65                  70                  75                  80
Ser Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn
                85                  90                  95
Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
            100                 105                 110
Thr Ala Val Tyr Tyr Cys Ala Arg Phe Asp Tyr Thr Ile Gly Phe Asp
        115                 120                 125
Phe Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly
    130                 135                 140
Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Asp Ile Gln Met
145                 150                 155                 160
Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr
                165                 170                 175
Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr
            180                 185                 190
Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser
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        195                 200                 205
Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
    210                 215                 220
Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala
225                 230                 235                 240
Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Arg Thr Phe Gly Gln
                245                 250                 255
Gly Thr Lys Val Glu Ile Lys Thr Gly Glu Pro Lys Ser Ser Asp Lys
            260                 265                 270
Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro
        275                 280                 285
Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
    290                 295                 300
Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
305                 310                 315                 320
Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
                325                 330                 335
Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
            340                 345                 350
Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Ala
        355                 360                 365
Tyr Ala Cys Ala Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
    370                 375                 380
Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
385                 390                 395                 400
Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
                405                 410                 415
Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
            420                 425                 430
Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
        435                 440                 445
Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
    450                 455                 460
Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
465                 470                 475                 480
Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
                485                 490                 495
Gln Arg His Asn Asn Ser Ser Leu Asn Thr Arg Thr Gln Lys Ala Arg
            500                 505                 510
His Ser Pro Asn Ser Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr Ala
        515                 520                 525
Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln Thr
    530                 535                 540
Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys Val
545                 550                 555                 560
Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp Ser
                565                 570                 575
Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys Gly
            580                 585                 590
Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg Glu
        595                 600                 605
Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu Ser
    610                 615                 620
Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg Pro
625                 630                 635                 640
Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val Cys
                645                 650                 655
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Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr Asp
            660                 665                 670
Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly Asn
        675                 680                 685
Ala Ser Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser Met
    690                 695                 700
Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser Gln
705                 710                 715                 720
His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser Phe
                725                 730                 735
Leu Leu Pro Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly Asp
            740                 745                 750

<210> 670
<211> 759
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 670
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1               5                  10                  15
Val Ile Met Ser Arg Gly Glu Val Gln Leu Leu Glu Ser Gly Gly Gly
            20                  25                  30
Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly
        35                  40                  45
Phe Thr Phe Ser Trp Tyr Leu Met His Trp Val Arg Gln Ala Pro Gly
    50                  55                  60
Lys Gly Leu Glu Trp Val Ser Gly Ile Trp Pro Ser Gly Gly His Thr
65                  70                  75                  80
Leu Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn
                85                  90                  95
Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
            100                 105                 110
Thr Ala Val Tyr Tyr Cys Ala Arg Glu Pro Leu Leu Trp Phe Gly Glu
        115                 120                 125
Leu Ser Tyr Asn Trp Phe Asp Pro Trp Gly Gln Gly Thr Leu Val Thr
    130                 135                 140
Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
145                 150                 155                 160
Gly Ser Gln Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Val Ser Ala
                165                 170                 175
Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile
            180                 185                 190
Ser Ser Trp Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys
        195                 200                 205
Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg
    210                 215                 220
Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser
225                 230                 235                 240
Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ala Asn Ser
                245                 250                 255
Phe Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Thr Gly
            260                 265                 270
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
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        275                 280                 285
Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
    290                 295                 300
Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
305                 310                 315                 320
Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
                325                 330                 335
Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
            340                 345                 350
Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
        355                 360                 365
Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala
    370                 375                 380
Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
385                 390                 395                 400
Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
                405                 410                 415
Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
            420                 425                 430
Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
        435                 440                 445
Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
    450                 455                 460
Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
465                 470                 475                 480
Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
                485                 490                 495
Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser Ser Leu Asn
            500                 505                 510
Thr Arg Thr Gln Lys Ala Arg His Ser Pro Asn Ser Leu Pro Ala Gln
        515                 520                 525
Val Ala Phe Thr Pro Tyr Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu
    530                 535                 540
Arg Glu Tyr Tyr Asp Gln Thr Ala Gln Met Cys Cys Ser Lys Cys Ser
545                 550                 555                 560
Pro Gly Gln His Ala Lys Val Phe Cys Thr Lys Thr Ser Asp Thr Val
                565                 570                 575
Cys Asp Ser Cys Glu Asp Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val
            580                 585                 590
Pro Glu Cys Leu Ser Cys Gly Ser Arg Cys Ser Ser Asp Gln Val Glu
        595                 600                 605
Thr Gln Ala Cys Thr Arg Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro
    610                 615                 620
Gly Trp Tyr Cys Ala Leu Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala
625                 630                 635                 640
Pro Leu Arg Lys Cys Arg Pro Gly Phe Gly Val Ala Arg Pro Gly Thr
                645                 650                 655
Glu Thr Ser Asp Val Val Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser
            660                 665                 670
Asn Thr Thr Ser Ser Thr Asp Ile Cys Arg Pro His Gln Ile Cys Asn
        675                 680                 685
Val Val Ala Ile Pro Gly Asn Ala Ser Met Asp Ala Val Cys Thr Ser
    690                 695                 700
Thr Ser Pro Thr Arg Ser Met Ala Pro Gly Ala Val His Leu Pro Gln
705                 710                 715                 720
Pro Val Ser Thr Arg Ser Gln His Thr Gln Pro Thr Pro Glu Pro Ser
                725                 730                 735
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Thr Ala Pro Ser Thr Ser Phe Leu Leu Pro Met Gly Pro Ser Pro Pro
740 745 750
Ala Glu Gly Ser Thr Gly Asp
755

<210> 671
<211> 2270
<212> DNA
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 671
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gtcataatgt cgcgaggatt gcccgcccag gtggcattta caccctacgc cccggagccc 120
gggagcacat gccggctcag agaatactat gaccagacag ctcagatgtg ctgcagcaaa 180
tgctcgccgg gccaacatgc aaaagtcttc tgtaccaaga cctcggacac cgtgtgtgac 240
tcctgtgagg acagcacata cacccagctc tggaactggg ttcccgagtg cttgagctgt 300
ggctcccgct gtagctctga ccaggtggaa actcaagcct gcactcggga acagaaccgc 360
atctgcacct gcaggcccgg ctggtactgc gcgctgagca agcaggaggg gtgccggctg 420
tgcgcgccgc tgcgcaagtg ccgcccgggc ttcggcgtgg ccagaccagg aactgaaaca 480
tcagacgtgg tgtgcaagcc ctgtgccccg gggacgttct ccaacacgac ttcatccacg 540
gatatttgca ggccccacca gatctgtaac gtggtggcca tccctgggaa tgcaagcatg 600
gatgcagtct gcacgtccac gtcccccacc cggagtatgg ccccaggggc agtacactta 660
ccccagccag tgtccacacg atcccaacac acgcagccaa ctccagaacc cagcactgct 720
ccaagcacct ccttcctgct cccaatgggc cccagccccc cagctgaagg gagcactggc 780
gacaccggtg agcccaaatc ttctgacaaa actcacacat gcccaccgtg cccagcacct 840
gaagccgcgg gtgcaccgtc agtcttcctc ttcccccaa aacccaagga caccctcatg 900
atctcccgga cccctgaggt cacatgcgtg gtggtggacg tgagccacga agaccctgag 960
gtcaagttca actggtacgt ggacggcgtg gaggtgcata atgccaagac aaagccgcgg 1020
gaggagcagt acaacagcac gtaccgtgtg gtcagcgtcc tcaccgtcct gcaccaggac 1080
tggctgaatg gcaaggcgta cgcgtgcgcg gtctccaaca aagccctccc agcccccatc 1140
gagaaaacca tctccaaagc caaagggcag ccccgagaac cacaggtgta cacctgccc 1200
ccatcccggg atgagctgac caagaaccag gtcagcctga cctgcctggt caaaggcttc 1260
tatccaagcg acatcgccgt ggagtgggag agcaatgggc agccggagaa caactacaag 1320
accacgcctc ccgtgctgga ctccgacggc tccttcttcc tctacagcaa gctcaccgtg 1380
gacaagagca ggtggcagca ggggaacgtc ttctcatgct ccgtgatgca tgaggctctg 1440
cacaaccact acacgcagaa gagcctctcc ctgtctccgg gtcagaggca caacaattct 1500
tccctgaata caagaactca gaaagcacgt cattctccga attctgaagt tcaattgtta 1560
gagtctggtg gcggtcttgt tcagcctggt ggttctttac gtctttcttg cgctgcttcc 1620
ggattcactt tctctaagta ctctatgcat tgggttcgcc aagctcctgg taaaggtttg 1680
gagtgggttt cttctatctg gccttctggt ggctggacta cttatgctga ctccgttaaa 1740
ggtcgcttca ctatctctag agacaactct aagaatactc tctacttgca gatgaacagc 1800
ttaagggctg aggacacggc cgtgtattac tgtgcgagag gtggttatta ctacgccctt 1860
gactactggg gccagggaac cctggtcacc gtctcaagcg gtggcggcgg ttcgggggt 1920
ggcggaagtg gaggtggagg gagtcagagc gaattgactc agccaccctc agtgtccgtg 1980
tccccaggac agacagccac catcacctgc tctggagaaa aattggggga tatatatgct 2040
tcctggtatc agcagaagcc aggccagtcc ccggtcttgg tcatctatca agataccaag 2100
cggccctcag ggatccctgt gcgattctct ggctccaact ctgggaacac agccactctg 2160
accatcagcg ggacccaggc tatggatgag gctgactatt actgtcaggc gtgggacagc 2220
agcacggtat tcggcggagg gaccaagctg accgtcctat gagcggccgc 2270

<210> 672
<211> 2297
<212> DNA

<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 672
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gtcataatgt cgcgaggatt gcccgcccag gtggcattta caccctacgc cccggagccc 120
gggagcacat gccggctcag agaatactat gaccagacag ctcagatgtg ctgcagcaaa 180
tgctcgccgg gccaacatgc aaaagtcttc tgtaccaaga cctcggacac cgtgtgtgac 240
tcctgtgagg acagcacata cacccagctc tggaactggg ttcccgagtg cttgagctgt 300
ggctcccgct gtagctctga ccaggtggaa actcaagcct gcactcggga acagaaccgc 360
atctgcacct gcaggcccgg ctggtactgc gcgctgagca agcaggaggg gtgccggctg 420
tgcgcgccgc tgcgcaagtg ccgcccgggc ttcggcgtgg ccagaccagg aactgaaaca 480
tcagacgtgg tgtgcaagcc ctgtgccccg gggacgttct ccaacacgac ttcatccacg 540
gatatttgca ggccccacca gatctgtaac gtggtggcca tccctgggaa tgcaagcatg 600
gatgcagtct gcacgtccac gtcccccacc cggagtatgg ccccaggggc agtacactta 660
ccccagccag tgtccacacg atcccaacac acgcagccaa ctccagaacc cagcactgct 720
ccaagcacct ccttcctgct cccaatgggc cccagccccc cagctgaagg gagcactggc 780
gacaccggtg agcccaaatc ttctgacaaa actcacacat gcccaccgtg cccagcacct 840
gaagccgcgg gtgcaccgtc agtcttcctc ttcccccaa aacccaagga caccctcatg 900
atctcccgga cccctgaggt cacatgcgtg gtggtggacg tgagccacga agaccctgag 960
gtcaagttca actggtacgt ggacggcgtg gaggtgcata atgccaagac aaagccgcgg 1020
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tggctgaatg gcaaggcgta cgcgtgcgcg gtctccaaca aagccctccc agcccccatc 1140
gagaaaacca tctccaaagc caaagggcag ccccgagaac cacaggtgta caccctgccc 1200
ccatcccggg atgagctgac caagaaccag gtcagcctga cctgcctggt caaaggcttc 1260
tatccaagcg acatcgccgt ggagtgggag agcaatgggc agccggagaa caactacaag 1320
accacgcctc ccgtgctgga ctccgacggc tccttcttcc tctacagcaa gctcaccgtg 1380
gacaagagca ggtggcagca ggggaacgtc ttctcatgct ccgtgatgca tgaggctctg 1440
cacaaccact acacgcagaa gagcctctcc ctgtctccgg gtcagaggca caacaattct 1500
tccctgaata caagaactca gaaagcacgt cattctccga attctgaagt tcaattgtta 1560
gagtctggtg gcggtcttgt tcagcctggt ggttctttac gtctttcttg cgctgcttcc 1620
ggattcactt tctctttta ccagatgcat tgggttcgcc aagctcctgg taaaggtttg 1680
gagtgggttt ctggtatcta tccttctggt ggctatacta agtatgctga ctccgttaaa 1740
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ttaagggctg aggacactgc agtctactat tgtgcgagag atctagggta cggcagcagc 1860
tggtactact ttgactactg gggccaggga accctggtca ccgtctcaag cggtggcggc 1920
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tccgtgtctg ggtctcctgg acagtcgatc accatctcct gcagtggaac cgacagtgac 2040
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ataatttatg atgtcgatca tcggccctca gggatctcta accgtttctc tggctccaag 2160
tctggcaaca cggcctccct gaccatctct gggctccagg ctgaggacga ggctgattat 2220
tactgcagct catatagaag cggtagcact tatgtcttcg gaactgggac caaggtcacc 2280
gtcctatgag cggccgc 2297

<210> 673
<211> 2276
<212> DNA
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 673
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gtcataatgt cgcgaggatt gcccgcccag gtggcattta caccctacgc cccggagccc 120

gggagcacat gccggctcag agaatactat gaccagacag ctcagatgtg ctgcagcaaa 180
tgctcgccgg gccaacatgc aaaagtcttc tgtaccaaga cctcggacac cgtgtgtgac 240
tcctgtgagg acagcacata cacccagctc tggaactggg ttcccgagtg cttgagctgt 300
ggctcccgct gtagctctga ccaggtggaa actcaagcct gcactcggga acagaaccgc 360
atctgcacct gcaggcccgg ctggtactgc gcgctgagca agcaggaggg gtgccggctg 420
tgcgcgccgc tgcgcaagtg ccgcccgggc ttcggcgtgg ccagaccagg aactgaaaca 480
tcagacgtgg tgtgcaagcc ctgtgccccg gggacgttct ccaacacgac ttcatccacg 540
gatatttgca ggccccacca gatctgtaac gtggtggcca tccctgggaa tgcaagcatg 600
gatgcagtct gcacgtccac gtcccccacc cggagtatgg ccccaggggc agtacactta 660
ccccagccag tgtccacacg atcccaacac acgcagccaa ctccagaacc cagcactgct 720
ccaagcacct ccttcctgct cccaatgggc cccagccccc cagctgaagg gagcactggc 780
gacaccggtg agcccaaatc ttctgacaaa actcacacat gcccaccgtg cccagcacct 840
gaagccgcgg gtgcaccgtc agtcttcctc ttcccccaa aacccaagga caccctcatg 900
atctcccgga cccctgaggt cacatgcgtg gtggtggacg tgagccacga agaccctgag 960
gtcaagttca actggtacgt ggacggcgtg gaggtgcata atgccaagac aaagccgcgg 1020
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gagaaaacca tctccaaagc caaagggcag ccccgagaac cacaggtgta caccctgccc 1200
ccatcccggg atgagctgac caagaaccag gtcagcctga cctgcctggt caaaggcttc 1260
tatccaagcg acatcgccgt ggagtgggag agcaatgggc agccggagaa caactacaag 1320
accacgcctc ccgtgctgga ctccgacggc tccttcttcc tctacagcaa gctcaccgtg 1380
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cacaaccact acacgcagaa gagcctctcc ctgtctccgg gtcagaggca caacaattct 1500
tccctgaata caagaactca gaaagcacgt cattctccga attctgaagt tcaattgtta 1560
gagtctggtg gcggtcttgt tcagcctggt ggttctttac gtctttcttg cgctgcttcc 1620
ggattcactt tctctaagta ctctatgcat tgggttcgcc aagctcctgg taaaggtttg 1680
gagtgggttt ctggtatctc tccttctggc tatactcgtt atgctgactc cgttaaaggt 1740
cgcttcacta tctctagaga caactctaag aatactctct acttgcagat gaacagctta 1800
agggctgagg acacggccgt gtattactgt gcgagggacc agctgctaga ggcttttgat 1860
atctggggcc aagggaccac ggtcaccgtc tcaagcggtg gcggcggttc gggggtggc 1920
ggaagtggag gtggagggag tcaagacatc cagatgaccc agtctccact ctccctgtct 1980
gcatctgtgg gagacagagt caccatcact tgccgggcaa gtcagagcat tagcagctat 2040
ttaaattggt atcagcaaaa accaggggaa gcccctaagc tcctcatcta tgctgcatcc 2100
gctttgcaaa gtggggtccc gtcaaggttc agtggcagtg gacttgggac agttttcact 2160
ctcaccatca ccagcctgca acctgaagat tctgcaactt actattgtca acagagttac 2220
agtcccccgg tcactttcgg cggagggacc aaggtggaga tcaaatgagc ggccgc 2276

<210> 674
<211> 2279
<212> DNA
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 674
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gggagcacat gccggctcag agaatactat gaccagacag ctcagatgtg ctgcagcaaa 180
tgctcgccgg gccaacatgc aaaagtcttc tgtaccaaga cctcggacac cgtgtgtgac 240
tcctgtgagg acagcacata cacccagctc tggaactggg ttcccgagtg cttgagctgt 300
ggctcccgct gtagctctga ccaggtggaa actcaagcct gcactcggga acagaaccgc 360
atctgcacct gcaggcccgg ctggtactgc gcgctgagca agcaggaggg gtgccggctg 420
tgcgcgccgc tgcgcaagtg ccgcccgggc ttcggcgtgg ccagaccagg aactgaaaca 480
tcagacgtgg tgtgcaagcc ctgtgccccg gggacgttct ccaacacgac ttcatccacg 540
gatatttgca ggccccacca gatctgtaac gtggtggcca tccctgggaa tgcaagcatg 600
gatgcagtct gcacgtccac gtcccccacc cggagtatgg ccccaggggc agtacactta 660

ccccagccag tgtccacacg atcccaacac acgcagccaa ctccagaacc cagcactgct 720
ccaagcacct ccttcctgct cccaatgggc cccagccccc cagctgaagg gagcactggc 780
gacaccggtg agcccaaatc ttctgacaaa actcacacat gcccaccgtg cccagcacct 840
gaagccgcgg gtgcaccgtc agtcttcctc ttccccccaa aacccaagga caccctcatg 900
atctcccgga cccctgaggt cacatgcgtg gtggtggacg tgagccacga agaccctgag 960
gtcaagttca actggtacgt ggacggcgtg gaggtgcata atgccaagac aaagccgcgg 1020
gaggagcagt acaacagcac gtaccgtgtg gtcagcgtcc tcaccgtcct gcaccaggac 1080
tggctgaatg gcaaggcgta cgcgtgcgcg gtctccaaca aagccctccc agcccccatc 1140
gagaaaacca tctccaaagc caaagggcag ccccgagaac cacaggtgta caccctgccc 1200
ccatcccggg atgagctgac caagaaccag gtcagcctga cctgcctggt caaaggcttc 1260
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gacaagagca ggtggcagca ggggaacgtc ttctcatgct ccgtgatgca tgaggctctg 1440
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tccctgaata caagaactca gaaagcacgt cattctccga attctgaagt tcaattgtta 1560
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gcatctagtt tagaaagtgg ggtcccatca aggttcagcg gcagtggatc tgggacagaa 2160
ttcactctca ccatcagcag cctgcagcct gatgattttg caacttatta ctgccaacag 2220
tataatagtt attggacgtt cggccaaggg accaaggtgg aaatcaaatg agcggccgc 2279

<210> 675
<211> 2306
<212> DNA
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 675
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ggagcacatg ccggctcaga gaatactatg accagacagc tcagatgtgc tgcagcaaat 180
gctcgccggg ccaacatgca aaagtcttct gtaccaagac ctcggacacc gtgtgtgact 240
cctgtgagga cagcacatac acccagctct ggaactgggt tcccgagtgc ttgagctgtg 300
gctcccgctg tagctctgac caggtggaaa ctcaagcctg cactcgggaa cagaaccgca 360
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gcgcgccgct gcgcaagtgc cgcccgggct tcggcgtggc cagaccagga actgaaacat 480
cagacgtggt gtgcaagccc tgtgccccgg ggacgttctc caacacgact tcatccacgg 540
atatttgcag gccccaccag atctgtaacg tggtggccat ccctgggaat gcaagcatgg 600
atgcagtctg cacgtccacg tcccccaccc ggagtatggc cccaggggca gtacacttac 660
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gcagtgggtc tgggacagac ttcactctca ccatcagcag cctagagcct gaagattctg 2220
cagtttatta ctgtcagcaa cgtagcaact ggcctccgtt cactttcggc ggagggacca 2280
aggtggagat caaatgagcg gccgcc 2306

<210> 676
<211> 2300
<212> DNA
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 676
aagcttgccg ccatggattt tcaagtgcag attttcagct tcctgctaat cagtgcttca 60
gtcataatgt cgcgaggatt gcccgcccag gtggcattta caccctacgc cccggagccc 120
gggagcacat gccggctcag agaatactat gaccagacag ctcagatgtg ctgcagcaaa 180
tgctcgccgg gccaacatgc aaaagtcttc tgtaccaaga cctcggacac cgtgtgtgac 240
tcctgtgagg acagcacata cacccagctc tggaactggg ttcccgagtg cttgagctgt 300
ggctcccgct gtagctctga ccaggtggaa actcaagcct gcactcggga acagaaccgc 360
atctgcacct gcaggcccgg ctggtactgc gcgctgagca agcaggaggg gtgccggctg 420
tgcgcgccgc tgcgcaagtg ccgcccgggc ttcggcgtgg ccagaccagg aactgaaaca 480
tcagacgtgg tgtgcaagcc ctgtgccccg gggacgttct ccaacacgac ttcatccacg 540
gatatttgca ggccccacca gatctgtaac gtggtggcca tccctgggaa tgcaagcatg 600
gatgcagtct gcacgtccac gtcccccacc cggagtatgg ccccaggggc agtacactta 660
ccccagccag tgtccacacg atcccaacac acgcagccaa ctccagaacc cagcactgct 720
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gacaccggtg agcccaaatc ttctgacaaa actcacacat gcccaccgtg cccagcacct 840
gaagccgcgg gtgcaccgtc agtcttcctc ttcccccaa aacccaagga caccctcatg 900
atctcccgga cccctgaggt cacatgcgtg gtggtggacg tgagccacga agaccctgag 960
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tggctgaatg gcaaggcgta cgcgtgcgcg gtctccaaca aagccctccc agcccccatc 1140
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ccatcccggg atgagctgac caagaaccag gtcagcctga cctgcctggt caaaggcttc 1260
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tccctgaata caagaactca gaaagcacgt cattctccga attctgaagt tcaattgtta 1560
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ggattcactt tctctcagta caatatgatt tgggttcgcc aagctcctgg taaaggtttg 1680

gagtgggttt cttggatctc ttcttctggc ggtactgagt atgctgactc cgttaaaggt 1740
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aaactcctga tctatgctgc atccagtttg caaagtgggg tcccatcaag gttcagtggc 2160
agtggatctg ggacagattt cactctcacc atcagcagtc tgcaacctga agattttgca 2220
agttactact gtcaacagag ttacaggacc ccccggacgt tcggccaagg gaccaaggtg 2280
gagatcaaat gagcggccgc 2300

<210> 677
<211> 2285
<212> DNA
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 677
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gtcataatgt cgcgaggatt gcccgcccag gtggcattta caccctacgc cccggagccc 120
gggagcacat gccggctcag agaatactat gaccagacag ctcagatgtg ctgcagcaaa 180
tgctcgccgg gccaacatgc aaaagtcttc tgtaccaaga cctcggacac cgtgtgtgac 240
tcctgtgagg acagcacata cacccagctc tggaactggg ttcccgagtg cttgagctgt 300
ggctcccgct gtagctctga ccaggtggaa actcaagcct gcactcggga acagaaccgc 360
atctgcacct gcaggcccgg ctggtactgc gcgctgagca agcaggaggg gtgccggctg 420
tgcgcgccgc tgcgcaagtg ccgcccgggc ttcggcgtgg ccagaccagg aactgaaaca 480
tcagacgtgg tgtgcaagcc ctgtgccccg gggacgttct ccaacacgac ttcatccacg 540
gatatttgca ggccccacca gatctgtaac gtggtggcca tccctgggaa tgcaagcatg 600
gatgcagtct gcacgtccac gtcccccacc cggagtatgg ccccaggggc agtacactta 660
ccccagccag tgtccacacg atcccaacac acgcagccaa ctccagaacc cagcactgct 720
ccaagcacct ccttcctgct cccaatgggc cccagccccc cagctgaagg gagcactggc 780
gacaccggtg agcccaaatc ttctgacaaa actcacacat gcccaccgtg cccagcacct 840
gaagccgcgg gtgcaccgtc agtcttcctc ttcccccaa aacccaagga caccctcatg 900
atctcccgga cccctgaggt cacatgcgtg gtggtggacg tgagccacga agaccctgag 960
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ttcactctca ccatcagcag actggagcct gaagattttg cagtgtatta ctgtcagcag 2220
tatggtagct cacctctctg gacgttcggc caagggacca aggtsgaaat caaatgagcg 2280
gccgc 2285

<210> 678
<211> 2279
<212> DNA
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 678
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gtcataatgt cgcgaggatt gcccgcccag gtggcattta caccctacgc cccggagccc 120
gggagcacat gccggctcag agaatactat gaccagacag ctcagatgtg ctgcagcaaa 180
tgctcgccgg gccaacatgc aaaagtcttc tgtaccaaga cctcggacac cgtgtgtgac 240
tcctgtgagg acagcacata cacccagctc tggaactggg ttcccgagtg cttgagctgt 300
ggctcccgct gtagctctga ccaggtggaa actcaagcct gcactcggga acagaaccgc 360
atctgcacct gcaggcccgg ctggtactgc gcgctgagca agcaggaggg gtgccggctg 420
tgcgcgccgc tgcgcaagtg ccgcccgggc ttcggcgtgg ccagaccagg aactgaaaca 480
tcagacgtgg tgtgcaagcc ctgtgccccg gggacgttct ccaacacgac ttcatccacg 540
gatatttgca ggccccacca gatctgtaac gtggtggcca tccctgggaa tgcaagcatg 600
gatgcagtct gcacgtccac gtcccccacc cggagtatgg ccccaggggc agtacactta 660
ccccagccag tgtccacacg atcccaacac acgcagccaa ctccagaacc cagcactgct 720
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gacaccggtg agcccaaatc ttctgacaaa actcacacat gcccaccgtg cccagcacct 840
gaagccgcgg gtgcaccgtc agtcttcctc ttcccccaa aacccaagga caccctcatg 900
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tatttaaatt ggtatcagca gaaaccaggg aaagccccta agctcctgat ctatgctgca 2100
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actctcacca tcagcagtct gcaacctgaa gattttgcaa cttactactg tcaacagagt 2220
tacagtaccc ctcggacgtt cggccaaggg accaaggtgg aaatcaaatg agcggccgc 2279

<210> 679
<211> 2376
<212> DNA
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 679
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aagtgcagat tttcagcttc ctgctaatca gtgcttcagt cataatgtcg cgaggattgc 120
ccgcccaggt ggcatttaca ccctacgccc cggagcccgg gagcacatgc cggctcagag 180
aatactatga ccagacagct cagatgtgct gcagcaaatg ctcgccgggc caacatgcaa 240
aagtcttctg taccaagacc tcggacaccg tgtgtgactc ctgtgaggac agcacataca 300
cccagctctg gaactgggtt cccgagtgct tgagctgtgg ctcccgctgt agctctgacc 360
aggtggaaac tcaagcctgc actcgggaac agaaccgcat ctgcacctgc aggcccggct 420
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gcccgggctt cggcgtggcc agaccaggaa ctgaaacatc agacgtggtg tgcaagccct 540
gtgccccggg gacgttctcc aacacgactt catccacgga tatttgcagg ccccaccaga 600
tctgtaacgt ggtggccatc cctgggaatg caagcatgga tgcagtctgc acgtccacgt 660
cccccacccg gagtatggcc ccaggggcag tacacttacc ccagccagtg tccacacgat 720
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aacaaatacc tgggcaggct cccaggctcc tcatgtatga tgcatccaag agggccagtg 2160
gcatcccggc caggttcagt ggcagtgggt ctgggacaga cctcactctc accatcagca 2220
gcctcgagcc tgaagattct gcggtttatt actgtcagct gcgtataaac tggcctccgg 2280
aattcacttt cggccctggg accaaagtgg atatcaaatg agcggccgcc tcgagtctag 2340
agggccctat tctatagtgt cacctaaatg ctagag 2376

<210> 680
<211> 2306
<212> DNA
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 680
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gggagcacat gccggctcag agaatactat gaccagacag ctcagatgtg ctgcagcaaa 180

tgctcgccgg gccaacatgc aaaagtcttc tgtaccaaga cctcggacac cgtgtgtgac 240
tcctgtgagg acagcacata cacccagctc tggaactggg ttcccgagtg cttgagctgt 300
ggctcccgct gtagctctga ccaggtggaa actcaagcct gcactcggga acagaaccgc 360
atctgcacct gcaggcccgg ctggtactgc gcgctgagca agcaggaggg gtgccggctg 420
tgcgcgccgc tgcgcaagtg ccgcccgggc ttcggcgtgg ccagaccagg aactgaaaca 480
tcagacgtgg tgtgcaagcc ctgtgccccg gggacgttct ccaacacgac ttcatccacg 540
gatatttgca ggccccacca gatctgtaac gtggtggcca tccctgggaa tgcaagcatg 600
gatgcagtct gcacgtccac gtcccccacc cggagtatgg ccccaggggc agtacactta 660
ccccagccag tgtccacacg atcccaacac acgcagccaa ctccagaacc cagcactgct 720
ccaagcacct ccttcctgct cccaatgggc cccagccccc cagctgaagg gagcactggc 780
gacaccggtg agcccaaatc ttctgacaaa actcacacat gcccaccgtg cccagcacct 840
gaagccgcgg gtgcaccgtc agtcttcctc ttcccccaa aacccaagga caccctcatg 900
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aaggtggaga tcaaatgagc ggccgc 2306

<210> 681
<211> 2288
<212> DNA
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 681
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gggagcacat gccggctcag agaatactat gaccagacag ctcagatgtg ctgcagcaaa 180
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tgcgcgccgc tgcgcaagtg ccgcccgggc ttcggcgtgg ccagaccagg aactgaaaca 480
tcagacgtgg tgtgcaagcc ctgtgccccg gggacgttct ccaacacgac ttcatccacg 540
gatatttgca ggccccacca gatctgtaac gtggtggcca tccctgggaa tgcaagcatg 600
gatgcagtct gcacgtccac gtcccccacc cggagtatgg ccccaggggc agtacactta 660

ccccagccag tgtccacacg atcccaacac acgcagccaa ctccagaacc cagcactgct 720
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aacacagcca ctctgaccat cagcggggcc caggctgcag atgaggctga ctattactgt 2220
cagacgtggg acagcgacac ttatgtcttc ggaagtggga gcacggtcac cgtcctgtga 2280
gcggccgc 2288

<210> 682
<211> 2389
<212> DNA
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 682
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aagtgcagat tttcagcttc ctgctaatca gtgcttcagt cataatgtcg cgaggattgc 120
ccgcccaggt ggcatttaca ccctacgccc cggagcccgg gagcacatgc cggctcagag 180
aatactatga ccagacagct cagatgtgct gcagcaaatg ctcgccgggc caacatgcaa 240
aagtcttctg taccaagacc tcggacaccg tgtgtgactc ctgtgaggac agcacataca 300
cccagctctg gaactgggtt cccgagtgct tgagctgtgg ctcccgctgt agctctgacc 360
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ggtactgcgc gctgagcaag caggaggggt gccggctgtg cgcgccgctg cgcaagtgcc 480
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tctgtaacgt ggtggccatc cctgggaatg caagcatgga tgcagtctgc acgtccacgt 660
cccccacccg gagtatggcc ccaggggcag tacacttacc ccagccagtg tccacacgat 720
cccaacacac gcagccaact ccagaaccca gcactgctcc aagcacctcc ttcctgctcc 780
caatgggccc cagcccccca gctgaaggga gcactggcga caccggtgag cccaaatctt 840
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tcttcctctt ccccccaaaa cccaaggaca ccctcatgat ctcccggacc cctgaggtca 960
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acggcgtgga ggtgcataat gccaagacaa agccgcggga ggagcagtac aacagcacgt 1080
accgtgtggt cagcgtcctc accgtcctgc accaggactg gctgaatggc aaggcgtacg 1140

cgtgcgcggt ctccaacaaa gccctcccag cccccatcga gaaaaccatc tccaaagcca 1200
aagggcagcc ccgagaacca caggtgtaca ccctgccccc atcccgggat gagctgacca 1260
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gcctctccct gtctccgggt cagaggcaca acaattcttc cctgaataca agaactcaga 1560
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acagtaccct atggacgttc ggccaaggga ccaaggtgga aatcaaatga gcggccgcct 2340
cgagtctaga gggccctatt ctatagtgtc acctaaatgc tagagctcg 2389

<210> 683
<211> 2290
<212> DNA
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 683
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tcataatgtc gcgaggattg cccgcccagg tggcatttac accctacgcc ccggagcccg 120
ggagcacatg ccggctcaga gaatactatg accagacagc tcagatgtgc tgcagcaaat 180
gctcgccggg ccaacatgca aaagtcttct gtaccaagac ctcggacacc gtgtgtgact 240
cctgtgagga cagcacatac acccagctct ggaactgggt tcccgagtgc ttgagctgtg 300
gctcccgctg tagctctgac caggtggaaa ctcaagcctg cactcgggaa cagaaccgca 360
tctgcacctg caggcccggc tggtactgcg cgctgagcaa gcaggagggg tgccggctgt 420
gcgcgccgct gcgcaagtgc cgcccgggct tcggcgtggc cagaccagga actgaaacat 480
cagacgtggt gtgcaagccc tgtgccccgg ggacgttctc caacacgact tcatccacgg 540
atatttgcag gccccaccag atctgtaacg tggtggccat ccctgggaat gcaagcatgg 600
atgcagtctg cacgtccacg tcccccaccc ggagtatggc cccaggggca gtacacttac 660
cccagccagt gtccacacga tcccaacaca cgcagccaac tccagaaccc agcactgctc 720
caagcacctc cttcctgctc ccaatgggcc ccagcccccc agctgaaggg agcactggcg 780
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aagccgcggg tgcaccgtca gtcttcctct tccccccaaa acccaaggac accctcatga 900
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agtctggtgg cggtcttgtt cagcctggtg gttctttacg tctttcttgc gctgcttccg 1620
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ggacagactt cactctcacc atcaccagcc tgcagcctga agatattgca acatattact 2220
gtcaacagta tgataacctc ccgctcactt tcggcggagg gaccaaggtg gagatcaaat 2280
gagcggccgc 2290

<210> 684
<211> 2300
<212> DNA
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 684
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gggagcacat gccggctcag agaatactat gaccagacag ctcagatgtg ctgcagcaaa 180
tgctcgccgg gccaacatgc aaaagtcttc tgtaccaaga cctcggacac cgtgtgtgac 240
tcctgtgagg acagcacata cacccagctc tggaactggg ttcccgagtg cttgagctgt 300
ggctcccgct gtagctctga ccaggtggaa actcaagcct gcactcggga acagaaccgc 360
atctgcacct gcaggcccgg ctggtactgc gcgctgagca agcaggaggg gtgccggctg 420
tgcgcgccgc tgcgcaagtg ccgcccgggc ttcggcgtgg ccagaccagg aactgaaaca 480
tcagacgtgg tgtgcaagcc ctgtgccccg gggacgttct ccaacacgac ttcatccacg 540
gatatttgca ggccccacca gatctgtaac gtggtggcca tccctgggaa tgcaagcatg 600
gatgcagtct gcacgtccac gtcccccacc cggagtatgg ccccaggggc agtacactta 660
ccccagccag tgtccacacg atcccaacac acgcagccaa ctccagaacc cagcactgct 720
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acaagtcaga gcgttgccac ctatgtaaat tggtatcagc agaaaccagg agaaggccct 2100
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agtggatctg ggacagattt cactctcacc atcggcagtc tgcaacctga agattttgca 2220
acttactact gtcaacagag ttacagtgtg ccaatcacct tcggccaagg gacacgactg 2280
gacattaaat gagcggccgc 2300

<210> 685
<211> 2376
<212> DNA
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 685
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caagtgcaga ttttcagctt cctgctaatc agtgcttcag tcataatgtc gcgaggattg 120
cccgcccagg tggcatttac accctacgcc ccggagcccg ggagcacatg ccggctcaga 180
gaatactatg accagacagc tcagatgtgc tgcagcaaat gctcgccggg ccaacatgca 240
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acccagctct ggaactgggt tcccgagtgc ttgagctgtg gctcccgctg tagctctgac 360
caggtggaaa ctcaagcctg cactcgggaa cagaaccgca tctgcacctg caggcccggc 420
tggtactgcg cgctgagcaa gcaggagggg tgccggctgt gcgcgccgct gcgcaagtgc 480
cgcccgggct tcggcgtggc cagaccagga actgaaacat cagacgtggt gtgcaagccc 540
tgtgccccgg ggacgttctc caacacgact tcatccacgg atatttgcag gccccaccag 600
atctgtaacg tggtggccat ccctgggaat gcaagcatgg atgcagtctg cacgtccacg 660
tcccccaccc ggagtatggc cccaggggca gtacacttac cccagccagt gtccacacga 720
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ccaatgggcc ccagcccccc agctgaaggg agcactggcg acaccggtga gcccaaatct 840
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taccgtgtgg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggcgtac 1140
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gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac 1380
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agcagcctgc agcctgatga ctttgcaact tattactgcc agcagtatag tgattattct 2280
gggatcactt tcggccctgg gaccgaagtg gatatcagat gagcggccgc ctcgagtcta 2340
gagggcccta ttctatagtg tcacctaaat gctaga 2376

<210> 686

<211> 2285
<212> DNA
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 686
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gtcataatgt cgcgaggatt gcccgcccag gtggcattta caccctacgc cccggagccc 120
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gccgc 2285

<210> 687
<211> 2361
<212> DNA
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 687

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agtgtcacct aaatgctaga g 2361

<210> 688
<211> 2276
<212> DNA
<213> Artificial Sequence

<220>
<223> Made in a lab

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<210> 689
<211> 2300
<212> DNA
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 689
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<210> 690
<211> 2294
<212> DNA
<213> Artificial Sequence

<220>
<223> Made in a lab

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gatgcagtct gcacgtccac gtcccccacc cggagtatgg ccccaggggc agtacactta 660
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aaatgagcgg ccgc 2294

<210> 691
<211> 2294
<212> DNA
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 691
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ggcggttcgg ggggtggcgg aagtggaggt ggagggagtc aagacatcca gatgacccag 1980
tctccatcct ccctgtctgc atctgtagga gacagagtca ccatcacttg ccgggcgagt 2040
cagggcatta gcaattattt agcctggtat cagcagaaac cagggaaagt tcctaagctc 2100
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tctgggacag aattcactct caccatcagc agtctgcaac ctgaagattt tgcaacttac 2220
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aaatgagcgg ccgc 2294

<210> 692
<211> 2297
<212> DNA
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 692
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gtcataatgt cgcgaggatt gcccgcccag gtggcattta caccctacgc cccggagccc 120
gggagcacat gccggctcag agaatactat gaccagacag ctcagatgtg ctgcagcaaa 180
tgctcgccgg gccaacatgc aaaagtcttc tgtaccaaga cctcggacac cgtgtgtgac 240
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ggctcccgct gtagctctga ccaggtggaa actcaagcct gcactcggga acagaaccgc 360
atctgcacct gcaggcccgg ctggtactgc gcgctgagca agcaggaggg gtgccggctg 420
tgcgcgccgc tgcgcaagtg ccgcccgggc ttcggcgtgg ccagaccagg aactgaaaca 480
tcagacgtgg tgtgcaagcc ctgtgccccg gggacgttct ccaacacgac ttcatccacg 540
gatatttgca ggccccacca gatctgtaac gtggtggcca tccctgggaa tgcaagcatg 600
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ggcacctcag cctccctggc catcagtggg ctccagtctg aggatgaggc tgattattac 2220
tgtgcagcat gggatgacag cctgaatggt tatgtcttcg gaattgggac caaggtcacc 2280
gtcctatgag cggccgc 2297

<210> 693
<211> 2303
<212> DNA
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 693
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gtcataatgt cgcgaggatt gcccgcccag gtggcattta caccctacgc cccggagccc 120
gggagcacat gccggctcag agaatactat gaccagacag ctcagatgtg ctgcagcaaa 180
tgctcgccgg gccaacatgc aaaagtcttc tgtaccaaga cctcggacac cgtgtgtgac 240
tcctgtgagg acagcacata cacccagctc tggaactggg ttcccgagtg cttgagctgt 300
ggctcccgct gtagctctga ccaggtggaa actcaagcct gcactcggga acagaaccgc 360
atctgcacct gcaggcccgg ctggtactgc gcgctgagca agcaggaggg gtgccggctg 420
tgcgcgccgc tgcgcaagtg ccgcccgggc ttcggcgtgg ccagaccagg aactgaaaca 480
tcagacgtgg tgtgcaagcc ctgtgccccg gggacgttct ccaacacgac ttcatccacg 540
gatatttgca ggccccacca gatctgtaac gtggtggcca tccctgggaa tgcaagcatg 600
gatgcagtct gcacgtccac gtcccccacc cggagtatgg ccccaggggc agtacactta 660
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gacaccggtg agcccaaatc ttctgacaaa actcacacat gcccaccgtg cccagcacct 840
gaagccgcgg gtgcaccgtc agtcttcctc ttcccccaa aacccaagga caccctcatg 900
atctcccgga cccctgaggt cacatgcgtg gtggtggacg tgagccacga agaccctgag 960
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tggctgaatg gcaaggcgta cgcgtgcgcg gtctccaaca aagccctccc agcccccatc 1140
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ccatcccggg atgagctgac caagaaccag gtcagcctga cctgcctggt caaaggcttc 1260
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gacaagagca ggtggcagca ggggaacgtc ttctcatgct ccgtgatgca tgaggctctg 1440
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gtggatatca aatgagcggc cgc 2303

<210> 694
<211> 2306
<212> DNA
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 694
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gtcataatgt cgcgaggatt gcccgcccag gtggcattta caccctacgc cccggagccc 120
gggagcacat gccggctcag agaatactat gaccagacag ctcagatgtg ctgcagcaaa 180
tgctcgccgg gccaacatgc aaaagtcttc tgtaccaaga cctcggacac cgtgtgtgac 240
tcctgtgagg acagcacata cacccagctc tggaactggg ttcccgagtg cttgagctgt 300
ggctcccgct gtagctctga ccaggtggaa actcaagcct gcactcggga acagaaccgc 360
atctgcacct gcaggcccgg ctggtactgc gcgctgagca agcaggaggg gtgccggctg 420
tgcgcgccgc tgcgcaagtg ccgcccgggc ttcggcgtgg ccagaccagg aactgaaaca 480
tcagacgtgg tgtgcaagcc ctgtgccccg gggacgttct ccaacacgac ttcatccacg 540
gatatttgca ggccccacca gatctgtaac gtggtggcca tccctgggaa tgcaagcatg 600
gatgcagtct gcacgtccac gtcccccacc cggagtatgg ccccaggggc agtacactta 660
ccccagccag tgtccacacg atcccaacac acgcagccaa ctccagaacc cagcactgct 720
ccaagcacct ccttcctgct cccaatgggc cccagccccc cagctgaagg gagcactggc 780
gacaccggtg agcccaaatc ttctgacaaa actcacacat gcccaccgtg cccagcacct 840
gaagccgcgg gtgcaccgtc agtcttcctc ttcccccaa aacccaagga caccctcatg 900
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tggctgaatg gcaaggcgta cgcgtgcgcg gtctccaaca aagccctccc agcccccatc 1140
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ccatcccggg atgagctgac caagaaccag gtcagcctga cctgcctggt caaaggcttc 1260
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gacaagagca ggtggcagca ggggaacgtc ttctcatgct ccgtgatgca tgaggctctg 1440
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tccaggtctg gcacctcagc ctccctggcc atcagtgggc tccagtctca ggatgaggct 2220
gattactact gtgcagcatg ggatgacagc ctgaatggtc cgctcttcgg cggagggacc 2280
aagytgaccg tcctatgagc ggccgc 2306

<210> 695
<211> 2279
<212> DNA
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 695
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gtcataatgt cgcgaggatt gcccgcccag gtggcattta caccctacgc cccggagccc 120
gggagcacat gccggctcag agaatactat gaccagacag ctcagatgtg ctgcagcaaa 180
tgctcgccgg gccaacatgc aaaagtcttc tgtaccaaga cctcggacac cgtgtgtgac 240
tcctgtgagg acagcacata cacccagctc tggaactggg ttcccgagtg cttgagctgt 300
ggctcccgct gtagctctga ccaggtggaa actcaagcct gcactcggga acagaaccgc 360
atctgcacct gcaggcccgg ctggtactgc gcgctgagca agcaggaggg gtgccggctg 420

tgcgcgccgc tgcgcaagtg ccgcccgggc ttcggcgtgg ccagaccagg aactgaaaca 480
tcagacgtgg tgtgcaagcc ctgtgccccg gggacgttct ccaacacgac ttcatccacg 540
gatatttgca ggccccacca gatctgtaac gtggtggcca tccctgggaa tgcaagcatg 600
gatgcagtct gcacgtccac gtcccccacc cggagtatgg ccccaggggc agtacactta 660
ccccagccag tgtccacacg atcccaacac acgcagccaa ctccagaacc cagcactgct 720
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gacaccggtg agcccaaatc ttctgacaaa actcacacat gcccaccgtg cccagcacct 840
gaagccgcgg gtgcaccgtc agtcttcctc ttcccccaa aacccaagga caccctcatg 900
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gtcatcagtg gaccccagtc tgaggatgag gctgattatt actgtgcagc atgggatgac 2220
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<210> 696
<211> 2306
<212> DNA
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 696
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gggagcacat gccggctcag agaatactat gaccagacag ctcagatgtg ctgcagcaaa 180
tgctcgccgg gccaacatgc aaaagtcttc tgtaccaaga cctcggacac cgtgtgtgac 240
tcctgtgagg acagcacata cacccagctc tggaactggg ttcccgagtg cttgagctgt 300
ggctcccgct gtagctctga ccaggtggaa actcaagcct gcactcggga acagaaccgc 360
atctgcacct gcaggcccgg ctggtactgc gcgctgagca agcaggaggg gtgccggctg 420
tgcgcgccgc tgcgcaagtg ccgcccgggc ttcggcgtgg ccagaccagg aactgaaaca 480
tcagacgtgg tgtgcaagcc ctgtgccccg gggacgttct ccaacacgac ttcatccacg 540
gatatttgca ggccccacca gatctgtaac gtggtggcca tccctgggaa tgcaagcatg 600
gatgcagtct gcacgtccac gtcccccacc cggagtatgg ccccaggggc agtacactta 660
ccccagccag tgtccacacg atcccaacac acgcagccaa ctccagaacc cagcactgct 720
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gacaccggtg agcccaaatc ttctgacaaa actcacacat gcccaccgtg cccagcacct 840
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tccaagtctg gcacctcagc ctccctggcc atcagtgggc tccagtctga ggatgaggct 2220
gattattact gtgcagcatg ggatgacagc ctgtatcaag gagtgttcgg cggagggacc 2280
aagctgaccg tcctatgagc ggccgc 2306

<210> 697
<211> 2371
<212> DNA
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 697
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caagtgcaga ttttcagctt cctgctaatc agtgcttcag tcataatgtc gcgaggattg 120
cccgcccagg tggcatttac accctacgcc ccggagcccg ggagcacatg ccggctcaga 180
gaatactatg accagacagc tcagatgtgc tgcagcaaat gctcgccggg ccaacatgca 240
aaagtcttct gtaccaagac ctcggacacc gtgtgtgact cctgtgagga cagcacatac 300
acccagctct ggaactgggt tcccgagtgc ttgagctgtg gctcccgctg tagctctgac 360
caggtggaaa ctcaagcctg cactcgggaa cagaaccgca tctgcacctg caggcccggc 420
tggtactgcg cgctgagcaa gcaggagggg tgccggctgt gcgcgccgct gcgcaagtgc 480
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tgtgccccgg ggacgttctc caacacgact tcatccacgg atatttgcag gccccaccag 600
atctgtaacg tggtggccat ccctgggaat gcaagcatgg atgcagtctg cacgtccacg 660
tcccccaccc ggagtatggc cccaggggca gtacacttac cccagccagt gtccacacga 720
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cctattctat agtgtcacct aaatgctaga g 2371

<210> 698
<211> 2294
<212> DNA
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 698
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gtcataatgt cgcgaggatt gcccgcccag gtggcattta caccctacgc cccggagccc 120
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gatatttgca ggccccacca gatctgtaac gtggtggcca tccctgggaa tgcaagcatg 600
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tctgggacag acttcactct caccatcagc agactggagc ctgaagattt tgcagtgtat 2220
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aaatgagcgg ccgc 2294

<210> 699
<211> 2359
<212> DNA
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 699
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ccgcccaggt ggcatttaca ccctacgccc cggagcccgg gagcacatgc cggctcagag 180
aatactatga ccagacagct cagatgtgct gcagcaaatg ctcgccgggc caacatgcaa 240
aagtcttctg taccaagacc tcggacaccg tgtgtgactc ctgtgaggac agcacataca 300
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ctgacaaaac tcacacatgc ccaccgtgcc cagcacctga agccgcgggt gcaccgtcag 900
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atgttgcaac ttattattgt caacagagtt acagtccccc gttcactttt ggccaaggga 2280
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acctaaatgc tagagctcg 2359

<210> 700
<211> 2288
<212> DNA
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 700
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gggagcacat gccggctcag agaatactat gaccagacag ctcagatgtg ctgcagcaaa 180
tgctcgccgg gccaacatgc aaaagtcttc tgtaccaaga cctcggacac cgtgtgtgac 240
tcctgtgagg acagcacata cacccagctc tggaactggg ttcccgagtg cttgagctgt 300
ggctcccgct gtagctctga ccaggtggaa actcaagcct gcactcggga acagaaccgc 360
atctgcacct gcaggcccgg ctggtactgc gcgctgagca agcaggaggg gtgccggctg 420
tgcgcgccgc tgcgcaagtg ccgcccgggc ttcggcgtgg ccagaccagg aactgaaaca 480
tcagacgtgg tgtgcaagcc ctgtgccccg gggacgttct ccaacacgac ttcatccacg 540
gatatttgca ggccccacca gatctgtaac gtggtggcca tccctgggaa tgcaagcatg 600
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acagatttca ctctcaccat cagcagcctg cagcctgaag attttgcaac ttattactgc 2220
caacagtata agagttaccc tttcactttc gggggaggga ccaaggtgga gatcaaatga 2280
gcggccgc 2288

<210> 701
<211> 2294
<212> DNA
<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 701
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gggagcacat gccggctcag agaatactat gaccagacag ctcagatgtg ctgcagcaaa 180
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tgcgcgccgc tgcgcaagtg ccgcccgggc ttcggcgtgg ccagaccagg aactgaaaca 480
tcagacgtgg tgtgcaagcc ctgtgccccg gggacgttct ccaacacgac ttcatccacg 540
gatatttgca ggccccacca gatctgtaac gtggtggcca tccctgggaa tgcaagcatg 600
gatgcagtct gcacgtccac gtcccccacc cggagtatgg ccccaggggc agtacactta 660
ccccagccag tgtccacacg atcccaacac acgcagccaa ctccagaacc cagcactgct 720
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aaatgagcgg ccgc 2294

<210> 702
<211> 2301
<212> DNA
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 702
gcgagggaag cttgccgcca tggattttca agtgcagatt ttcagcttcc tgctaatcag 60
tgcttcagtc ataatgtcgc gaggattgcc cgcccaggtg gcatttacac cctacgcccc 120
ggagcccggg agcacatgcc ggctcagaga atactatgac cagacagctc agatgtgctg 180
cagcaaatgc tcgccgggcc aacatgcaaa agtcttctgt accaagacct cggacaccgt 240
gtgtgactcc tgtgaggaca gcacatacac ccagctctgg aactgggttc ccgagtgctt 300

gagctgtggc tcccgctgta gctctgacca ggtggaaact caagcctgca ctcgggaaca 360
gaaccgcatc tgcacctgca ggcccggctg gtactgcgcg ctgagcaagc aggaggggtg 420
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tgaaacatca gacgtggtgt gcaagccctg tgccccgggg acgttctcca acacgacttc 540
atccacggat atttgcaggc cccaccagat ctgtaacgtg gtggccatcc ctgggaatgc 600
aagcatggat gcagtctgca cgtccacgtc ccccacccgg agtatggccc caggggcagt 660
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aacttactac tgtcaacaga gttacagtac ctcgggaacg ttcggccaag ggaccaaggt 2280
ggaaatcaaa tgagcggccg c 2301

<210> 703
<211> 2279
<212> DNA
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 703
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gtcataatgt cgcgaggatt gcccgcccag gtggcattta caccctacgc cccggagccc 120
gggagcacat gccggctcag agaatactat gaccagacag ctcagatgtg ctgcagcaaa 180
tgctcgccgg gccaacatgc aaaagtcttc tgtaccaaga cctcggacac cgtgtgtgac 240
tcctgtgagg acagcacata cacccagctc tggaactggg ttcccgagtg cttgagctgt 300
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<210> 704
<211> 2288
<212> DNA
<213> Artificial Sequence

<220>
<223> Made in a lab

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gcggccgc 2288

<210> 705
<211> 2291
<212> DNA
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 705
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gggagcacat gccggctcag agaatactat gaccagacag ctcagatgtg ctgcagcaaa 180
tgctcgccgg gccaacatgc aaaagtcttc tgtaccaaga cctcggacac cgtgtgtgac 240
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tgagcggccg c 2291

<210> 706
<211> 2264
<212> DNA
<213> Artificial Sequence

<220>
<223> Made in a lab

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gggagcacat gccggctcag agaatactat gaccagacag ctcagatgtg ctgcagcaaa 180
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tgcgcgccgc tgcgcaagtg ccgcccgggc ttcggcgtgg ccagaccagg aactgaaaca 480
tcagacgtgg tgtgcaagcc ctgtgccccg gggacgttct ccaacacgac ttcatccacg 540
gatatttgca ggccccacca gatctgtaac gtggtggcca tccctgggaa tgcaagcatg 600
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<210> 707
<211> 2300
<212> DNA
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 707
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accgtcctat gagcggccgc 2300

<210> 708
<211> 2378
<212> DNA
<213> Artificial Sequence

<220>
<223> Made in a lab

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ccattcattt tcggccctgg gaccaaagtg gatatcaaat gagcggccgc ctcgagtcta 2340
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<210> 709
<211> 2369
<212> DNA
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 709
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ttgcccgccc aggtggcatt tacaccctac gccccggagc ccgggagcac atgccggctc 180
agagaatact atgaccagac agctcagatg tgctgcagca aatgctcgcc gggccaacat 240
gcaaaagtct tctgtaccaa gacctcggac accgtgtgtg actcctgtga ggacagcaca 300

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gaccaggtgg aaactcaagc ctgcactcgg gaacagaacc gcatctgcac ctgcaggccc 420
ggctggtact gcgcgctgag caagcaggag gggtgccggc tgtgcgcgcc gctgcgcaag 480
tgccgcccgg gcttcggcgt ggccagacca ggaactgaaa catcagacgt ggtgtgcaag 540
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ctatagtgtc acctaaatgc tagagctcg 2369

<210> 710
<211> 2291
<212> DNA
<213> Artificial Sequence

<220>
<223> Made in a lab

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gtcataatgt cgcgaggatt gcccgcccag gtggcattta caccctacgc cccggagccc 120
gggagcacat gccggctcag agaatactat gaccagacag ctcagatgtg ctgcagcaaa 180
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gatatttgca ggccccacca gatctgtaac gtggtggcca tccctgggaa tgcaagcatg 600
gatgcagtct gcacgtccac gtcccccacc cggagtatgg ccccaggggc agtacactta 660
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ccaagcacct ccttcctgct cccaatgggc cccagccccc cagctgaagg gagcactggc 780
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tgagcggccg c 2291

<210> 711
<211> 2299
<212> DNA
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 711
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ggagcacatg ccggctcaga gaatactatg accagacagc tcagatgtgc tgcagcaaat 180
gctcgccggg ccaacatgca aaagtcttct gtaccaagac ctcggacacc gtgtgtgact 240
cctgtgagga cagcacatac acccagctct ggaactgggt tcccgagtgc ttgagctgtg 300
gctcccgctg tagctctgac caggtggaaa ctcaagcctg cactcgggaa cagaaccgca 360
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gcgcgccgct gcgcaagtgc cgcccgggct tcggcgtggc cagaccagga actgaaacat 480
cagacgtggt gtgcaagccc tgtgccccgg ggacgttctc caacacgact tcatccacgg 540
atatttgcag gccccaccag atctgtaacg tggtggccat ccctgggaat gcaagcatgg 600
atgcagtctg cacgtccacg tcccccaccc ggagtatggc cccaggggca gtacacttac 660
cccagccagt gtccacacga tcccaacaca cgcagccaac tccagaaccc agcactgctc 720
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acaccggtga gcccaaatct tctgacaaaa ctcacacatg cccaccgtgc ccagcacctg 840
aagccgcggg tgcaccgtca gtcttcctct tccccccaaa acccaaggac accctcatga 900
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cttactattg tcaacaggct aacagtttcc ctctcacttt cggcggaggg accaaggtgg 2280
agatcaaatg agcggccgc 2299

<210> 712
<211> 2362
<212> DNA
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 712
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aggtggcatt tacaccctac gccccggagc ccgggagcac atgccggctc agagaatact 180
atgaccagac agctcagatg tgctgcagca aatgctcgcc gggccaacat gcaaaagtct 240
tctgtaccaa gacctcggac accgtgtgtg actcctgtga ggacagcaca tacacccagc 300
tctggaactg ggttcccgag tgcttgagct gtggctcccg ctgtagctct gaccaggtgg 360
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gcgcgctgag caagcaggag gggtgccggc tgtgcgcgcc gctgcgcaag tgccgcccgg 480
gcttcggcgt ggccagacca ggaactgaaa catcagacgt ggtgtgcaag ccctgtgccc 540
cggggacgtt ctccaacacg acttcatcca cggatatttg caggccccac cagatctgta 600
acgtggtggc catccctggg aatgcaagca tggatgcagt ctgcacgtcc acgtccccca 660
cccggagtat ggccccaggg gcagtacact taccccagcc agtgtccaca cgatcccaac 720
acacgcagcc aactccagaa cccagcactg ctccaagcac ctccttcctg ctcccaatgg 780
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aacctgaaga ttttgcaact tactactgtc aacagagtta cagtaccccg tacacttttg 2280
gccaggggac caagctggag atcaaatgag cggccgcctc gagtctagag ggccctattc 2340
tatagtgtca cctaaatgct ag 2362

<210> 713
<211> 2294
<212> DNA
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 713
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gtcataatgt cgcgaggatt gcccgcccag gtggcattta caccctacgc cccggagccc 120
gggagcacat gccggctcag agaatactat gaccagacag ctcagatgtg ctgcagcaaa 180
tgctcgccgg gccaacatgc aaaagtcttc tgtaccaaga cctcggacac cgtgtgtgac 240
tcctgtgagg acagcacata cacccagctc tggaactggg ttcccgagtg cttgagctgt 300
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tcagacgtgg tgtgcaagcc ctgtgccccg gggacgttct ccaacacgac ttcatccacg 540
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aaatgagcgg ccgc 2294

<210> 714
<211> 2308
<212> DNA
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 714
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ggagcacatg ccggctcaga gaatactatg accagacagc tcagatgtgc tgcagcaaat 180
gctcgccggg ccaacatgca aaagtcttct gtaccaagac ctcggacacc gtgtgtgact 240
cctgtgagga cagcacatac acccagctct ggaactgggt tcccgagtgc ttgagctgtg 300
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cagacgtggt gtgcaagccc tgtgccccgg ggacgttctc caacacgact tcatccacgg 540
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atgcagtctg cacgtccacg tcccccaccc ggagtatggc cccaggggca gtacacttac 660
cccagccagt gtccacacga tcccaacaca cgcagccaac tccagaaccc agcactgctc 720
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ccaaggtgga gatcaaatga gcggccgc 2308

<210> 715
<211> 2288
<212> DNA

<213> Artificial Sequence

<220>
<223> Made in a lab

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gggagcacat gccggctcag agaatactat gaccagacag ctcagatgtg ctgcagcaaa 180
tgctcgccgg gccaacatgc aaaagtcttc tgtaccaaga cctcggacac cgtgtgtgac 240
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gatatttgca ggccccacca gatctgtaac gtggtggcca tccctgggaa tgcaagcatg 600
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gaagccgcgg gtgcaccgtc agtcttcctc ttcccccaa aacccaagga caccctcatg 900
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gcggccgc 2288

<210> 716
<211> 2282
<212> DNA
<213> Artificial Sequence

<220>
<223> Made in a lab

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gtcataatgt cgcgaggatt gcccgcccag gtggcattta caccctacgc cccggagccc 120

gggagcacat gccggctcag agaatactat gaccagacag ctcagatgtg ctgcagcaaa 180
tgctcgccgg gccaacatgc aaaagtcttc tgtaccaaga cctcggacac cgtgtgtgac 240
tcctgtgagg acagcacata cacccagctc tggaactggg ttcccgagtg cttgagctgt 300
ggctcccgct gtagctctga ccaggtggaa actcaagcct gcactcggga acagaaccgc 360
atctgcacct gcaggcccgg ctggtactgc gcgctgagca agcaggaggg gtgccggctg 420
tgcgcgccgc tgcgcaagtg ccgcccgggc ttcggcgtgg ccagaccagg aactgaaaca 480
tcagacgtgg tgtgcaagcc ctgtgccccg gggacgttct ccaacacgac ttcatccacg 540
gatatttgca ggccccacca gatctgtaac gtggtggcca tccctgggaa tgcaagcatg 600
gatgcagtct gcacgtccac gtcccccacc cggagtatgg ccccaggggc agtacactta 660
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gaagccgcgg gtgcaccgtc agtcttcctc ttcccccaa aacccaagga caccctcatg 900
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gctaacagtt ttccgatcac tttcggcgga gggaccaaag tggagatcaa ctgagcggcc 2280
gc 2282

<210> 717
<211> 2285
<212> DNA
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 717
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gggagcacat gccggctcag agaatactat gaccagacag ctcagatgtg ctgcagcaaa 180
tgctcgccgg gccaacatgc aaaagtcttc tgtaccaaga cctcggacac cgtgtgtgac 240
tcctgtgagg acagcacata cacccagctc tggaactggg ttcccgagtg cttgagctgt 300
ggctcccgct gtagctctga ccaggtggaa actcaagcct gcactcggga acagaaccgc 360
atctgcacct gcaggcccgg ctggtactgc gcgctgagca agcaggaggg gtgccggctg 420
tgcgcgccgc tgcgcaagtg ccgcccgggc ttcggcgtgg ccagaccagg aactgaaaca 480
tcagacgtgg tgtgcaagcc ctgtgccccg gggacgttct ccaacacgac ttcatccacg 540
gatatttgca ggccccacca gatctgtaac gtggtggcca tccctgggaa tgcaagcatg 600

gatgcagtct gcacgtccac gtcccccacc cggagtatgg ccccaggggc agtacactta 660
ccccagccag tgtccacacg atcccaacac acgcagccaa ctccagaacc cagcactgct 720
ccaagcacct ccttcctgct cccaatgggc cccagccccc cagctgaagg gagcactggc 780
gacaccggtg agcccaaatc ttctgacaaa actcacacat gcccaccgtg cccagcacct 840
gaagccgcgg gtgcaccgtc agtcttcctc ttcccccaa aacccaagga caccctcatg 900
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gattttactt tcaccatcac tagcctgcag cctgaagatt ttggaacata ttactgtcaa 2220
cagtatgata ctttacatcc ctctttcggc cctgggacca cagtggatat caaatgagcg 2280
gccgc 2285

<210> 718
<211> 2300
<212> DNA
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 718
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gtcataatgt cgcgaggatt gcccgcccag gtggcattta caccctacgc cccggagccc 120
gggagcacat gccggctcag agaatactat gaccagacag ctcagatgtg ctgcagcaaa 180
tgctcgccgg gccaacatgc aaaagtcttc tgtaccaaga cctcggacac cgtgtgtgac 240
tcctgtgagg acagcacata cacccagctc tggaactggg ttcccgagtg cttgagctgt 300
ggctcccgct gtagctctga ccaggtggaa actcaagcct gcactcggga acagaaccgc 360
atctgcacct gcaggcccgg ctggtactgc gcgctgagca agcaggaggg gtgccggctg 420
tgcgcgccgc tgcgcaagtg ccgcccgggc ttcggcgtgg ccagaccagg aactgaaaca 480
tcagacgtgg tgtgcaagcc ctgtgccccg gggacgttct ccaacacgac ttcatccacg 540
gatatttgca ggccccacca gatctgtaac gtggtggcca tccctgggaa tgcaagcatg 600
gatgcagtct gcacgtccac gtcccccacc cggagtatgg ccccaggggc agtacactta 660
ccccagccag tgtccacacg atcccaacac acgcagccaa ctccagaacc cagcactgct 720
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gaagccgcgg gtgcaccgtc agtcttcctc ttcccccaa aacccaagga caccctcatg 900
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accgtcctat gagcggccgc 2300

<210> 719
<211> 2282
<212> DNA
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 719
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gtcataatgt cgcgaggatt gcccgcccag gtggcattta caccctacgc cccggagccc 120
gggagcacat gccggctcag agaatactat gaccagacag ctcagatgtg ctgcagcaaa 180
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ggctcccgct gtagctctga ccaggtggaa actcaagcct gcactcggga acagaaccgc 360
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tcagacgtgg tgtgcaagcc ctgtgccccg gggacgttct ccaacacgac ttcatccacg 540
gatatttgca ggccccacca gatctgtaac gtggtggcca tccctgggaa tgcaagcatg 600
gatgcagtct gcacgtccac gtcccccacc cggagtatgg ccccaggggc agtacactta 660
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gc 2282

<210> 720
<211> 2294
<212> DNA
<213> Artificial Sequence

<220>
<223> Made in a lab

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gggagcacat gccggctcag agaatactat gaccagacag ctcagatgtg ctgcagcaaa 180
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tcctgtgagg acagcacata cacccagctc tggaactggg ttcccgagtg cttgagctgt 300
ggctcccgct gtagctctga ccaggtggaa actcaagcct gcactcggga acagaaccgc 360
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gatatttgca ggccccacca gatctgtaac gtggtggcca tccctgggaa tgcaagcatg 600
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ctatgagcgg ccgc 2294

<210> 721
<211> 2279
<212> DNA
<213> Artificial Sequence

<220>
<223> Made in a lab

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gggagcacat gccggctcag agaatactat gaccagacag ctcagatgtg ctgcagcaaa 180
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<210> 722
<211> 2285
<212> DNA

<213> Artificial Sequence

<220>
<223> Made in a lab

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gggagcacat gccggctcag agaatactat gaccagacag ctcagatgtg ctgcagcaaa 180
tgctcgccgg gccaacatgc aaaagtcttc tgtaccaaga cctcggacac cgtgtgtgac 240
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gatatttgca ggccccacca gatctgtaac gtggtggcca tccctgggaa tgcaagcatg 600
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gccgc 2285

<210> 723
<211> 2285
<212> DNA
<213> Artificial Sequence

<220>
<223> Made in a lab

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gggagcacat gccggctcag agaatactat gaccagacag ctcagatgtg ctgcagcaaa 180
tgctcgccgg gccaacatgc aaaagtcttc tgtaccaaga cctcggacac cgtgtgtgac 240
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tcagacgtgg tgtgcaagcc ctgtgccccg gggacgttct ccaacacgac ttcatccacg 540
gatatttgca ggccccacca gatctgtaac gtggtggcca tccctgggaa tgcaagcatg 600
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gccgc 2285

<210> 724
<211> 2306
<212> DNA
<213> Artificial Sequence

<220>
<223> Made in a lab

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tcagacgtgg tgtgcaagcc ctgtgccccg gggacgttct ccaacacgac ttcatccacg 540
gatatttgca ggccccacca gatctgtaac gtggtggcca tccctgggaa tgcaagcatg 600

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agggtggaaa tcaaatgagc ggccgc 2306

<210> 725
<211> 2383
<212> DNA
<213> Artificial Sequence

<220>
<223> Made in a lab

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agagaatact atgaccagac agctcagatg tgctgcagca aatgctcgcc gggccaacat 240
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ggctggtact gcgcgctgag caagcaggag gggtgccggc tgtgcgcgcc gctgcgcaag 480
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<210> 726
<211> 2412
<212> DNA
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 726
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<211> 2288
<212> DNA
<213> Artificial Sequence

<220>
<223> Made in a lab

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<210> 728
<211> 2279
<212> DNA
<213> Artificial Sequence

<220>
<223> Made in a lab

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<210> 729
<211> 2409
<212> DNA
<213> Artificial Sequence

<220>
<223> Made in a lab

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acatgccggc tcagagaata ctatgaccag acagctcaga tgtgctgcag caaatgctcg 240
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gaggacagca catacaccca gctctggaac tgggttcccg agtgcttgag ctgtggctcc 360
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<210> 730
<211> 2297
<212> DNA
<213> Artificial Sequence

<220>

<223> Made in a lab

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<210> 731
<211> 2303
<212> DNA
<213> Artificial Sequence

<220>
<223> Made in a lab

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gagtgggttt cttctatcgt tccttctggt ggccttactc gttatgctga ctccgttaaa 1740
ggtcgcttca ctatctctag agacaactct aagaatactc tctacttgca gatgaacagc 1800
ttaagggctg aggacacagc cacatattac tgtgcgagac tcgcgtatta cgatttttgg 1860
agtggtcgtg atgctttga tatctggggc caagggacaa tggtcaccgt ctcaagcggt 1920
ggcggcggtt cgggggtgg cggaagtgga ggtggaggga gtcagagcgt cttgactcag 1980
cctgcctccg tgtctgggtc tcctggacag tcgatcacca tctcctgcag tggaagcagc 2040
agtgacgttg gtcattatga ctatgtctcc tggtaccaac agcacccagg caaggccccc 2100
aaactcatga tttatgatgt cagtaatcgg ccctcagggg tttctaatcg cttctctggc 2160
tccaagtctg gcaacacggc ctccctgacc atctctgggc tccaggctga cgacgaggct 2220
gagtattact gcagctcata tacaagcagc ggcactcgag tcttcggaac tgggaccaag 2280
gtcaccgtcc tatgagcggc cgc 2303

<210> 732
<211> 2326
<212> DNA
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 732
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gggagcacat gccggctcag agaatactat gaccagacag ctcagatgtg ctgcagcaaa 180
tgctcgccgg gccaacatgc aaaagtcttc tgtaccaaga cctcggacac cgtgtgtgac 240
tcctgtgagg acagcacata cacccagctc tggaactggg ttcccgagtg cttgagctgt 300
ggctcccgct gtagctctga ccaggtggaa actcaagcct gcactcggga acagaaccgc 360
atctgcacct gcaggcccgg ctggtactgc gcgctgagca agcaggaggg gtgccggctg 420
tgcgcgccgc tgcgcaagtg ccgcccgggc ttcggcgtgg ccagaccagg aactgaaaca 480
tcagacgtgg tgtgcaagcc ctgtgccccg gggacgttct ccaacacgac ttcatccacg 540
gatatttgca ggccccacca gatctgtaac gtggtggcca tccctgggaa tgcaagcatg 600
gatgcagtct gcacgtccac gtcccccacc cggagtatgg ccccaggggc agtacactta 660
ccccagccag tgtccacacg atcccaacac acgcagccaa ctccagaacc cagcactgct 720
ccaagcacct ccttcctgct cccaatgggc cccagccccc cagctgaagg gagcactggc 780

gacaccggtg agcccaaatc ttctgacaaa actcacacat gcccaccgtg cccagcacct 840
gaagccgcgg gtgcaccgtc agtcttcctc ttcccccaa aacccaagga caccctcatg 900
atctcccgga cccctgaggt cacatgcgtg gtggtggacg tgagccacga agaccctgag 960
gtcaagttca actggtacgt ggacggcgtg gaggtgcata atgccaagac aaagccgcgg 1020
gaggagcagt acaacagcac gtaccgtgtg gtcagcgtcc tcaccgtcct gcaccaggac 1080
tggctgaatg gcaaggcgta cgcgtgcgcg gtctccaaca aagccctccc agcccccatc 1140
gagaaaacca tctccaaagc caaagggcag ccccgagaac cacaggtgta caccctgccc 1200
ccatcccggg atgagctgac caagaaccag gtcagcctga cctgcctggt caaaggcttc 1260
tatccaagcg acatcgccgt ggagtgggag agcaatgggc agccggagaa caactacaag 1320
accacgcctc ccgtgctgga ctccgacggc tccttcttcc tctacagcaa gctcaccgtg 1380
gacaagagca ggtggcagca ggggaacgtc ttctcatgct ccgtgatgca tgaggctctg 1440
cacaaccact acacgcagaa gagcctctcc ctgtctccgg gtcagaggca caacaattct 1500
tccctgaata caagaactca gaaagcacgt cattctccga attctgaagt tcaattgtta 1560
gagtctggtg gcggtcttgt tcagcctggt ggttctttac gtctttcttg cgctgcttcc 1620
ggattcactt tctctcatta cggtatggat tgggttcgcc aagctcctgg taaaggtttg 1680
gagtgggttt cttctatcta ttcttctggt ggctatactc tttatgctga ctccgttaaa 1740
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ttaagggctg aggacacagc cacatattac tgtgccacta gaacgtgggc ggatgctttt 1860
gatgtctggg gccaagggac cacggtcacc gtctcaagcg gtggcggcgg ttcgggggt 1920
ggcggaagtg gaggtggagg gagtcaagac atccagatga cccagtctcc ctccaccttg 1980
tctgcatctg tgggagacag agtcactttc acttgccggg ccagtcagag tgtcaacaac 2040
tgggtggcct ggtatcagca gaaaccaggg aaagccccta agctcctgat ctatgctgca 2100
tccagtttgc aaagtggggt cccatcaagg ttcagtggca gtggatctgg gacagatttc 2160
actctcacca tcagcagtct gcaacctgaa gattttgcaa cttactactg tcaacagagt 2220
tacagtatgc cgctcacttt cggcggaggg accaaggtgg agatcaaatg agcggccgcc 2280
tcgagtctag agggccctat tctatagtgt cacctaaatg ctagag 2326

<210> 733
<211> 2280
<212> DNA
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 733
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gtcataatgt cgcgaggaga agttcaattg ttagagtctg gtggcggtct tgttcagcct 120
ggtggttctt tacgtctttc ttgcgctgct tccggattca ctttctctca ttacatgatg 180
gcttgggttc gccaagctcc tggtaaaggt ttggagtggg tttcttatat ctatccttct 240
ggtggctgga cttcttatgc tgactccgtt aaaggtcgct tcactatctc tagagacaac 300
tctaagaata ctctctactt gcagatgaac agcttaaggg ctgaggacac ggccgtgtat 360
tactgtgcga gattcgacta tactataggt tttgacttct ggggccaggg aaccctggtc 420
accgtctcaa gcggtggcgg cggttcgggg ggtggcggaa gtggaggtgg agggagtcaa 480
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 540
atcacttgcc gggcaagtca gagcattagc agctatttaa attggtatca gcagaaacca 600
gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 660
aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 720
gaagattttg caacttacta ctgtcaacag agttacagta cccctcggac gttcggccaa 780
gggaccaagg tggaaatcaa aaccggtgag cccaaatctt ctgacaaaac tcacacatgc 840
ccaccgtgcc cagcacctga agccgcgggt gcaccgtcag tcttcctctt ccccccaaaa 900
cccaaggaca ccctcatgat ctcccggacc cctgaggtca catgcgtggt ggtggacgtg 960
agccacgaag accctgaggt caagttcaac tggtacgtgg acggcgtgga ggtgcataat 1020
gccaagacaa agccgcggga ggagcagtac aacagcacgt accgtgtggt cagcgtcctc 1080
accgtcctgc accaggactg gctgaatggc aaggcgtacg cgtgcgcggt ctccaacaaa 1140
gccctcccag cccccatcga gaaaaccatc tccaaagcca aagggcagcc ccgagaacca 1200
caggtgtaca ccctgccccc atcccgggat gagctgacca agaaccaggt cagcctgacc 1260

tgcctggtca aaggcttcta tccaagcgac atcgccgtgg agtgggagag caatgggcag 1320
ccggagaaca actacaagac cacgcctccc gtgctggact ccgacggctc cttcttcctc 1380
tacagcaagc tcaccgtgga caagagcagg tggcagcagg ggaacgtctt ctcatgctcc 1440
gtgatgcatg aggctctgca caaccactac acgcagaaga gcctctccct gtctccgggt 1500
cagaggcaca acaattcttc cctgaataca agaactcaga aagcacgtca ttctccgaat 1560
tctttgcccg cccaggtggc atttacaccc tacgccccgg agcccgggag cacatgccgg 1620
ctcagagaat actatgacca gacagctcag atgtgctgca gcaaatgctc gccgggccaa 1680
catgcaaaag tcttctgtac caagacctcg gacaccgtgt gtgactcctg tgaggacagc 1740
acatacaccc agctctggaa ctgggttccc gagtgcttga gctgtggctc ccgctgtagc 1800
tctgaccagg tggaaactca agcctgcact cgggaacaga accgcatctg cacctgcagg 1860
cccggctggt actgcgcgct gagcaagcag gaggggtgcc ggctgtgcgc gccgctgcgc 1920
aagtgccgcc cgggcttcgg cgtggccaga ccaggaactg aaacatcaga cgtggtgtgc 1980
aagccctgtg ccccggggac gttctccaac acgacttcat ccacggatat ttgcaggccc 2040
caccagatct gtaacgtggt ggccatccct gggaatgcaa gcatggatgc agtctgcacg 2100
tccacgtccc ccacccggag tatggcccca ggggcagtac acttacccca gccagtgtcc 2160
acacgatccc aacacacgca gccaactcca gaacccagca ctgctccaag cacctccttc 2220
ctgctcccaa tgggccccag ccccccagct gaagggagca ctggcgactg agcggccgcc 2280

<210> 734
<211> 2300
<212> DNA
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 734
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ggtggttctt tacgtctttc ctgcgctgct tccggattca ctttctcttg gtaccttatg 180
cattgggttc gccaagctcc tggtaaaggt ttggagtggg tttctggtat ctggccttct 240
ggtggccata ctctttatgc tgactccgtt aaaggtcgct tcactatctc tagagacaac 300
tctaagaata ctctctactt gcagatgaac agcttaaggg ctgaggacac ggccgtgtat 360
tactgtgcga gagagccgtt actatggttc ggggagttat cgtacaactg gttcgacccc 420
tggggccagg gcaccctggt caccgtctca agcggtggcg gcggttcggg gggtggcgga 480
agtggaggtg gagggagtca agacatccag atgacccagt ctccatcttc cgtgtctgca 540
tctgtaggag acagagtcac catcacttgt cgggcgagtc agggtattag cagctggtta 600
gcctggtatc agcagaaacc agggaaagcc cctaagctcc tgatctatgc tgcatccagt 660
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accatcagca gcctgcagcc tgaagatttt gcaacttact attgtcaaca ggctaacagt 780
ttccctctca ctttcggcgg agggaccaag gtggagatca aaaccggtga gcccaaatct 840
tctgacaaaa ctcacacatg cccaccgtgc ccagcacctg aagccgcggg tgcaccgtca 900
gtcttcctct tccccccaaa acccaaggac accctcatga tctcccggac ccctgaggtc 960
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gacggcgtgg aggtgcataa tgccaagaca aagccgcggg aggagcagta caacagcacg 1080
taccgtgtgg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggcgtac 1140
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aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccggga tgagctgacc 1260
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gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac 1380
tccgacggct ccttcttcct ctacagcaag ctcaccgtgg acaagagcag gtggcagcag 1440
gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag 1500
agcctctccc tgtctccggg tcagaggcac aacaattctt ccctgaatac aagaactcag 1560
aaagcacgtc attctccgaa ttctttgccc gcccaggtgg catttacacc ctacgccccg 1620
gagcccggga gcacatgccg gctcagagaa tactatgacc agacagctca gatgtgctgc 1680
agcaaatgct cgccgggcca acatgcaaaa gtcttctgta ccaagacctc ggacaccgtg 1740
tgtgactcct gtgaggacag cacatacacc cagctctgga actgggttcc cgagtgcttg 1800

agctgtggct cccgctgtag ctctgaccag gtggaaactc aagcctgcac tcgggaacag 1860
aaccgcatct gcacctgcag gcccggctgg tactgcgcgc tgagcaagca ggaggggtgc 1920
cggctgtgcg cgccgctgcg caagtgccgc ccgggcttcg gcgtggccag accaggaact 1980
gaaacatcag acgtggtgtg caagccctgt gccccgggga cgttctccaa cacgacttca 2040
tccacggata tttgcaggcc ccaccagatc tgtaacgtgg tggccatccc tgggaatgca 2100
agcatggatg cagtctgcac gtccacgtcc cccacccgga gtatggcccc aggggcagta 2160
cacttacccc agccagtgtc cacacgatcc caacacacgc agccaactcc agaacccagc 2220
actgctccaa gcacctcctt cctgctccca atgggcccca gccccccagc tgaagggagc 2280
actggcgact gagcggccgc 2300

<210> 735
<211> 693
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 735
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
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Val Ile Met Ser Arg Gly Glu Val Gln Leu Leu Glu Ser Gly Gly Gly
            20   25   30
Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly
        35   40   45
Phe Thr Phe Ser Trp Tyr Leu Met His Trp Val Arg Gln Ala Pro Gly
    50   55   60
Lys Gly Leu Glu Trp Val Ser Gly Ile Trp Pro Ser Gly Gly His Thr
65   70   75   80
Leu Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn
                85   90   95
Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
            100   105   110
Thr Ala Val Tyr Tyr Cys Ala Arg Glu Pro Leu Leu Trp Phe Gly Glu
        115   120   125
Leu Ser Tyr Asn Trp Phe Asp Pro Trp Gly Gln Gly Thr Leu Val Thr
    130   135   140
Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
145   150   155   160
Gly Ser Gln Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Val Ser Ala
                165   170   175
Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile
            180   185   190
Ser Ser Trp Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys
        195   200   205
Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg
    210   215   220
Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser
225   230   235   240
Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ala Asn Ser
                245   250   255
Phe Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Thr Gly
            260   265   270
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
        275   280   285
Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
    290   295   300

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Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
305                 310                 315                 320
Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
                325                 330                 335
Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
            340                 345                 350
Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
        355                 360                 365
Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala
    370                 375                 380
Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
385                 390                 395                 400
Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
                405                 410                 415
Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
            420                 425                 430
Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
        435                 440                 445
Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
    450                 455                 460
Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
465                 470                 475                 480
Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
                485                 490                 495
Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser Ser Leu Asn
            500                 505                 510
Thr Arg Thr Gln Lys Ala Arg His Ser Pro Asn Ser Thr Ile Pro Pro
        515                 520                 525
His Val Gln Lys Ser Asp Val Glu Met Glu Ala Gln Lys Asp Glu Ile
    530                 535                 540
Ile Cys Pro Ser Cys Asn Arg Thr Ala His Pro Leu Arg His Ile Asn
545                 550                 555                 560
Asn Asp Met Ile Val Thr Asp Asn Asn Gly Ala Val Lys Phe Pro Gln
                565                 570                 575
Leu Cys Lys Phe Cys Asp Val Arg Phe Ser Thr Cys Asp Asn Gln Lys
            580                 585                 590
Ser Cys Met Ser Asn Cys Ser Ile Thr Ser Ile Cys Glu Lys Pro Gln
        595                 600                 605
Glu Val Cys Val Ala Val Trp Arg Lys Asn Asp Glu Asn Ile Thr Leu
    610                 615                 620
Glu Thr Val Cys His Asp Pro Lys Leu Pro Tyr His Asp Phe Ile Leu
625                 630                 635                 640
Glu Asp Ala Ala Ser Pro Lys Cys Ile Met Lys Glu Lys Lys Lys Pro
                645                 650                 655
Gly Glu Thr Phe Phe Met Cys Ser Cys Ser Ser Asp Glu Cys Asn Asp
            660                 665                 670
Asn Ile Ile Phe Ser Glu Glu Tyr Asn Thr Ser Asn Pro Asp Leu Leu
        675                 680                 685
Leu Val Ile Phe Gln
    690

<210> 736
<211> 668
<212> PRT
<213> Artificial Sequence

<220>
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<223> Made in a lab

<400> 736
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1   5   10   15
Val Ile Met Ser Arg Gly Glu Val Gln Leu Leu Glu Ser Gly Gly Gly
            20   25   30
Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly
        35   40   45
Phe Thr Phe Ser Trp Tyr Leu Met His Trp Val Arg Gln Ala Pro Gly
    50   55   60
Lys Gly Leu Glu Trp Val Ser Gly Ile Trp Pro Ser Gly Gly His Thr
65   70   75   80
Leu Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn
                85   90   95
Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
            100   105   110
Thr Ala Val Tyr Tyr Cys Ala Arg Glu Pro Leu Leu Trp Phe Gly Glu
        115   120   125
Leu Ser Tyr Asn Trp Phe Asp Pro Trp Gly Gln Gly Thr Leu Val Thr
    130   135   140
Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
145   150   155   160
Gly Ser Gln Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Val Ser Ala
                165   170   175
Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile
            180   185   190
Ser Ser Trp Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys
        195   200   205
Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg
    210   215   220
Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser
225   230   235   240
Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ala Asn Ser
                245   250   255
Phe Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Thr Gly
            260   265   270
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
        275   280   285
Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
    290   295   300
Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
305   310   315   320
Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
                325   330   335
Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
            340   345   350
Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
        355   360   365
Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala
    370   375   380
Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
385   390   395   400
Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
                405   410   415
Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

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            420                 425                 430
Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
        435                 440                 445
Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
    450                 455                 460
Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
465                 470                 475                 480
Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
                485                 490                 495
Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser Ser Leu Asn
            500                 505                 510
Thr Arg Thr Gln Lys Ala Arg His Ser Pro Asn Ser Thr Ile Pro Pro
        515                 520                 525
His Val Gln Lys Ser Val Asn Asn Asp Met Ile Val Thr Asp Asn Asn
    530                 535                 540
Gly Ala Val Lys Phe Pro Gln Leu Cys Lys Phe Cys Asp Val Arg Phe
545                 550                 555                 560
Ser Thr Cys Asp Asn Gln Lys Ser Cys Met Ser Asn Cys Ser Ile Thr
                565                 570                 575
Ser Ile Cys Glu Lys Pro Gln Glu Val Cys Val Ala Val Trp Arg Lys
            580                 585                 590
Asn Asp Glu Asn Ile Thr Leu Glu Thr Val Cys His Asp Pro Lys Leu
        595                 600                 605
Pro Tyr His Asp Phe Ile Leu Glu Asp Ala Ala Ser Pro Lys Cys Ile
    610                 615                 620
Met Lys Glu Lys Lys Lys Pro Gly Glu Thr Phe Phe Met Cys Ser Cys
625                 630                 635                 640
Ser Ser Asp Glu Cys Asn Asp Asn Ile Ile Phe Ser Glu Glu Tyr Asn
                645                 650                 655
Thr Ser Asn Pro Asp Leu Leu Leu Val Ile Phe Gln
            660                 665
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<210> 737
<211> 693
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 737

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Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1               5                  10                  15
Val Ile Met Ser Arg Gly Thr Ile Pro Pro His Val Gln Lys Ser Asp
            20                  25                  30
Val Glu Met Glu Ala Gln Lys Asp Glu Ile Ile Cys Pro Ser Cys Asn
        35                  40                  45
Arg Thr Ala His Pro Leu Arg His Ile Asn Asn Asp Met Ile Val Thr
    50                  55                  60
Asp Asn Asn Gly Ala Val Lys Phe Pro Gln Leu Cys Lys Phe Cys Asp
65                  70                  75                  80
Val Arg Phe Ser Thr Cys Asp Asn Gln Lys Ser Cys Met Ser Asn Cys
                85                  90                  95
Ser Ile Thr Ser Ile Cys Glu Lys Pro Gln Glu Val Cys Val Ala Val
            100                 105                 110
Trp Arg Lys Asn Asp Glu Asn Ile Thr Leu Glu Thr Val Cys His Asp
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        115                 120                 125
Pro Lys Leu Pro Tyr His Asp Phe Ile Leu Glu Asp Ala Ala Ser Pro
    130                 135                 140
Lys Cys Ile Met Lys Glu Lys Lys Lys Pro Gly Glu Thr Phe Phe Met
145                 150                 155                 160
Cys Ser Cys Ser Ser Asp Glu Cys Asn Asp Asn Ile Ile Phe Ser Glu
                165                 170                 175
Glu Tyr Asn Thr Ser Asn Pro Asp Leu Leu Leu Val Ile Phe Gln Thr
            180                 185                 190
Gly Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro
        195                 200                 205
Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys
    210                 215                 220
Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
225                 230                 235                 240
Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
                245                 250                 255
Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
            260                 265                 270
Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
        275                 280                 285
Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys
    290                 295                 300
Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
305                 310                 315                 320
Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
                325                 330                 335
Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
            340                 345                 350
Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
        355                 360                 365
Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
    370                 375                 380
Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
385                 390                 395                 400
Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
                405                 410                 415
Lys Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser Ser Leu
            420                 425                 430
Asn Thr Arg Thr Gln Lys Ala Arg His Ser Pro Asn Ser Glu Val Gln
        435                 440                 445
Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg
    450                 455                 460
Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Trp Tyr Leu Met His
465                 470                 475                 480
Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Gly Ile
                485                 490                 495
Trp Pro Ser Gly Gly His Thr Leu Tyr Ala Asp Ser Val Lys Gly Arg
            500                 505                 510
Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met
        515                 520                 525
Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Glu
    530                 535                 540
Pro Leu Leu Trp Phe Gly Glu Leu Ser Tyr Asn Trp Phe Asp Pro Trp
545                 550                 555                 560
Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
                565                 570                 575
```

```
Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Asp Ile Gln Met Thr Gln
            580                 585                 590
Ser Pro Ser Ser Val Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr
        595                 600                 605
Cys Arg Ala Ser Gln Gly Ile Ser Ser Trp Leu Ala Trp Tyr Gln Gln
    610                 615                 620
Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu
625                 630                 635                 640
Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
                645                 650                 655
Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr
            660                 665                 670
Tyr Cys Gln Gln Ala Asn Ser Phe Pro Leu Thr Phe Gly Gly Gly Thr
        675                 680                 685
Lys Val Glu Ile Lys
    690
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<210> 738
<211> 668
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 738

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Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1                5                  10                  15
Val Ile Met Ser Arg Gly Thr Ile Pro Pro His Val Gln Lys Ser Val
            20                  25                  30
Asn Asn Asp Met Ile Val Thr Asp Asn Asn Gly Ala Val Lys Phe Pro
        35                  40                  45
Gln Leu Cys Lys Phe Cys Asp Val Arg Phe Ser Thr Cys Asp Asn Gln
    50                  55                  60
Lys Ser Cys Met Ser Asn Cys Ser Ile Thr Ser Ile Cys Glu Lys Pro
65                  70                  75                  80
Gln Glu Val Cys Val Ala Val Trp Arg Lys Asn Asp Glu Asn Ile Thr
                85                  90                  95
Leu Glu Thr Val Cys His Asp Pro Lys Leu Pro Tyr His Asp Phe Ile
            100                 105                 110
Leu Glu Asp Ala Ala Ser Pro Lys Cys Ile Met Lys Glu Lys Lys Lys
        115                 120                 125
Pro Gly Glu Thr Phe Phe Met Cys Ser Cys Ser Ser Asp Glu Cys Asn
    130                 135                 140
Asp Asn Ile Ile Phe Ser Glu Glu Tyr Asn Thr Ser Asn Pro Asp Leu
145                 150                 155                 160
Leu Leu Val Ile Phe Gln Thr Gly Glu Pro Lys Ser Ser Asp Lys Thr
                165                 170                 175
His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser
            180                 185                 190
Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
        195                 200                 205
Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
    210                 215                 220
Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
225                 230                 235                 240
```

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Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
                245                 250                 255
Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Ala Tyr
            260                 265                 270
Ala Cys Ala Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
        275                 280                 285
Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
    290                 295                 300
Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
305                 310                 315                 320
Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
                325                 330                 335
Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
            340                 345                 350
Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
        355                 360                 365
Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
    370                 375                 380
Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gln
385                 390                 395                 400
Arg His Asn Asn Ser Ser Leu Asn Thr Arg Thr Gln Lys Ala Arg His
                405                 410                 415
Ser Pro Asn Ser Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val
            420                 425                 430
Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr
        435                 440                 445
Phe Ser Trp Tyr Leu Met His Trp Val Arg Gln Ala Pro Gly Lys Gly
    450                 455                 460
Leu Glu Trp Val Ser Gly Ile Trp Pro Ser Gly Gly His Thr Leu Tyr
465                 470                 475                 480
Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys
                485                 490                 495
Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala
            500                 505                 510
Val Tyr Tyr Cys Ala Arg Glu Pro Leu Leu Trp Phe Gly Glu Leu Ser
        515                 520                 525
Tyr Asn Trp Phe Asp Pro Trp Gly Gln Gly Thr Leu Val Thr Val Ser
    530                 535                 540
Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
545                 550                 555                 560
Gln Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val
                565                 570                 575
Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Ser
            580                 585                 590
Trp Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu
        595                 600                 605
Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser
    610                 615                 620
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln
625                 630                 635                 640
Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ala Asn Ser Phe Pro
                645                 650                 655
Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            660                 665
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<210> 739
<211> 2102

<212> DNA
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 739
aagcttgccg ccatggattt tcaagtgcag attttcagct tcctgctaat cagtgcttca 60
gtcataatgt cgcgaggaga agttcaattg ttagagtctg gtggcggtct tgttcagcct 120
ggtggttctt tacgtctttc ctgcgctgct tccggattca ctttctcttg gtaccttatg 180
cattgggttc gccaagctcc tggtaaaggt ttggagtggg tttctggtat ctggccttct 240
ggtggccata ctctttatgc tgactccgtt aaaggtcgct tcactatctc tagagacaac 300
tctaagaata ctctctactt gcagatgaac agcttaaggg ctgaggacac ggccgtgtat 360
tactgtgcga gagagccgtt actatggttc ggggagttat cgtacaactg gttcgacccc 420
tggggccagg gcaccctggt caccgtctca agcggtggcg gcggttcggg gggtggcgga 480
agtggaggtg gagggagtca agacatccag atgacccagt ctccatcttc cgtgtctgca 540
tctgtaggag acagagtcac catcacttgt cgggcgagtc agggtattag cagctggtta 600
gcctggtatc agcagaaacc agggaaagcc cctaagctcc tgatctatgc tgcatccagt 660
ttgcaaagtg gggtcccatc aaggttcagc ggcagtggat ctgggacaga tttcactctc 720
accatcagca gcctgcagcc tgaagatttt gcaacttact attgtcaaca ggctaacagt 780
ttccctctca ctttcggcgg agggaccaag gtggagatca aaaccggtga gcccaaatct 840
tctgacaaaa ctcacacatg cccaccgtgc ccagcacctg aagccgcggg tgcaccgtca 900
gtcttcctct tccccccaaa acccaaggac accctcatga tctcccggac ccctgaggtc 960
acatgcgtgg tggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg 1020
gacggcgtgg aggtgcataa tgccaagaca aagccgcggg aggagcagta caacagcacg 1080
taccgtgtgg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggcgtac 1140
gcgtgcgcgg tctccaacaa agccctccca gcccccatcg agaaaaccat ctccaaagcc 1200
aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccggga tgagctgacc 1260
aagaaccagg tcagcctgac ctgcctggtc aaaggcttct atccaagcga catcgccgtg 1320
gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac 1380
tccgacggct ccttcttcct ctacagcaag ctcaccgtgg acaagagcag gtggcagcag 1440
gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag 1500
agcctctccc tgtctccggg tcagaggcac aacaattctt ccctgaatac aagaactcag 1560
aaagcacgtc attctccgaa ttctacgatc ccaccgcacg ttcagaagtc ggatgtggaa 1620
atggaggccc agaaagatga aatcatctgc cccagctgta ataggactgc ccatccactg 1680
agacatatta ataacgacat gatagtcact gacaacaacg gtgcagtcaa gtttccacaa 1740
ctgtgtaaat tttgtgatgt gagattttcc acctgtgaca accagaaatc ctgcatgagc 1800
aactgcagca tcacctccat ctgtgagaag ccacaggaag tctgtgtggc tgtatggaga 1860
aagaatgacg agaacataac actagagaca gtttgccatg accccaagct cccctaccat 1920
gactttattc tggaagatgc tgcttctcca aagtgcatta tgaaggaaaa aaaaaagcct 1980
ggtgagactt tcttcatgtg ttcctgtagc tctgatgagt gcaatgacaa catcatcttc 2040
tcagaagaat ataacaccag caatcctgac ttgttgctag tcatatttca atgagcggcc 2100
gc 2102

<210> 740
<211> 2027
<212> DNA
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 740
aagcttgccg ccatggattt tcaagtgcag attttcagct tcctgctaat cagtgcttca 60
gtcataatgt cgcgaggaga agttcaattg ttagagtctg gtggcggtct tgttcagcct 120

ggtggttctt tacgtctttc ctgcgctgct tccggattca ctttctcttg gtaccttatg 180
cattgggttc gccaagctcc tggtaaaggt ttggagtggg tttctggtat ctggccttct 240
ggtggccata ctctttatgc tgactccgtt aaaggtcgct tcactatctc tagagacaac 300
tctaagaata ctctctactt gcagatgaac agcttaaggg ctgaggacac ggccgtgtat 360
tactgtgcga gagagccgtt actatggttc ggggagttat cgtacaactg gttcgacccc 420
tggggccagg gcaccctggt caccgtctca agcggtggcg gcggttcggg gggtggcgga 480
agtggaggtg gagggagtca agacatccag atgacccagt ctccatcttc cgtgtctgca 540
tctgtaggag acagagtcac catcacttgt cgggcgagtc agggtattag cagctggtta 600
gcctggtatc agcagaaacc agggaaagcc cctaagctcc tgatctatgc tgcatccagt 660
ttgcaaagtg gggtcccatc aaggttcagc ggcagtggat ctgggacaga tttcactctc 720
accatcagca gcctgcagcc tgaagatttt gcaacttact attgtcaaca ggctaacagt 780
ttccctctca ctttcggcgg agggaccaag gtggagatca aaaccggtga gcccaaatct 840
tctgacaaaa ctcacacatg cccaccgtgc ccagcacctg aagccgcggg tgcaccgtca 900
gtcttcctct tccccccaaa acccaaggac accctcatga tctcccggac ccctgaggtc 960
acatgcgtgg tggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg 1020
gacggcgtgg aggtgcataa tgccaagaca aagccgcggg aggagcagta caacagcacg 1080
taccgtgtgg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggcgtac 1140
gcgtgcgcgg tctccaacaa agccctccca gcccccatcg agaaaaccat ctccaaagcc 1200
aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccggga tgagctgacc 1260
aagaaccagg tcagcctgac ctgcctggtc aaaggcttct atccaagcga catcgccgtg 1320
gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac 1380
tccgacggct ccttcttcct ctacagcaag ctcaccgtgg acaagagcag gtggcagcag 1440
gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag 1500
agcctctccc tgtctccggg tcagaggcac aacaattctt ccctgaatac aagaactcag 1560
aaagcacgtc attctccgaa ttctacgatc ccaccgcacg ttcagaagtc ggttaataac 1620
gacatgatag tcactgacaa caacggtgca gtcaagtttc cacaactgtg taaattttgt 1680
gatgtgagat tttccacctg tgacaaccag aaatcctgca tgagcaactg cagcatcacc 1740
tccatctgtg agaagccaca ggaagtctgt gtggctgtat ggagaaagaa tgacgagaac 1800
ataacactag agacagtttg ccatgacccc aagctcccct accatgactt tattctggaa 1860
gatgctgctt ctccaaagtg cattatgaag gaaaaaaaaa agcctggtga gactttcttc 1920
atgtgttcct gtagctctga tgagtgcaat gacaacatca tcttctcaga agaatataac 1980
accagcaatc ctgacttgtt gctagtcata tttcaatgag cggccgc 2027

<210> 741
<211> 2102
<212> DNA
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 741
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gcccagaaag atgaaatcat ctgccccagc tgtaatagga ctgcccatcc actgagacat 180
attaataacg acatgatagt cactgacaac aacggtgcag tcaagtttcc acaactgtgt 240
aaattttgtg atgtgagatt ttccacctgt gacaaccaga aatcctgcat gagcaactgc 300
agcatcacct ccatctgtga gaagccacag gaagtctgtg tggctgtatg gagaaagaat 360
gacgagaaca taacactaga gacagtttgc catgacccca agctccccta ccatgacttt 420
attctggaag atgctgcttc tccaaagtgc attatgaagg aaaaaaaaaa gcctggtgag 480
actttcttca tgtgttcctg tagctctgat gagtgcaatg acaacatcat cttctcagaa 540
gaatataaca ccagcaatcc tgacttgttg ctagtcatat ttcaaaccgg tgagcccaaa 600
tcttctgaca aaactcacac atgcccaccg tgcccagcac ctgaagccgc gggtgcaccg 660
tcagtcttcc tcttcccccc aaaacccaag gacaccctca tgatctcccg gaccctgag 720
gtcacatgcg tggtggtgga cgtgagccac gaagaccctg aggtcaagtt caactggtac 780
gtggacggcg tggaggtgca taatgccaag acaaagccgc gggaggagca gtacaacagc 840

acgtaccgtg tggtcagcgt cctcaccgtc ctgcaccagg actggctgaa tggcaaggcg 900
tacgcgtgcg cggtctccaa caaagccctc ccagccccca tcgagaaaac catctccaaa 960
gccaaagggc agccccgaga accacaggtg tacaccctgc ccccatcccg ggatgagctg 1020
accaagaacc aggtcagcct gacctgcctg gtcaaaggct tctatccaag cgacatcgcc 1080
gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacgcc tcccgtgctg 1140
gactccgacg gctccttctt cctctacagc aagctcaccg tggacaagag caggtggcag 1200
caggggaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacgcag 1260
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cagaaagcac gtcattctcc gaattctgaa gttcaattgt tagagtctgg tggcggtctt 1380
gttcagcctg gtggttcttt acgtctttct tgcgctgctt ccggattcac tttctcttgg 1440
taccttatgc attgggttcg ccaagctcct ggtaaaggtt tggagtgggt ttctggtatc 1500
tggccttctg gtggccatac tctttatgct gactccgtta aaggtcgctt cactatctct 1560
agagacaact ctaagaatac tctctacttg cagatgaaca gcttaagggc tgaggacacg 1620
gccgtgtatt actgtgcgag agagccgtta ctatggttcg gggagttatc gtacaactgg 1680
ttcgacccct ggggccaggg caccctggtc accgtctcaa gcggtggcgg cggttcgggg 1740
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gtgtctgcat ctgtaggaga cagagtcacc atcacttgtc gggcgagtca gggtattagc 1860
agctggttag cctggtatca gcagaaacca gggaaagccc ctaagctcct gatctatgct 1920
gcatccagtt tgcaaagtgg ggtcccatca aggttcagcg gcagtggatc tgggacagat 1980
ttcactctca ccatcagcag cctgcagcct gaagattttg caacttacta ttgtcaacag 2040
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gc 2102

<210> 742
<211> 2027
<212> DNA
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 742
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atagtcactg acaacaacgg tgcagtcaag tttccacaac tgtgtaaatt ttgtgatgtg 180
agattttcca cctgtgacaa ccagaaatcc tgcatgagca actgcagcat cacctccatc 240
tgtgagaagc cacaggaagt ctgtgtggct gtatggagaa agaatgacga gaacataaca 300
ctagagacag tttgccatga ccccaagctc ccctaccatg actttattct ggaagatgct 360
gcttctccaa agtgcattat gaaggaaaaa aaaaagcctg gtgagacttt cttcatgtgt 420
tcctgtagct ctgatgagtg caatgacaac atcatcttct cagaagaata taacaccagc 480
aatcctgact tgttgctagt catatttcaa accggtgagc ccaaatcttc tgacaaaact 540
cacacatgcc caccgtgccc agcacctgaa gccgcgggtg caccgtcagt cttcctcttc 600
cccccaaaac ccaaggacac cctcatgatc tcccggaccc ctgaggtcac atgcgtggtg 660
gtggacgtga gccacgaaga ccctgaggtc aagttcaact ggtacgtgga cggcgtggag 720
gtgcataatg ccaagacaaa gccgcgggag gagcagtaca acagcacgta ccgtgtggtc 780
agcgtcctca ccgtcctgca ccaggactgg ctgaatggca aggcgtacgc gtgcgcggtc 840
tccaacaaag ccctcccagc ccccatcgag aaaaccatct ccaaagccaa agggcagccc 900
cgagaaccac aggtgtacac cctgccccca tcccgggatg agctgaccaa gaaccaggtc 960
agcctgacct gcctggtcaa aggcttctat ccaagcgaca tcgccgtgga gtgggagagc 1020
aatgggcagc cggagaacaa ctacaagacc acgcctcccg tgctggactc cgacggctcc 1080
ttcttcctct acagcaagct caccgtggac aagagcaggt ggcagcaggg gaacgtcttc 1140
tcatgctccg tgatgcatga ggctctgcac aaccactaca cgcagaagag cctctccctg 1200
tctccgggtc agaggcacaa caattcttcc ctgaatacaa gaactcagaa agcacgtcat 1260
tctccgaatt ctgaagttca attgttagag tctggtggcg gtcttgttca gcctggtggt 1320
tctttacgtc tttcttgcgc tgcttccgga ttcactttct cttggtacct tatgcattgg 1380
gttcgccaag ctcctggtaa aggtttggag tgggtttctg gtatctggcc ttctggtggc 1440

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catactcttt atgctgactc cgttaaaggt cgcttcacta tctctagaga caactctaag    1500
aatactctct acttgcagat gaacagctta agggctgagg acacggccgt gtattactgt    1560
gcgagagagc cgttactatg gttcggggag ttatcgtaca actggttcga cccctggggc    1620
cagggcaccc tggtcaccgt ctcaagcggt ggcggcggtt cgggggtgg cggaagtgga    1680
ggtggaggga gtcaagacat ccagatgacc cagtctccat cttccgtgtc tgcatctgta    1740
ggagacagag tcaccatcac ttgtcgggcg agtcagggta ttagcagctg gttagcctgg    1800
tatcagcaga aaccagggaa agcccctaag ctcctgatct atgctgcatc cagtttgcaa    1860
agtggggtcc catcaaggtt cagcggcagt ggatctggga cagatttcac tctcaccatc    1920
agcagcctgc agcctgaaga ttttgcaact tactattgtc aacaggctaa cagtttccct    1980
ctcactttcg gcggagggac caaggtggag atcaaatgag cggccgc                  2027

<210> 743
<211> 191
<212> PRT
<213> Human

<400> 743
Met Gly Arg Gly Leu Leu Arg Gly Leu Trp Pro Leu His Ile Val Leu
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Trp Thr Arg Ile Ala Ser Thr Ile Pro Pro His Val Gln Lys Ser Asp
            20                  25                  30
Val Glu Met Glu Ala Gln Lys Asp Glu Ile Ile Cys Pro Ser Cys Asn
        35                  40                  45
Arg Thr Ala His Pro Leu Arg His Ile Asn Asn Asp Met Ile Val Thr
    50                  55                  60
Asp Asn Asn Gly Ala Val Lys Phe Pro Gln Leu Cys Lys Phe Cys Asp
65                  70                  75                  80
Val Arg Phe Ser Thr Cys Asp Asn Gln Lys Ser Cys Met Ser Asn Cys
                85                  90                  95
Ser Ile Thr Ser Ile Cys Glu Lys Pro Gln Glu Val Cys Val Ala Val
            100                 105                 110
Trp Arg Lys Asn Asp Glu Asn Ile Thr Leu Glu Thr Val Cys His Asp
        115                 120                 125
Pro Lys Leu Pro Tyr His Asp Phe Ile Leu Glu Asp Ala Ala Ser Pro
    130                 135                 140
Lys Cys Ile Met Lys Glu Lys Lys Lys Pro Gly Glu Thr Phe Phe Met
145                 150                 155                 160
Cys Ser Cys Ser Ser Asp Glu Cys Asn Asp Asn Ile Ile Phe Ser Glu
                165                 170                 175
Glu Tyr Asn Thr Ser Asn Pro Asp Leu Leu Leu Val Ile Phe Gln
            180                 185                 190

<210> 744
<211> 166
<212> PRT
<213> Human

<400> 744
Met Gly Arg Gly Leu Leu Arg Gly Leu Trp Pro Leu His Ile Val Leu
 1               5                  10                  15
Trp Thr Arg Ile Ala Ser Thr Ile Pro Pro His Val Gln Lys Ser Val
            20                  25                  30
Asn Asn Asp Met Ile Val Thr Asp Asn Asn Gly Ala Val Lys Phe Pro
        35                  40                  45
Gln Leu Cys Lys Phe Cys Asp Val Arg Phe Ser Thr Cys Asp Asn Gln
    50                  55                  60
Lys Ser Cys Met Ser Asn Cys Ser Ile Thr Ser Ile Cys Glu Lys Pro
```

65 70 75 80
Gln Glu Val Cys Val Ala Val Trp Arg Lys Asn Asp Glu Asn Ile Thr
85 90 95
Leu Glu Thr Val Cys His Asp Pro Lys Leu Pro Tyr His Asp Phe Ile
100 105 110
Leu Glu Asp Ala Ala Ser Pro Lys Cys Ile Met Lys Glu Lys Lys Lys
115 120 125
Pro Gly Glu Thr Phe Phe Met Cys Ser Cys Ser Ser Asp Glu Cys Asn
130 135 140
Asp Asn Ile Ile Phe Ser Glu Glu Tyr Asn Thr Ser Asn Pro Asp Leu
145 150 155 160
Leu Leu Val Ile Phe Gln
165

<210> 745
<211> 233
<212> PRT
<213> Human

<400> 745
Met Leu Pro Cys Leu Val Val Leu Leu Ala Ala Leu Leu Ser Leu Arg
1 5 10 15
Leu Gly Ser Asp Ala His Gly Thr Glu Leu Pro Ser Pro Pro Ser Val
20 25 30
Trp Phe Glu Ala Glu Phe Phe His His Ile Leu His Trp Thr Pro Ile
35 40 45
Pro Asn Gln Ser Glu Ser Thr Cys Tyr Glu Val Ala Leu Leu Arg Tyr
50 55 60
Gly Ile Glu Ser Trp Asn Ser Ile Ser Asn Cys Ser Gln Thr Leu Ser
65 70 75 80
Tyr Asp Leu Thr Ala Val Thr Leu Asp Leu Tyr His Ser Asn Gly Tyr
85 90 95
Arg Ala Arg Val Arg Ala Val Asp Gly Ser Arg His Ser Asn Trp Thr
100 105 110
Val Thr Asn Thr Arg Phe Ser Val Asp Glu Val Thr Leu Thr Val Gly
115 120 125
Ser Val Asn Leu Glu Ile His Asn Gly Phe Ile Leu Gly Lys Ile Gln
130 135 140
Leu Pro Arg Pro Lys Met Ala Pro Ala Asn Asp Thr Tyr Glu Ser Ile
145 150 155 160
Phe Ser His Phe Arg Glu Tyr Glu Ile Ala Ile Arg Lys Val Pro Gly
165 170 175
Asn Phe Thr Phe Thr His Lys Lys Val Lys His Glu Asn Phe Ser Leu
180 185 190
Leu Thr Ser Gly Glu Val Gly Glu Phe Cys Val Gln Val Lys Pro Ser
195 200 205
Val Ala Ser Arg Ser Asn Lys Gly Met Trp Ser Lys Glu Glu Cys Ile
210 215 220
Ser Leu Thr Arg Gln Tyr Phe Thr Val
225 230

<210> 746
<211> 126
<212> PRT
<213> Human

<400> 746

```
Glu Thr Ala Lys Glu Pro Cys Met Ala Lys Phe Gly Pro Leu Pro Ser
 1               5                  10                  15
Lys Trp Gln Met Ala Ser Ser Glu Pro Pro Cys Val Asn Lys Val Ser
            20                  25                  30
Asp Trp Lys Leu Glu Ile Leu Gln Asn Gly Leu Tyr Leu Ile Tyr Gly
        35                  40                  45
Gln Val Ala Pro Asn Ala Asn Tyr Asn Asp Val Ala Pro Phe Glu Val
    50                  55                  60
Arg Leu Tyr Lys Asn Lys Asp Met Ile Gln Thr Leu Thr Asn Lys Ser
65                  70                  75                  80
Lys Ile Gln Asn Val Gly Gly Thr Tyr Glu Leu His Val Gly Asp Thr
                85                  90                  95
Ile Asp Leu Ile Phe Asn Ser Glu His Gln Val Leu Lys Asn Asn Thr
            100                 105                 110
Tyr Trp Gly Ile Ile Leu Leu Ala Asn Pro Gln Phe Ile Ser
        115                 120                 125

<210> 747
<211> 1356
<212> PRT
<213> Human

<400> 747
Met Gln Ser Lys Val Leu Leu Ala Val Ala Leu Trp Leu Cys Val Glu
 1               5                  10                  15
Thr Arg Ala Ala Ser Val Gly Leu Pro Ser Val Ser Leu Asp Leu Pro
            20                  25                  30
Arg Leu Ser Ile Gln Lys Asp Ile Leu Thr Ile Lys Ala Asn Thr Thr
        35                  40                  45
Leu Gln Ile Thr Cys Arg Gly Gln Arg Asp Leu Asp Trp Leu Trp Pro
    50                  55                  60
Asn Asn Gln Ser Gly Ser Glu Gln Arg Val Glu Val Thr Glu Cys Ser
65                  70                  75                  80
Asp Gly Leu Phe Cys Lys Thr Leu Thr Ile Pro Lys Val Ile Gly Asn
                85                  90                  95
Asp Thr Gly Ala Tyr Lys Cys Phe Tyr Arg Glu Thr Asp Leu Ala Ser
            100                 105                 110
Val Ile Tyr Val Tyr Val Gln Asp Tyr Arg Ser Pro Phe Ile Ala Ser
        115                 120                 125
Val Ser Asp Gln His Gly Val Val Tyr Ile Thr Glu Asn Lys Asn Lys
    130                 135                 140
Thr Val Val Ile Pro Cys Leu Gly Ser Ile Ser Asn Leu Asn Val Ser
145                 150                 155                 160
Leu Cys Ala Arg Tyr Pro Glu Lys Arg Phe Val Pro Asp Gly Asn Arg
                165                 170                 175
Ile Ser Trp Asp Ser Lys Lys Gly Phe Thr Ile Pro Ser Tyr Met Ile
            180                 185                 190
Ser Tyr Ala Gly Met Val Phe Cys Glu Ala Lys Ile Asn Asp Glu Ser
        195                 200                 205
Tyr Gln Ser Ile Met Tyr Ile Val Val Val Val Gly Tyr Arg Ile Tyr
    210                 215                 220
Asp Val Val Leu Ser Pro Ser His Gly Ile Glu Leu Ser Val Gly Glu
225                 230                 235                 240
Lys Leu Val Leu Asn Cys Thr Ala Arg Thr Glu Leu Asn Val Gly Ile
                245                 250                 255
Asp Phe Asn Trp Glu Tyr Pro Ser Ser Lys His Gln His Lys Lys Leu
            260                 265                 270
```

```
Val Asn Arg Asp Leu Lys Thr Gln Ser Gly Ser Glu Met Lys Lys Phe
        275                 280                 285
Leu Ser Thr Leu Thr Ile Asp Gly Val Thr Arg Ser Asp Gln Gly Leu
    290                 295                 300
Tyr Thr Cys Ala Ala Ser Ser Gly Leu Met Thr Lys Lys Asn Ser Thr
305                 310                 315                 320
Phe Val Arg Val His Glu Lys Pro Phe Val Ala Phe Gly Ser Gly Met
                325                 330                 335
Glu Ser Leu Val Glu Ala Thr Val Gly Glu Arg Val Arg Ile Pro Ala
            340                 345                 350
Lys Tyr Leu Gly Tyr Pro Pro Pro Glu Ile Lys Trp Tyr Lys Asn Gly
        355                 360                 365
Ile Pro Leu Glu Ser Asn His Thr Ile Lys Ala Gly His Val Leu Thr
    370                 375                 380
Ile Met Glu Val Ser Glu Arg Asp Thr Gly Asn Tyr Thr Val Ile Leu
385                 390                 395                 400
Thr Asn Pro Ile Ser Lys Glu Lys Gln Ser His Val Val Ser Leu Val
                405                 410                 415
Val Tyr Val Pro Pro Gln Ile Gly Glu Lys Ser Leu Ile Ser Pro Val
            420                 425                 430
Asp Ser Tyr Gln Tyr Gly Thr Thr Gln Thr Leu Thr Cys Thr Val Tyr
        435                 440                 445
Ala Ile Pro Pro Pro His His Ile His Trp Tyr Trp Gln Leu Glu Glu
    450                 455                 460
Glu Cys Ala Asn Glu Pro Ser Gln Ala Val Ser Val Thr Asn Pro Tyr
465                 470                 475                 480
Pro Cys Glu Glu Trp Arg Ser Val Glu Asp Phe Gln Gly Gly Asn Lys
                485                 490                 495
Ile Glu Val Asn Lys Asn Gln Phe Ala Leu Ile Glu Gly Lys Asn Lys
            500                 505                 510
Thr Val Ser Thr Leu Val Ile Gln Ala Ala Asn Val Ser Ala Leu Tyr
        515                 520                 525
Lys Cys Glu Ala Val Asn Lys Val Gly Arg Gly Glu Arg Val Ile Ser
    530                 535                 540
Phe His Val Thr Arg Gly Pro Glu Ile Thr Leu Gln Pro Asp Met Gln
545                 550                 555                 560
Pro Thr Glu Gln Glu Ser Val Ser Leu Trp Cys Thr Ala Asp Arg Ser
                565                 570                 575
Thr Phe Glu Asn Leu Thr Trp Tyr Lys Leu Gly Pro Gln Pro Leu Pro
            580                 585                 590
Ile His Val Gly Glu Leu Pro Thr Pro Val Cys Lys Asn Leu Asp Thr
        595                 600                 605
Leu Trp Lys Leu Asn Ala Thr Met Phe Ser Asn Ser Thr Asn Asp Ile
    610                 615                 620
Leu Ile Met Glu Leu Lys Asn Ala Ser Leu Gln Asp Gln Gly Asp Tyr
625                 630                 635                 640
Val Cys Leu Ala Gln Asp Arg Lys Thr Lys Lys Arg His Cys Val Val
                645                 650                 655
Arg Gln Leu Thr Val Leu Glu Arg Val Ala Pro Thr Ile Thr Gly Asn
            660                 665                 670
Leu Glu Asn Gln Thr Thr Ser Ile Gly Glu Ser Ile Glu Val Ser Cys
        675                 680                 685
Thr Ala Ser Gly Asn Pro Pro Pro Gln Ile Met Trp Phe Lys Asp Asn
    690                 695                 700
Glu Thr Leu Val Glu Asp Ser Gly Ile Val Leu Lys Asp Gly Asn Arg
705                 710                 715                 720
Asn Leu Thr Ile Arg Arg Val Arg Lys Glu Asp Glu Gly Leu Tyr Thr
```

```
                725                 730                 735
Cys Gln Ala Cys Ser Val Leu Gly Cys Ala Lys Val Glu Ala Phe Phe
            740                 745                 750
Ile Ile Glu Gly Ala Gln Glu Lys Thr Asn Leu Glu Ile Ile Ile Leu
        755                 760                 765
Val Gly Thr Ala Val Ile Ala Met Phe Phe Trp Leu Leu Leu Val Ile
    770                 775                 780
Ile Leu Arg Thr Val Lys Arg Ala Asn Gly Gly Glu Leu Lys Thr Gly
785                 790                 795                 800
Tyr Leu Ser Ile Val Met Asp Pro Asp Glu Leu Pro Leu Asp Glu His
                805                 810                 815
Cys Glu Arg Leu Pro Tyr Asp Ala Ser Lys Trp Glu Phe Pro Arg Asp
            820                 825                 830
Arg Leu Lys Leu Gly Lys Pro Leu Gly Arg Gly Ala Phe Gly Gln Val
        835                 840                 845
Ile Glu Ala Asp Ala Phe Gly Ile Asp Lys Thr Ala Thr Cys Arg Thr
    850                 855                 860
Val Ala Val Lys Met Leu Lys Glu Gly Ala Thr His Ser Glu His Arg
865                 870                 875                 880
Ala Leu Met Ser Glu Leu Lys Ile Leu Ile His Ile Gly His His Leu
                885                 890                 895
Asn Val Val Asn Leu Leu Gly Ala Cys Thr Lys Pro Gly Gly Pro Leu
            900                 905                 910
Met Val Ile Val Glu Phe Cys Lys Phe Gly Asn Leu Ser Thr Tyr Leu
        915                 920                 925
Arg Ser Lys Arg Asn Glu Phe Val Pro Tyr Lys Thr Lys Gly Ala Arg
    930                 935                 940
Phe Arg Gln Gly Lys Asp Tyr Val Gly Ala Ile Pro Val Asp Leu Lys
945                 950                 955                 960
Arg Arg Leu Asp Ser Ile Thr Ser Ser Gln Ser Ser Ala Ser Ser Gly
                965                 970                 975
Phe Val Glu Glu Lys Ser Leu Ser Asp Val Glu Glu Glu Glu Ala Pro
            980                 985                 990
Glu Asp Leu Tyr Lys Asp Phe Leu Thr Leu Glu His Leu Ile Cys Tyr
        995                 1000                1005
Ser Phe Gln Val Ala Lys Gly Met Glu Phe Leu Ala Ser Arg Lys Cys
    1010                1015                1020
Ile His Arg Asp Leu Ala Ala Arg Asn Ile Leu Leu Ser Glu Lys Asn
1025                1030                1035                1040
Val Val Lys Ile Cys Asp Phe Gly Leu Ala Arg Asp Ile Tyr Lys Asp
                1045                1050                1055
Pro Asp Tyr Val Arg Lys Gly Asp Ala Arg Leu Pro Leu Lys Trp Met
            1060                1065                1070
Ala Pro Glu Thr Ile Phe Asp Arg Val Tyr Thr Ile Gln Ser Asp Val
        1075                1080                1085
Trp Ser Phe Gly Val Leu Leu Trp Glu Ile Phe Ser Leu Gly Ala Ser
    1090                1095                1100
Pro Tyr Pro Gly Val Lys Ile Asp Glu Glu Phe Cys Arg Arg Leu Lys
1105                1110                1115                1120
Glu Gly Thr Arg Met Arg Ala Pro Asp Tyr Thr Thr Pro Glu Met Tyr
                1125                1130                1135
Gln Thr Met Leu Asp Cys Trp His Gly Glu Pro Ser Gln Arg Pro Thr
            1140                1145                1150
Phe Ser Glu Leu Val Glu His Leu Gly Asn Leu Leu Gln Ala Asn Ala
        1155                1160                1165
Gln Gln Asp Gly Lys Asp Tyr Ile Val Leu Pro Ile Ser Glu Thr Leu
    1170                1175                1180
```

```
Ser Met Glu Glu Asp Ser Gly Leu Ser Leu Pro Thr Ser Pro Val Ser
1185                1190                1195                1200
Cys Met Glu Glu Glu Glu Val Cys Asp Pro Lys Phe His Tyr Asp Asn
                1205                1210                1215
Thr Ala Gly Ile Ser Gln Tyr Leu Gln Asn Ser Lys Arg Lys Ser Arg
            1220                1225                1230
Pro Val Ser Val Lys Thr Phe Glu Asp Ile Pro Leu Glu Glu Pro Glu
        1235                1240                1245
Val Lys Val Ile Pro Asp Asp Asn Gln Thr Asp Ser Gly Met Val Leu
    1250                1255                1260
Ala Ser Glu Glu Leu Lys Thr Leu Glu Asp Arg Thr Lys Leu Ser Pro
1265                1270                1275                1280
Ser Phe Gly Gly Met Val Pro Ser Lys Ser Arg Glu Ser Val Ala Ser
                1285                1290                1295
Glu Gly Ser Asn Gln Thr Ser Gly Tyr Gln Ser Gly Tyr His Ser Asp
            1300                1305                1310
Asp Thr Asp Thr Thr Val Tyr Ser Ser Glu Glu Ala Glu Leu Leu Lys
        1315                1320                1325
Leu Ile Glu Ile Gly Val Gln Thr Gly Ser Thr Ala Gln Ile Leu Gln
    1330                1335                1340
Pro Asp Ser Gly Thr Thr Leu Ser Ser Pro Pro Val
1345                1350                1355


<210> 748
<211> 257
<212> PRT
<213> Human

<400> 748
Met Ala Pro Val Ala Val Trp Ala Ala Leu Ala Val Gly Leu Glu Leu
 1               5                  10                  15
Trp Ala Ala Ala His Ala Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr
            20                  25                  30
Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln
        35                  40                  45
Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys
    50                  55                  60
Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp
65                  70                  75                  80
Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys
                85                  90                  95
Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
            100                 105                 110
Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu
        115                 120                 125
Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg
    130                 135                 140
Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val
145                 150                 155                 160
Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr
                165                 170                 175
Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly
            180                 185                 190
Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser
        195                 200                 205
Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser
```

```
    210                 215                 220
Gln His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser
225                 230                 235                 240
Phe Leu Leu Pro Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly
                245                 250                 255
Asp
```

<210> 749
<211> 211
<212> PRT
<213> Human

<400> 749

```
Met Gly Leu Ser Thr Val Pro Asp Leu Leu Leu Pro Leu Val Leu Leu
 1               5                  10                  15
Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu Val Pro
            20                  25                  30
His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro Gln Gly Lys
        35                  40                  45
Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys
    50                  55                  60
Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp
65                  70                  75                  80
Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu
                85                  90                  95
Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val
            100                 105                 110
Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg
        115                 120                 125
Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe
    130                 135                 140
Asn Cys Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu
145                 150                 155                 160
Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu
                165                 170                 175
Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr
            180                 185                 190
Lys Leu Cys Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser
        195                 200                 205
Gly Thr Thr
    210
```

<210> 750
<211> 950
<212> PRT
<213> Human

<400> 750

```
Met Lys Ala Pro Ala Val Leu Ala Pro Gly Ile Leu Val Leu Leu Phe
 1               5                  10                  15
Thr Leu Val Gln Arg Ser Asn Gly Glu Cys Lys Glu Ala Leu Ala Lys
            20                  25                  30
Ser Glu Met Asn Val Asn Met Lys Tyr Gln Leu Pro Asn Phe Thr Ala
        35                  40                  45
Glu Thr Pro Ile Gln Asn Val Ile Leu His Glu His His Ile Phe Leu
    50                  55                  60
```

```
Gly Ala Thr Asn Tyr Ile Tyr Val Leu Asn Glu Glu Asp Leu Gln Lys
65                  70                  75                  80
Val Ala Glu Tyr Lys Thr Gly Pro Val Leu Glu His Pro Asp Cys Phe
                85                  90                  95
Pro Cys Gln Asp Cys Ser Ser Lys Ala Asn Leu Ser Gly Gly Val Trp
            100                 105                 110
Lys Asp Asn Ile Asn Met Ala Leu Val Val Asp Thr Tyr Tyr Asp Asp
        115                 120                 125
Gln Leu Ile Ser Cys Gly Ser Val Asn Arg Gly Thr Cys Gln Arg His
    130                 135                 140
Val Phe Pro His Asn His Thr Ala Asp Ile Gln Ser Glu Val His Cys
145                 150                 155                 160
Ile Phe Ser Pro Gln Ile Glu Glu Pro Ser Gln Cys Pro Asp Cys Val
                165                 170                 175
Val Ser Ala Leu Gly Ala Lys Val Leu Ser Ser Val Lys Asp Arg Phe
            180                 185                 190
Ile Asn Phe Phe Val Gly Asn Thr Ile Asn Ser Ser Tyr Phe Pro Asp
        195                 200                 205
His Pro Leu His Ser Ile Ser Val Arg Arg Leu Lys Glu Thr Lys Asp
    210                 215                 220
Gly Phe Met Phe Leu Thr Asp Gln Ser Tyr Ile Asp Val Leu Pro Glu
225                 230                 235                 240
Phe Arg Asp Ser Tyr Pro Ile Lys Tyr Val His Ala Phe Glu Ser Asn
                245                 250                 255
Asn Phe Ile Tyr Phe Leu Thr Val Gln Arg Glu Thr Leu Asp Ala Gln
            260                 265                 270
Thr Phe His Thr Arg Ile Ile Arg Phe Cys Ser Ile Asn Ser Gly Leu
        275                 280                 285
His Ser Tyr Met Glu Met Pro Leu Glu Cys Ile Leu Thr Glu Lys Arg
    290                 295                 300
Lys Lys Arg Ser Thr Lys Lys Glu Val Phe Asn Ile Leu Gln Ala Ala
305                 310                 315                 320
Tyr Val Ser Lys Pro Gly Ala Gln Leu Ala Arg Gln Ile Gly Ala Ser
                325                 330                 335
Leu Asn Asp Asp Ile Leu Phe Gly Val Phe Ala Gln Ser Lys Pro Asp
            340                 345                 350
Ser Ala Glu Pro Met Asp Arg Ser Ala Met Cys Ala Phe Pro Ile Lys
        355                 360                 365
Tyr Val Asn Asp Phe Phe Asn Lys Ile Val Asn Lys Asn Asn Val Arg
    370                 375                 380
Cys Leu Gln His Phe Tyr Gly Pro Asn His Glu His Cys Phe Asn Arg
385                 390                 395                 400
Thr Leu Leu Arg Asn Ser Ser Gly Cys Glu Ala Arg Arg Asp Glu Tyr
                405                 410                 415
Arg Thr Glu Phe Thr Thr Ala Leu Gln Arg Val Asp Leu Phe Met Gly
            420                 425                 430
Gln Phe Ser Glu Val Leu Leu Thr Ser Ile Ser Thr Phe Ile Lys Gly
        435                 440                 445
Asp Leu Thr Ile Ala Asn Leu Gly Thr Ser Glu Gly Arg Phe Met Gln
    450                 455                 460
Val Val Val Ser Arg Ser Gly Pro Ser Thr Pro His Val Asn Phe Leu
465                 470                 475                 480
Leu Asp Ser His Pro Val Ser Pro Glu Val Ile Val Glu His Thr Leu
                485                 490                 495
Asn Gln Asn Gly Tyr Thr Leu Val Ile Thr Gly Lys Lys Ile Thr Lys
            500                 505                 510
Ile Pro Leu Asn Gly Leu Gly Cys Arg His Phe Gln Ser Cys Ser Gln
```

```
        515                 520                 525
Cys Leu Ser Ala Pro Pro Phe Val Gln Cys Gly Trp Cys His Asp Lys
    530                 535                 540
Cys Val Arg Ser Glu Glu Cys Leu Ser Gly Thr Trp Thr Gln Gln Ile
545                 550                 555                 560
Cys Leu Pro Ala Ile Tyr Lys Val Phe Pro Asn Ser Ala Pro Leu Glu
                565                 570                 575
Gly Gly Thr Arg Leu Thr Ile Cys Gly Trp Asp Phe Gly Phe Arg Arg
            580                 585                 590
Asn Asn Lys Phe Asp Leu Lys Lys Thr Arg Val Leu Leu Gly Asn Glu
        595                 600                 605
Ser Cys Thr Leu Thr Leu Ser Glu Ser Thr Met Asn Thr Leu Lys Cys
    610                 615                 620
Thr Val Gly Pro Ala Met Asn Lys His Phe Asn Met Ser Ile Ile Ile
625                 630                 635                 640
Ser Asn Gly His Gly Thr Thr Gln Tyr Ser Thr Phe Ser Tyr Val Asp
                645                 650                 655
Pro Val Ile Thr Ser Ile Ser Pro Lys Tyr Gly Pro Met Ala Gly Gly
            660                 665                 670
Thr Leu Leu Thr Leu Thr Gly Asn Tyr Leu Asn Ser Gly Asn Ser Arg
        675                 680                 685
His Ile Ser Ile Gly Gly Lys Thr Cys Thr Leu Lys Ser Val Ser Asn
    690                 695                 700
Ser Ile Leu Glu Cys Tyr Thr Pro Ala Gln Thr Ile Ser Thr Glu Phe
705                 710                 715                 720
Ala Val Lys Leu Lys Ile Asp Leu Ala Asn Arg Glu Thr Ser Ile Phe
                725                 730                 735
Ser Tyr Arg Glu Asp Pro Ile Val Tyr Glu Ile His Pro Thr Lys Ser
            740                 745                 750
Phe Ile Ser Thr Trp Trp Lys Glu Pro Leu Asn Ile Val Ser Phe Leu
        755                 760                 765
Phe Cys Phe Ala Ser Gly Gly Ser Thr Ile Thr Gly Val Gly Lys Asn
    770                 775                 780
Leu Asn Ser Val Ser Val Pro Arg Met Val Ile Asn Val His Glu Ala
785                 790                 795                 800
Gly Arg Asn Phe Thr Val Ala Cys Gln His Arg Ser Asn Ser Glu Ile
                805                 810                 815
Ile Cys Cys Thr Thr Pro Ser Leu Gln Gln Leu Asn Leu Gln Leu Pro
            820                 825                 830
Leu Lys Thr Lys Ala Phe Phe Met Leu Asp Gly Ile Leu Ser Lys Tyr
        835                 840                 845
Phe Asp Leu Ile Tyr Val His Asn Pro Val Phe Lys Pro Phe Glu Lys
    850                 855                 860
Pro Val Met Ile Ser Met Gly Asn Glu Asn Val Leu Glu Ile Lys Gly
865                 870                 875                 880
Asn Asp Ile Asp Pro Glu Ala Val Lys Gly Glu Val Leu Lys Val Gly
                885                 890                 895
Asn Lys Ser Cys Glu Asn Ile His Leu His Ser Glu Ala Val Leu Cys
            900                 905                 910
Thr Val Pro Asn Asp Leu Leu Lys Leu Asn Ser Glu Leu Asn Ile Glu
        915                 920                 925
Trp Lys Gln Ala Ile Ser Ser Thr Val Leu Gly Lys Val Ile Val Gln
    930                 935                 940
Pro Asp Gln Asn Phe Thr
945                 950
```

<210> 751

<211> 500
<212> PRT
<213> Human

<400> 751
Met Lys Ala Pro Ala Val Leu Ala Pro Gly Ile Leu Val Leu Leu Phe
 1   5   10   15
Thr Leu Val Gln Arg Ser Asn Gly Glu Cys Lys Glu Ala Leu Ala Lys
            20   25   30
Ser Glu Met Asn Val Asn Met Lys Tyr Gln Leu Pro Asn Phe Thr Ala
        35   40   45
Glu Thr Pro Ile Gln Asn Val Ile Leu His Glu His His Ile Phe Leu
    50   55   60
Gly Ala Thr Asn Tyr Ile Tyr Val Leu Asn Glu Glu Asp Leu Gln Lys
65   70   75   80
Val Ala Glu Tyr Lys Thr Gly Pro Val Leu Glu His Pro Asp Cys Phe
                85   90   95
Pro Cys Gln Asp Cys Ser Ser Lys Ala Asn Leu Ser Gly Gly Val Trp
            100   105   110
Lys Asp Asn Ile Asn Met Ala Leu Val Val Asp Thr Tyr Tyr Asp Asp
        115   120   125
Gln Leu Ile Ser Cys Gly Ser Val Asn Arg Gly Thr Cys Gln Arg His
    130   135   140
Val Phe Pro His Asn His Thr Ala Asp Ile Gln Ser Glu Val His Cys
145   150   155   160
Ile Phe Ser Pro Gln Ile Glu Glu Pro Ser Gln Cys Pro Asp Cys Val
                165   170   175
Val Ser Ala Leu Gly Ala Lys Val Leu Ser Ser Val Lys Asp Arg Phe
            180   185   190
Ile Asn Phe Phe Val Gly Asn Thr Ile Asn Ser Ser Tyr Phe Pro Asp
        195   200   205
His Pro Leu His Ser Ile Ser Val Arg Arg Leu Lys Glu Thr Lys Asp
    210   215   220
Gly Phe Met Phe Leu Thr Asp Gln Ser Tyr Ile Asp Val Leu Pro Glu
225   230   235   240
Phe Arg Asp Ser Tyr Pro Ile Lys Tyr Val His Ala Phe Glu Ser Asn
                245   250   255
Asn Phe Ile Tyr Phe Leu Thr Val Gln Arg Glu Thr Leu Asp Ala Gln
            260   265   270
Thr Phe His Thr Arg Ile Ile Arg Phe Cys Ser Ile Asn Ser Gly Leu
        275   280   285
His Ser Tyr Met Glu Met Pro Leu Glu Cys Ile Leu Thr Glu Lys Arg
    290   295   300
Lys Lys Arg Ser Thr Lys Lys Glu Val Phe Asn Ile Leu Gln Ala Ala
305   310   315   320
Tyr Val Ser Lys Pro Gly Ala Gln Leu Ala Arg Gln Ile Gly Ala Ser
                325   330   335
Leu Asn Asp Asp Ile Leu Phe Gly Val Phe Ala Gln Ser Lys Pro Asp
            340   345   350
Ser Ala Glu Pro Met Asp Arg Ser Ala Met Cys Ala Phe Pro Ile Lys
        355   360   365
Tyr Val Asn Asp Phe Phe Asn Lys Ile Val Asn Lys Asn Asn Val Arg
    370   375   380
Cys Leu Gln His Phe Tyr Gly Pro Asn His Glu His Cys Phe Asn Arg
385   390   395   400
Thr Leu Leu Arg Asn Ser Ser Gly Cys Glu Ala Arg Arg Asp Glu Tyr
                405   410   415

```
Arg Thr Glu Phe Thr Thr Ala Leu Gln Arg Val Asp Leu Phe Met Gly
            420                 425                 430
Gln Phe Ser Glu Val Leu Leu Thr Ser Ile Ser Thr Phe Ile Lys Gly
        435                 440                 445
Asp Leu Thr Ile Ala Asn Leu Gly Thr Ser Glu Gly Arg Phe Met Gln
    450                 455                 460
Val Val Val Ser Arg Ser Gly Pro Ser Thr Pro His Val Asn Phe Leu
465                 470                 475                 480
Leu Asp Ser His Pro Val Ser Pro Glu Val Ile Val Glu His Thr Leu
                485                 490                 495
Asn Gln Asn Gly
            500

<210> 752
<211> 567
<212> PRT
<213> Human

<400> 752
Met Lys Ala Pro Ala Val Leu Ala Pro Gly Ile Leu Val Leu Leu Phe
 1               5                  10                  15
Thr Leu Val Gln Arg Ser Asn Gly Glu Cys Lys Glu Ala Leu Ala Lys
            20                  25                  30
Ser Glu Met Asn Val Asn Met Lys Tyr Gln Leu Pro Asn Phe Thr Ala
        35                  40                  45
Glu Thr Pro Ile Gln Asn Val Ile Leu His Glu His His Ile Phe Leu
    50                  55                  60
Gly Ala Thr Asn Tyr Ile Tyr Val Leu Asn Glu Glu Asp Leu Gln Lys
65                  70                  75                  80
Val Ala Glu Tyr Lys Thr Gly Pro Val Leu Glu His Pro Asp Cys Phe
                85                  90                  95
Pro Cys Gln Asp Cys Ser Ser Lys Ala Asn Leu Ser Gly Gly Val Trp
            100                 105                 110
Lys Asp Asn Ile Asn Met Ala Leu Val Val Asp Thr Tyr Tyr Asp Asp
        115                 120                 125
Gln Leu Ile Ser Cys Gly Ser Val Asn Arg Gly Thr Cys Gln Arg His
    130                 135                 140
Val Phe Pro His Asn His Thr Ala Asp Ile Gln Ser Glu Val His Cys
145                 150                 155                 160
Ile Phe Ser Pro Gln Ile Glu Glu Pro Ser Gln Cys Pro Asp Cys Val
                165                 170                 175
Val Ser Ala Leu Gly Ala Lys Val Leu Ser Ser Val Lys Asp Arg Phe
            180                 185                 190
Ile Asn Phe Phe Val Gly Asn Thr Ile Asn Ser Ser Tyr Phe Pro Asp
        195                 200                 205
His Pro Leu His Ser Ile Ser Val Arg Arg Leu Lys Glu Thr Lys Asp
    210                 215                 220
Gly Phe Met Phe Leu Thr Asp Gln Ser Tyr Ile Asp Val Leu Pro Glu
225                 230                 235                 240
Phe Arg Asp Ser Tyr Pro Ile Lys Tyr Val His Ala Phe Glu Ser Asn
                245                 250                 255
Asn Phe Ile Tyr Phe Leu Thr Val Gln Arg Glu Thr Leu Asp Ala Gln
            260                 265                 270
Thr Phe His Thr Arg Ile Ile Arg Phe Cys Ser Ile Asn Ser Gly Leu
        275                 280                 285
His Ser Tyr Met Glu Met Pro Leu Glu Cys Ile Leu Thr Glu Lys Arg
    290                 295                 300
```

```
Lys Lys Arg Ser Thr Lys Lys Glu Val Phe Asn Ile Leu Gln Ala Ala
305                 310                 315                 320
Tyr Val Ser Lys Pro Gly Ala Gln Leu Ala Arg Gln Ile Gly Ala Ser
                325                 330                 335
Leu Asn Asp Asp Ile Leu Phe Gly Val Phe Ala Gln Ser Lys Pro Asp
            340                 345                 350
Ser Ala Glu Pro Met Asp Arg Ser Ala Met Cys Ala Phe Pro Ile Lys
        355                 360                 365
Tyr Val Asn Asp Phe Phe Asn Lys Ile Val Asn Lys Asn Asn Val Arg
    370                 375                 380
Cys Leu Gln His Phe Tyr Gly Pro Asn His Glu His Cys Phe Asn Arg
385                 390                 395                 400
Thr Leu Leu Arg Asn Ser Ser Gly Cys Glu Ala Arg Arg Asp Glu Tyr
                405                 410                 415
Arg Thr Glu Phe Thr Thr Ala Leu Gln Arg Val Asp Leu Phe Met Gly
            420                 425                 430
Gln Phe Ser Glu Val Leu Leu Thr Ser Ile Ser Thr Phe Ile Lys Gly
        435                 440                 445
Asp Leu Thr Ile Ala Asn Leu Gly Thr Ser Glu Gly Arg Phe Met Gln
    450                 455                 460
Val Val Val Ser Arg Ser Gly Pro Ser Thr Pro His Val Asn Phe Leu
465                 470                 475                 480
Leu Asp Ser His Pro Val Ser Pro Glu Val Ile Val Glu His Thr Leu
                485                 490                 495
Asn Gln Asn Gly Tyr Thr Leu Val Ile Thr Gly Lys Lys Ile Thr Lys
            500                 505                 510
Ile Pro Leu Asn Gly Leu Gly Cys Arg His Phe Gln Ser Cys Ser Gln
        515                 520                 525
Cys Leu Ser Ala Pro Pro Phe Val Gln Cys Gly Trp Cys His Asp Lys
    530                 535                 540
Cys Val Arg Ser Glu Glu Cys Leu Ser Gly Thr Trp Thr Gln Gln Ile
545                 550                 555                 560
Cys Leu Pro Ala Ile Tyr Lys
                565
```

<210> 753
<211> 1367
<212> PRT
<213> Human

<400> 753

```
Met Lys Ser Gly Ser Gly Gly Gly Ser Pro Thr Ser Leu Trp Gly Leu
 1               5                  10                  15
Leu Phe Leu Ser Ala Ala Leu Ser Leu Trp Pro Thr Ser Gly Glu Ile
            20                  25                  30
Cys Gly Pro Gly Ile Asp Ile Arg Asn Asp Tyr Gln Gln Leu Lys Arg
        35                  40                  45
Leu Glu Asn Cys Thr Val Ile Glu Gly Tyr Leu His Ile Leu Leu Ile
    50                  55                  60
Ser Lys Ala Glu Asp Tyr Arg Ser Tyr Arg Phe Pro Lys Leu Thr Val
65                  70                  75                  80
Ile Thr Glu Tyr Leu Leu Leu Phe Arg Val Ala Gly Leu Glu Ser Leu
                85                  90                  95
Gly Asp Leu Phe Pro Asn Leu Thr Val Ile Arg Gly Trp Lys Leu Phe
            100                 105                 110
Tyr Asn Tyr Ala Leu Val Ile Phe Glu Met Thr Asn Leu Lys Asp Ile
        115                 120                 125
```

```
Gly Leu Tyr Asn Leu Arg Asn Ile Thr Arg Gly Ala Ile Arg Ile Glu
    130                 135                 140
Lys Asn Ala Asp Leu Cys Tyr Leu Ser Thr Val Asp Trp Ser Leu Ile
145                 150                 155                 160
Leu Asp Ala Val Ser Asn Asn Tyr Ile Val Gly Asn Lys Pro Pro Lys
                165                 170                 175
Glu Cys Gly Asp Leu Cys Pro Gly Thr Met Glu Glu Lys Pro Met Cys
            180                 185                 190
Glu Lys Thr Thr Ile Asn Asn Glu Tyr Asn Tyr Arg Cys Trp Thr Thr
        195                 200                 205
Asn Arg Cys Gln Lys Met Cys Pro Ser Thr Cys Gly Lys Arg Ala Cys
    210                 215                 220
Thr Glu Asn Asn Glu Cys Cys His Pro Glu Cys Leu Gly Ser Cys Ser
225                 230                 235                 240
Ala Pro Asp Asn Asp Thr Ala Cys Val Ala Cys Arg His Tyr Tyr Tyr
                245                 250                 255
Ala Gly Val Cys Val Pro Ala Cys Pro Pro Asn Thr Tyr Arg Phe Glu
            260                 265                 270
Gly Trp Arg Cys Val Asp Arg Asp Phe Cys Ala Asn Ile Leu Ser Ala
        275                 280                 285
Glu Ser Ser Asp Ser Glu Gly Phe Val Ile His Asp Gly Glu Cys Met
    290                 295                 300
Gln Glu Cys Pro Ser Gly Phe Ile Arg Asn Gly Ser Gln Ser Met Tyr
305                 310                 315                 320
Cys Ile Pro Cys Glu Gly Pro Cys Pro Lys Val Cys Glu Glu Glu Lys
                325                 330                 335
Lys Thr Lys Thr Ile Asp Ser Val Thr Ser Ala Gln Met Leu Gln Gly
            340                 345                 350
Cys Thr Ile Phe Lys Gly Asn Leu Leu Ile Asn Ile Arg Arg Gly Asn
        355                 360                 365
Asn Ile Ala Ser Glu Leu Glu Asn Phe Met Gly Leu Ile Glu Val Val
    370                 375                 380
Thr Gly Tyr Val Lys Ile Arg His Ser His Ala Leu Val Ser Leu Ser
385                 390                 395                 400
Phe Leu Lys Asn Leu Arg Leu Ile Leu Gly Glu Glu Gln Leu Glu Gly
                405                 410                 415
Asn Tyr Ser Phe Tyr Val Leu Asp Asn Gln Asn Leu Gln Gln Leu Trp
            420                 425                 430
Asp Trp Asp His Arg Asn Leu Thr Ile Lys Ala Gly Lys Met Tyr Phe
        435                 440                 445
Ala Phe Asn Pro Lys Leu Cys Val Ser Glu Ile Tyr Arg Met Glu Glu
    450                 455                 460
Val Thr Gly Thr Lys Gly Arg Gln Ser Lys Gly Asp Ile Asn Thr Arg
465                 470                 475                 480
Asn Asn Gly Glu Arg Ala Ser Cys Glu Ser Asp Val Leu His Phe Thr
                485                 490                 495
Ser Thr Thr Thr Ser Lys Asn Arg Ile Ile Ile Thr Trp His Arg Tyr
            500                 505                 510
Arg Pro Pro Asp Tyr Arg Asp Leu Ile Ser Phe Thr Val Tyr Tyr Lys
        515                 520                 525
Glu Ala Pro Phe Lys Asn Val Thr Glu Tyr Asp Gly Gln Asp Ala Cys
    530                 535                 540
Gly Ser Asn Ser Trp Asn Met Val Asp Val Asp Leu Pro Pro Asn Lys
545                 550                 555                 560
Asp Val Glu Pro Gly Ile Leu Leu His Gly Leu Lys Pro Trp Thr Gln
                565                 570                 575
Tyr Ala Val Tyr Val Lys Ala Val Thr Leu Thr Met Val Glu Asn Asp
```

```
            580                 585                 590
His Ile Arg Gly Ala Lys Ser Glu Ile Leu Tyr Ile Arg Thr Asn Ala
        595                 600                 605
Ser Val Pro Ser Ile Pro Leu Asp Val Leu Ser Ala Ser Asn Ser Ser
    610                 615                 620
Ser Gln Leu Ile Val Lys Trp Asn Pro Pro Ser Leu Pro Asn Gly Asn
625                 630                 635                 640
Leu Ser Tyr Tyr Ile Val Arg Trp Gln Arg Gln Pro Gln Asp Gly Tyr
                645                 650                 655
Leu Tyr Arg His Asn Tyr Cys Ser Lys Asp Lys Ile Pro Ile Arg Lys
            660                 665                 670
Tyr Ala Asp Gly Thr Ile Asp Ile Glu Glu Val Thr Glu Asn Pro Lys
        675                 680                 685
Thr Glu Val Cys Gly Gly Glu Lys Gly Pro Cys Cys Ala Cys Pro Lys
    690                 695                 700
Thr Glu Ala Glu Lys Gln Ala Glu Lys Glu Glu Ala Glu Tyr Arg Lys
705                 710                 715                 720
Val Phe Glu Asn Phe Leu His Asn Ser Ile Phe Val Pro Arg Pro Glu
                725                 730                 735
Arg Lys Arg Arg Asp Val Met Gln Val Ala Asn Thr Thr Met Ser Ser
            740                 745                 750
Arg Ser Arg Asn Thr Thr Ala Ala Asp Thr Tyr Asn Ile Thr Asp Pro
        755                 760                 765
Glu Glu Leu Glu Thr Glu Tyr Pro Phe Phe Glu Ser Arg Val Asp Asn
    770                 775                 780
Lys Glu Arg Thr Val Ile Ser Asn Leu Arg Pro Phe Thr Leu Tyr Arg
785                 790                 795                 800
Ile Asp Ile His Ser Cys Asn His Glu Ala Glu Lys Leu Gly Cys Ser
                805                 810                 815
Ala Ser Asn Phe Val Phe Ala Arg Thr Met Pro Ala Glu Gly Ala Asp
            820                 825                 830
Asp Ile Pro Gly Pro Val Thr Trp Glu Pro Arg Pro Glu Asn Ser Ile
        835                 840                 845
Phe Leu Lys Trp Pro Glu Pro Glu Asn Pro Asn Gly Leu Ile Leu Met
    850                 855                 860
Tyr Glu Ile Lys Tyr Gly Ser Gln Val Glu Asp Gln Arg Glu Cys Val
865                 870                 875                 880
Ser Arg Gln Glu Tyr Arg Lys Tyr Gly Gly Ala Lys Leu Asn Arg Leu
                885                 890                 895
Asn Pro Gly Asn Tyr Thr Ala Arg Ile Gln Ala Thr Ser Leu Ser Gly
            900                 905                 910
Asn Gly Ser Trp Thr Asp Pro Val Phe Phe Tyr Val Gln Ala Lys Thr
        915                 920                 925
Gly Tyr Glu Asn Phe Ile His Leu Ile Ile Ala Leu Pro Val Ala Val
    930                 935                 940
Leu Leu Ile Val Gly Gly Leu Val Ile Met Leu Tyr Val Phe His Arg
945                 950                 955                 960
Lys Arg Asn Asn Ser Arg Leu Gly Asn Gly Val Leu Tyr Ala Ser Val
                965                 970                 975
Asn Pro Glu Tyr Phe Ser Ala Ala Asp Val Tyr Val Pro Asp Glu Trp
            980                 985                 990
Glu Val Ala Arg Glu Lys Ile Thr Met Ser Arg Glu Leu Gly Gln Gly
        995                 1000                1005
Ser Phe Gly Met Val Tyr Glu Gly Val Ala Lys Gly Val Val Lys Asp
    1010                1015                1020
Glu Pro Glu Thr Arg Val Ala Ile Lys Thr Val Asn Glu Ala Ala Ser
1025                1030                1035                1040
```

```
Met Arg Glu Arg Ile Glu Phe Leu Asn Glu Ala Ser Val Met Lys Glu
                1045                1050                1055
Phe Asn Cys His His Val Val Arg Leu Leu Gly Val Val Ser Gln Gly
            1060                1065                1070
Gln Pro Thr Leu Val Ile Met Glu Leu Met Thr Arg Gly Asp Leu Lys
        1075                1080                1085
Ser Tyr Leu Arg Ser Leu Arg Pro Glu Met Glu Asn Asn Pro Val Leu
    1090                1095                1100
Ala Pro Pro Ser Leu Ser Lys Met Ile Gln Met Ala Gly Glu Ile Ala
1105                1110                1115                1120
Asp Gly Met Ala Tyr Leu Asn Ala Asn Lys Phe Val His Arg Asp Leu
                1125                1130                1135
Ala Ala Arg Asn Cys Met Val Ala Glu Asp Phe Thr Val Lys Ile Gly
            1140                1145                1150
Asp Phe Gly Met Thr Arg Asp Ile Tyr Glu Thr Asp Tyr Tyr Arg Lys
        1155                1160                1165
Gly Gly Lys Gly Leu Leu Pro Val Arg Trp Met Ser Pro Glu Ser Leu
    1170                1175                1180
Lys Asp Gly Val Phe Thr Thr Tyr Ser Asp Val Trp Ser Phe Gly Val
1185                1190                1195                1200
Val Leu Trp Glu Ile Ala Thr Leu Ala Glu Gln Pro Tyr Gln Gly Leu
                1205                1210                1215
Ser Asn Glu Gln Val Leu Arg Phe Val Met Glu Gly Gly Leu Leu Asp
            1220                1225                1230
Lys Pro Asp Asn Cys Pro Asp Met Leu Phe Glu Leu Met Arg Met Cys
        1235                1240                1245
Trp Gln Tyr Asn Pro Lys Met Arg Pro Ser Phe Leu Glu Ile Ile Ser
    1250                1255                1260
Ser Ile Lys Glu Glu Met Glu Pro Gly Phe Arg Glu Val Ser Phe Tyr
1265                1270                1275                1280
Tyr Ser Glu Glu Asn Lys Leu Pro Glu Pro Glu Glu Leu Asp Leu Glu
                1285                1290                1295
Pro Glu Asn Met Glu Ser Val Pro Leu Asp Pro Ser Ala Ser Ser Ser
            1300                1305                1310
Ser Leu Pro Leu Pro Asp Arg His Ser Gly His Lys Ala Glu Asn Gly
        1315                1320                1325
Pro Gly Pro Gly Val Leu Val Leu Arg Ala Ser Phe Asp Glu Arg Gln
    1330                1335                1340
Pro Tyr Ala His Met Asn Gly Gly Arg Lys Asn Glu Arg Ala Leu Pro
1345                1350                1355                1360
Leu Pro Gln Ser Ser Thr Cys
                1365

<210> 754
<211> 259
<212> PRT
<213> Human

<400> 754
Met Ser Glu Val Pro Val Ala Arg Val Trp Leu Val Leu Leu Leu Leu
 1               5                  10                  15
Thr Val Gln Val Gly Val Thr Ala Gly Ala Pro Trp Gln Cys Ala Pro
            20                  25                  30
Cys Ser Ala Glu Lys Leu Ala Leu Cys Pro Pro Val Ser Ala Ser Cys
        35                  40                  45
Ser Glu Val Thr Arg Ser Ala Gly Cys Gly Cys Cys Pro Met Cys Ala
    50                  55                  60
```

```
Leu Pro Leu Gly Ala Ala Cys Gly Val Ala Thr Ala Arg Cys Ala Arg
65                  70                  75                  80
Gly Leu Ser Cys Arg Ala Leu Pro Gly Glu Gln Gln Pro Leu His Ala
                85                  90                  95
Leu Thr Arg Gly Gln Gly Ala Cys Val Gln Glu Ser Asp Ala Ser Ala
            100                 105                 110
Pro His Ala Ala Glu Ala Gly Ser Pro Glu Ser Pro Glu Ser Thr Glu
        115                 120                 125
Ile Thr Glu Glu Glu Leu Leu Asp Asn Phe His Leu Met Ala Pro Ser
    130                 135                 140
Glu Glu Asp His Ser Ile Leu Trp Asp Ala Ile Ser Thr Tyr Asp Gly
145                 150                 155                 160
Ser Lys Ala Leu His Val Thr Asn Ile Lys Lys Trp Lys Glu Pro Cys
                165                 170                 175
Arg Ile Glu Leu Tyr Arg Val Val Glu Ser Leu Ala Lys Ala Gln Glu
            180                 185                 190
Thr Ser Gly Glu Glu Ile Ser Lys Phe Tyr Leu Pro Asn Cys Asn Lys
        195                 200                 205
Asn Gly Phe Tyr His Ser Arg Gln Cys Glu Thr Ser Met Asp Gly Glu
    210                 215                 220
Ala Gly Leu Cys Trp Cys Val Tyr Pro Trp Asn Gly Lys Arg Ile Pro
225                 230                 235                 240
Gly Ser Pro Glu Ile Arg Gly Asp Pro Asn Cys Gln Ile Tyr Phe Asn
                245                 250                 255
Val Gln Asn
```

<210> 755
<211> 328
<212> PRT
<213> Human

<400> 755

```
Met Leu Pro Arg Val Gly Cys Pro Ala Leu Pro Leu Pro Pro Pro Pro
 1               5                  10                  15
Leu Leu Pro Leu Leu Pro Leu Leu Leu Leu Leu Leu Gly Ala Ser Gly
            20                  25                  30
Gly Gly Gly Gly Ala Arg Ala Glu Val Leu Phe Arg Cys Pro Pro Cys
        35                  40                  45
Thr Pro Glu Arg Leu Ala Ala Cys Gly Pro Pro Pro Val Ala Pro Pro
    50                  55                  60
Ala Ala Val Ala Ala Val Ala Gly Gly Ala Arg Met Pro Cys Ala Glu
65                  70                  75                  80
Leu Val Arg Glu Pro Gly Cys Gly Cys Cys Ser Val Cys Ala Arg Leu
                85                  90                  95
Glu Gly Glu Ala Cys Gly Val Tyr Thr Pro Arg Cys Gly Gln Gly Leu
            100                 105                 110
Arg Cys Tyr Pro His Pro Gly Ser Glu Leu Pro Leu Gln Ala Leu Val
        115                 120                 125
Met Gly Glu Gly Thr Cys Glu Lys Arg Arg Asp Ala Glu Tyr Gly Ala
    130                 135                 140
Ser Pro Glu Gln Val Ala Asp Asn Gly Asp Asp His Ser Glu Gly Gly
145                 150                 155                 160
Leu Val Glu Asn His Val Asp Ser Thr Met Asn Met Leu Gly Gly Gly
                165                 170                 175
Gly Ser Ala Gly Arg Lys Pro Leu Lys Ser Gly Met Lys Glu Leu Ala
            180                 185                 190
Val Phe Arg Glu Lys Val Thr Glu Gln His Arg Gln Met Gly Lys Gly
```

```
        195                 200                 205
Gly Lys His His Leu Gly Leu Glu Glu Pro Lys Lys Leu Arg Pro Pro
    210                 215                 220
Pro Ala Arg Thr Pro Cys Gln Gln Glu Leu Asp Gln Val Leu Glu Arg
225                 230                 235                 240
Ile Ser Thr Met Arg Leu Pro Asp Glu Arg Gly Pro Leu Glu His Leu
                245                 250                 255
Tyr Ser Leu His Ile Pro Asn Cys Asp Lys His Gly Leu Tyr Asn Leu
            260                 265                 270
Lys Gln Cys Lys Met Ser Leu Asn Gly Gln Arg Gly Glu Cys Trp Cys
        275                 280                 285
Val Asn Pro Asn Thr Gly Lys Leu Ile Gln Gly Ala Pro Thr Ile Arg
    290                 295                 300
Gly Asp Pro Glu Cys His Leu Phe Tyr Asn Glu Gln Gln Glu Ala Arg
305                 310                 315                 320
Gly Val His Thr Gln Arg Met Gln
                325
```

<210> 756
<211> 297
<212> PRT
<213> Human

<400> 756

```
Met Gln Arg Ala Arg Pro Thr Leu Trp Ala Ala Ala Leu Thr Leu Leu
 1               5                  10                  15
Val Leu Leu Arg Gly Pro Pro Val Ala Arg Ala Gly Ala Ser Ser Ala
            20                  25                  30
Gly Leu Gly Pro Val Val Arg Cys Glu Pro Cys Asp Ala Arg Ala Leu
        35                  40                  45
Ala Gln Cys Ala Pro Pro Pro Ala Val Cys Ala Glu Leu Val Arg Glu
    50                  55                  60
Pro Gly Cys Gly Cys Cys Leu Thr Cys Ala Leu Ser Glu Gly Gln Pro
65                  70                  75                  80
Cys Gly Ile Tyr Thr Glu Arg Cys Gly Ser Gly Leu Arg Cys Gln Pro
                85                  90                  95
Ser Pro Asp Glu Ala Arg Pro Leu Gln Ala Leu Leu Asp Gly Arg Gly
            100                 105                 110
Leu Cys Val Asn Ala Ser Ala Val Ser Arg Leu Arg Ala Tyr Leu Leu
        115                 120                 125
Pro Ala Pro Pro Ala Pro Gly Glu Pro Pro Ala Pro Gly Asn Ala Ser
    130                 135                 140
Glu Ser Glu Glu Asp Arg Ser Ala Gly Ser Val Glu Ser Pro Ser Val
145                 150                 155                 160
Ser Ser Thr His Arg Val Ser Asp Pro Lys Phe His Pro Leu His Ser
                165                 170                 175
Lys Ile Ile Ile Ile Lys Lys Gly His Ala Lys Asp Ser Gln Arg Tyr
            180                 185                 190
Lys Val Asp Tyr Glu Ser Gln Ser Thr Asp Thr Gln Asn Phe Ser Ser
        195                 200                 205
Glu Ser Lys Arg Glu Thr Glu Tyr Gly Pro Cys Arg Arg Glu Met Glu
    210                 215                 220
Asp Thr Leu Asn His Leu Lys Phe Leu Asn Val Leu Ser Pro Arg Gly
225                 230                 235                 240
Val His Ile Pro Asn Cys Asp Lys Lys Gly Phe Tyr Lys Lys Lys Gln
                245                 250                 255
Cys Arg Pro Ser Lys Gly Arg Lys Arg Gly Phe Cys Trp Cys Val Asp
```

```
            260                 265                 270
Lys Tyr Gly Gln Pro Leu Pro Gly Tyr Thr Thr Lys Gly Lys Glu Asp
        275                 280                 285
Val His Cys Tyr Ser Met Gln Ser Lys
    290                 295
```

<210> 757
<211> 291
<212> PRT
<213> Human

<400> 757

```
Met Gln Arg Ala Arg Pro Thr Leu Trp Ala Ala Ala Leu Thr Leu Leu
 1               5                  10                  15
Val Leu Leu Arg Gly Pro Pro Val Ala Arg Ala Gly Ala Ser Ser Ala
            20                  25                  30
Gly Leu Gly Pro Val Val Arg Cys Glu Pro Cys Asp Ala Arg Ala Leu
        35                  40                  45
Ala Gln Cys Ala Pro Pro Pro Ala Val Cys Ala Glu Leu Val Arg Glu
    50                  55                  60
Pro Gly Cys Gly Cys Cys Leu Thr Cys Ala Leu Ser Glu Gly Gln Pro
65                  70                  75                  80
Cys Gly Ile Tyr Thr Glu Arg Cys Gly Ser Gly Leu Arg Cys Gln Pro
                85                  90                  95
Ser Pro Asp Glu Ala Arg Pro Leu Gln Ala Leu Leu Asp Gly Arg Gly
            100                 105                 110
Leu Cys Val Asn Ala Ser Ala Val Ser Arg Leu Arg Ala Tyr Leu Leu
        115                 120                 125
Pro Ala Pro Pro Ala Pro Gly Asn Ala Ser Glu Ser Glu Glu Asp Arg
    130                 135                 140
Ser Ala Gly Ser Val Glu Ser Pro Ser Val Ser Ser Thr His Arg Val
145                 150                 155                 160
Ser Asp Pro Lys Phe His Pro Leu His Ser Lys Ile Ile Ile Ile Lys
                165                 170                 175
Lys Gly His Ala Lys Asp Ser Gln Arg Tyr Lys Val Asp Tyr Glu Ser
            180                 185                 190
Gln Ser Thr Asp Thr Gln Asn Phe Ser Ser Glu Ser Lys Arg Glu Thr
        195                 200                 205
Glu Tyr Gly Pro Cys Arg Arg Glu Met Glu Asp Thr Leu Asn His Leu
    210                 215                 220
Lys Phe Leu Asn Val Leu Ser Pro Arg Gly Val His Ile Pro Asn Cys
225                 230                 235                 240
Asp Lys Lys Gly Phe Tyr Lys Lys Lys Gln Cys Arg Pro Ser Lys Gly
                245                 250                 255
Arg Lys Arg Gly Phe Cys Trp Cys Val Asp Lys Tyr Gly Gln Pro Leu
            260                 265                 270
Pro Gly Tyr Thr Thr Lys Gly Lys Glu Asp Val His Cys Tyr Ser Met
        275                 280                 285
Gln Ser Lys
    290
```

<210> 758
<211> 258
<212> PRT
<213> Human

<400> 758

```
Met Leu Pro Leu Cys Leu Val Ala Ala Leu Leu Leu Ala Ala Gly Pro
 1               5                  10                  15
Gly Pro Ser Leu Gly Asp Glu Ala Ile His Cys Pro Pro Cys Ser Glu
            20                  25                  30
Glu Lys Leu Ala Arg Cys Arg Pro Pro Val Gly Cys Glu Glu Leu Val
        35                  40                  45
Arg Glu Pro Gly Cys Gly Cys Cys Ala Thr Cys Ala Leu Gly Leu Gly
    50                  55                  60
Met Pro Cys Gly Val Tyr Thr Pro Arg Cys Gly Ser Gly Leu Arg Cys
65                  70                  75                  80
Tyr Pro Pro Arg Gly Val Glu Lys Pro Leu His Thr Leu Met His Gly
                85                  90                  95
Gln Gly Val Cys Met Glu Leu Ala Glu Ile Glu Ala Ile Gln Glu Ser
            100                 105                 110
Leu Gln Pro Ser Asp Lys Asp Glu Gly Asp His Pro Asn Asn Ser Phe
        115                 120                 125
Ser Pro Cys Ser Ala His Asp Arg Arg Cys Leu Gln Lys His Phe Ala
    130                 135                 140
Lys Ile Arg Asp Arg Ser Thr Ser Gly Gly Lys Met Lys Val Asn Gly
145                 150                 155                 160
Ala Pro Arg Glu Asp Ala Arg Pro Val Pro Gln Gly Ser Cys Gln Ser
                165                 170                 175
Glu Leu His Arg Ala Leu Glu Arg Leu Ala Ala Ser Gln Ser Arg Thr
            180                 185                 190
His Glu Asp Leu Tyr Ile Ile Pro Ile Pro Asn Cys Asp Arg Asn Gly
        195                 200                 205
Asn Phe His Pro Lys Gln Cys His Pro Ala Leu Asp Gly Gln Arg Gly
    210                 215                 220
Lys Cys Trp Cys Val Asp Arg Lys Thr Gly Val Lys Leu Pro Gly Gly
225                 230                 235                 240
Leu Glu Pro Lys Gly Glu Leu Asp Cys His Gln Leu Ala Asp Ser Phe
                245                 250                 255
Arg Glu
```

<210> 759
<211> 272
<212> PRT
<213> Human

<400> 759

```
Met Val Leu Leu Thr Ala Val Leu Leu Leu Leu Ala Ala Tyr Ala Gly
 1               5                  10                  15
Pro Ala Gln Ser Leu Gly Ser Phe Val His Cys Glu Pro Cys Asp Glu
            20                  25                  30
Lys Ala Leu Ser Met Cys Pro Pro Ser Pro Leu Gly Cys Glu Leu Val
        35                  40                  45
Lys Glu Pro Gly Cys Gly Cys Cys Met Thr Cys Ala Leu Ala Glu Gly
    50                  55                  60
Gln Ser Cys Gly Val Tyr Thr Glu Arg Cys Ala Gln Gly Leu Arg Cys
65                  70                  75                  80
Leu Pro Arg Gln Asp Glu Glu Lys Pro Leu His Ala Leu Leu His Gly
                85                  90                  95
Arg Gly Val Cys Leu Asn Glu Lys Ser Tyr Arg Glu Gln Val Lys Ile
            100                 105                 110
Glu Arg Asp Ser Arg Glu His Glu Glu Pro Thr Thr Ser Glu Met Ala
        115                 120                 125
Glu Glu Thr Tyr Ser Pro Lys Ile Phe Arg Pro Lys His Thr Arg Ile
```

```
    130                 135                 140
Ser Glu Leu Lys Ala Glu Ala Val Lys Lys Asp Arg Arg Lys Lys Leu
145                 150                 155                 160
Thr Gln Ser Lys Phe Val Gly Gly Ala Glu Asn Thr Ala His Pro Arg
                165                 170                 175
Ile Ile Ser Ala Pro Glu Met Arg Gln Glu Ser Glu Gln Gly Pro Cys
            180                 185                 190
Arg Arg His Met Glu Ala Ser Leu Gln Glu Leu Lys Ala Ser Pro Arg
        195                 200                 205
Met Val Pro Arg Ala Val Tyr Leu Pro Asn Cys Asp Arg Lys Gly Phe
    210                 215                 220
Tyr Lys Arg Lys Gln Cys Lys Pro Ser Arg Gly Arg Lys Arg Gly Ile
225                 230                 235                 240
Cys Trp Cys Val Asp Lys Tyr Gly Met Lys Leu Pro Gly Met Glu Tyr
                245                 250                 255
Val Asp Gly Asp Phe Gln Cys His Thr Phe Asp Ser Ser Asn Val Glu
            260                 265                 270

<210> 760
<211> 240
<212> PRT
<213> Human

<400> 760
Met Thr Pro His Arg Leu Leu Pro Pro Leu Leu Leu Leu Leu Ala Leu
 1               5                  10                  15
Leu Leu Ala Ala Ser Pro Gly Gly Ala Leu Ala Arg Cys Pro Gly Cys
            20                  25                  30
Gly Gln Gly Val Gln Ala Gly Cys Pro Gly Gly Cys Val Glu Glu Glu
        35                  40                  45
Asp Gly Gly Ser Pro Ala Glu Gly Cys Ala Glu Ala Glu Gly Cys Leu
    50                  55                  60
Arg Arg Glu Gly Gln Glu Cys Gly Val Tyr Thr Pro Asn Cys Ala Pro
65                  70                  75                  80
Gly Leu Gln Cys His Pro Pro Lys Asp Asp Glu Ala Pro Leu Arg Ala
                85                  90                  95
Leu Leu Leu Gly Arg Gly Arg Cys Leu Pro Ala Arg Ala Pro Ala Val
            100                 105                 110
Ala Glu Glu Asn Pro Lys Glu Ser Lys Pro Gln Ala Gly Thr Ala Arg
        115                 120                 125
Pro Gln Asp Val Asn Arg Arg Asp Gln Gln Arg Asn Pro Gly Thr Ser
    130                 135                 140
Thr Thr Pro Ser Gln Pro Asn Ser Ala Gly Val Gln Asp Thr Glu Met
145                 150                 155                 160
Gly Pro Cys Arg Arg His Leu Asp Ser Val Leu Gln Gln Leu Gln Thr
                165                 170                 175
Glu Val Tyr Arg Gly Ala Gln Thr Leu Tyr Val Pro Asn Cys Asp His
            180                 185                 190
Arg Gly Phe Tyr Arg Lys Arg Gln Cys Arg Ser Ser Gln Gly Gln Arg
        195                 200                 205
Arg Gly Pro Cys Trp Cys Val Asp Arg Met Gly Lys Ser Leu Pro Gly
    210                 215                 220
Ser Pro Asp Gly Asn Gly Ser Ser Ser Cys Pro Thr Gly Ser Ser Gly
225                 230                 235                 240

<210> 761
<211> 79
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<212> PRT
<213> Human

<400> 761
Met Ala Arg Gly Ser Leu Arg Arg Leu Leu Arg Leu Leu Val Leu Gly
 1   5   10   15
Leu Trp Leu Ala Leu Leu Arg Ser Val Ala Gly Glu Gln Ala Pro Gly
            20   25   30
Thr Ala Pro Cys Ser Arg Gly Ser Ser Trp Ser Ala Asp Leu Asp Lys
        35   40   45
Cys Met Asp Cys Ala Ser Cys Arg Ala Arg Pro His Ser Asp Phe Cys
    50   55   60
Leu Gly Cys Ala Ala Ala Pro Pro Ala Pro Phe Arg Leu Leu Trp
65   70   75

<210> 762
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 762
Gln Gly Asp Ser Leu Arg Asn Tyr His Pro Ser
 1   5   10

<210> 763
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 763
Gly Lys Asn Asn Arg Pro Ser
 1   5

<210> 764
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 764
Asn Ser Arg Asp Ser Ser Gly Asn Leu Val Phe
 1   5   10

<210> 765
<211> 11
<212> PRT
<213> Artificial Sequence

<220>

<223> Made in lab

<400> 765
Ser Gly Asp Lys Leu Gly Asp Lys Tyr Ala Ser
 1   5   10

<210> 766
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 766
Gln Asp Arg Lys Arg Pro Ser
 1   5

<210> 767
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 767
Gln Ala Trp Asp Ser Asn Thr Val Val
 1   5

<210> 768
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 768
Ser Gly Ser Ser Ser Asn Ile Gly Ser Asp Tyr Val His
 1   5   10

<210> 769
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 769
Arg Asn Asn Lys Arg Pro Ser
 1   5

<210> 770
<211> 11
<212> PRT

<213> Artificial Sequence

<220>
<223> Made in lab

<400> 770
Ala Ala Trp Asp Asp Ser Leu Asn Gly Trp Val
 1   5   10

<210> 771
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 771
Ser Gly Asp Lys Leu Gly Asp Lys Tyr Ala Ser
 1   5   10

<210> 772
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 772
Glu Asp Asn Lys Arg Pro Ser
 1   5

<210> 773
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 773
Gln Thr Trp Ala Ser Gly Thr Val Leu
 1   5

<210> 774
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 774
Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn Thr Val Asn
 1   5   10

<210> 775
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 775
Ala Asn Asn Gln Arg Pro Ser
 1   5

<210> 776
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 776
Ala Val Trp Asp Asp Ser Leu Asn Ala Trp Val
 1   5   10

<210> 777
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 777
Ser Gly Asp Lys Leu Glu Asn Lys Tyr Thr Ser
 1   5   10

<210> 778
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 778
Glu Asp Ile Glu Arg Pro Ser
 1   5

<210> 779
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
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<400> 779

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Gly

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Gly

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Tyr Tyr Asp Met Gln
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<210> 1017
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
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<400> 1017
Tyr Ile Gly Pro Ser Gly Gly Asp Thr Asp Tyr Ala Asp Ser Val Lys
 1   5   10   15
Gly

<210> 1018
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1018
Ser Ser Tyr Tyr Tyr Asp Ser Ser Gly Tyr Tyr His Glu Ala Phe Asp
 1   5   10   15
Ile

<210> 1019
<211> 5
<212> PRT
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<220>
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<400> 1019
Tyr Tyr Met Met Arg
 1   5

<210> 1020
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1020

Tyr Ile Gly Pro Ser Gly Gly Ala Thr Thr Tyr Ala Asp Ser Val Lys
 1   5   10   15
Gly

<210> 1021
<211> 18
<212> PRT
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<220>
<223> Made in lab

<400> 1021
Gly Arg Ser Val Lys Tyr Tyr Tyr Asp Ser Ser Gly Tyr Leu Leu Phe
 1   5   10   15
Asp Tyr

<210> 1022
<211> 5
<212> PRT
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<220>
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<400> 1022
His Tyr Ser Met Tyr
 1   5

<210> 1023
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1023
Gly Ile Tyr Ser Ser Gly Gly Pro Thr Ile Tyr Ala Asp Ser Val Lys
 1   5   10   15
Gly

<210> 1024
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1024
Leu Gln Ile Glu Met Ala Thr Ile Gly His Phe Asp Tyr
 1   5   10

<210> 1025
<211> 5
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<220>
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<400> 1025
Gln Tyr Asp Met Val
 1   5

<210> 1026
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1026
Tyr Ile Tyr Ser Ser Gly Gly His Thr Leu Tyr Val Asp Ser Val Lys
 1   5   10   15
Gly

<210> 1027
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1027
Ile Arg Ser Ser Gly Tyr Tyr His Glu Val Leu Asp Tyr
 1   5   10

<210> 1028
<211> 5
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<220>
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<400> 1028
His Tyr Trp Met Met
 1   5

<210> 1029
<211> 17
<212> PRT
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<220>
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<400> 1029
Ser Ile Val Pro Ser Gly Gly Asp Thr Tyr Tyr Ala Asp Ser Val Lys
 1   5   10   15
Gly

<210> 1030
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<220>
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<400> 1030
Asp Pro Val Met Thr Pro Val Asp Tyr
 1   5

<210> 1031
<211> 5
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<220>
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<400> 1031
Pro Tyr Phe Met Asn
 1   5

<210> 1032
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1032
Ser Ile Tyr Pro Ser Gly Gly Ile Thr Lys Tyr Ala Asp Ser Val Lys
 1   5   10   15
Gly

<210> 1033
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1033
Glu Thr Tyr Tyr Tyr Gly Ser Gly Ser Tyr Ala Phe Asp Ile
 1   5   10

<210> 1034
<211> 5
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<220>
<223> Made in lab

<400> 1034
Gln Tyr Tyr Met Tyr
 1   5

<210> 1035
<211> 17
<212> PRT
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<220>
<223> Made in lab

<400> 1035
Arg Ile Ser Pro Ser Gly Gly Met Thr Ser Tyr Ala Asp Ser Val Lys
 1   5   10   15
Gly

<210> 1036
<211> 8
<212> PRT
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<220>
<223> Made in lab

<400> 1036
His Lys Tyr Gly Gly Pro Asp Phe
 1   5

<210> 1037
<211> 5
<212> PRT
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<220>
<223> Made in lab

<400> 1037
Arg Tyr Gln Met Asn
 1   5

<210> 1038
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1038
Ser Ile Arg Ser Ser Gly Gly Val Thr Lys Tyr Ala Asp Ser Val Lys
 1   5   10   15
Gly

<210> 1039
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1039
Gly Arg Gly Leu Ser Ser
 1   5

<210> 1040
<211> 5
<212> PRT
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<220>
<223> Made in lab

<400> 1040
Leu Tyr Thr Met Ala
 1   5

<210> 1041
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1041
Tyr Ile Ser Pro Ser Gly Gly Phe Thr Gly Tyr Ala Asp Ser Val Lys
 1   5   10   15
Gly

<210> 1042
<211> 4
<212> PRT
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<220>
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<400> 1042
Trp Gly Asp Pro
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<210> 1043
<211> 5
<212> PRT
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<220>
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<400> 1043
Asp Tyr Phe Met Gly
 1   5

<210> 1044
<211> 17
<212> PRT
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<220>
<223> Made in lab

<400> 1044
Arg Ile Ser Ser Ser Gly Gly His Thr Met Tyr Ala Asp Ser Val Lys
 1   5   10   15
Gly

<210> 1045
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1045
Glu Glu Asp Tyr Tyr Asp Ser Ser Gly Tyr Tyr Pro Pro Ala Phe Asp
 1   5   10   15
Ile

<210> 1046
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1046
Ile Tyr Trp Met Tyr
 1   5

<210> 1047
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1047
Gly Ile Gly Pro Ser Gly Gly Tyr Thr Ser Tyr Ala Asp Ser Val Lys
 1   5   10   15
Gly

<210> 1048
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1048
Gly Asn Gly Gly Phe Asp Ser
 1   5

<210> 1049
<211> 5
<212> PRT
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<220>
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<400> 1049
Pro Tyr His Met Ser
 1   5

<210> 1050
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1050
Ser Ile Tyr Pro Ser Gly Gly Phe Thr Ala Tyr Ala Asp Ser Val Lys
 1   5   10   15
Gly

<210> 1051
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1051
Glu Ser Ala Tyr Tyr Tyr Asp Ser Ser Pro Pro Ala Phe Asp Ile

1 5 10 15

<210> 1052
<211> 5
<212> PRT
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<220>
<223> Made in lab

<400> 1052
Thr Tyr Ala Met Tyr
1 5

<210> 1053
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1053
Ser Ile Tyr Ser Ser Gly Gly Ala Thr Trp Tyr Ala Asp Ser Val Lys
1 5 10 15
Gly

<210> 1054
<211> 8
<212> PRT
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<220>
<223> Made in lab

<400> 1054
Ser Thr Phe Asp Tyr Phe Asp Tyr
1 5

<210> 1055
<211> 5
<212> PRT
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<220>
<223> Made in lab

<400> 1055
Lys Tyr Arg Met Met
1 5

<210> 1056
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1056
Tyr Ile Ser Ser Ser Gly Gly Ala Thr Ile Tyr Ala Asp Ser Val Lys
 1   5   10   15
Gly

<210> 1057
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1057
His Gly Pro Gln Ile Ala Ala Trp Tyr Phe Asp Leu
 1   5   10

<210> 1058
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1058
Pro Tyr Ser Met Asp
 1   5

<210> 1059
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1059
Gly Ile Ser Ser Ser Gly Gly Arg Thr Val Tyr Ala Asp Ser Val Lys
 1   5   10   15
Gly

<210> 1060
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1060
Gly Pro Tyr Tyr Asp Phe Trp Ser Gly Tyr Tyr Ile Asp Arg Gly Pro

1 5 10 15
Leu Asp Tyr

<210> 1061
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1061
Trp Tyr Met Met Ala
1 5

<210> 1062
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1062
Trp Ile Ser Ser Ser Gly Gly Phe Thr Pro Tyr Ala Asp Ser Val Lys
1 5 10 15
Gly

<210> 1063
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1063
Gly Gln Gln Trp Pro Gly Val Ala Phe Asp Ile
1 5 10

<210> 1064
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1064
Phe Tyr Pro Met Met
1 5

<210> 1065
<211> 15
<212> PRT

<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1065
Tyr Ile Gly Pro Ser Gly Gly Asn Asn Ala Asp Ser Val Lys Gly
 1   5   10   15

<210> 1066
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1066
Gly Leu Trp Phe Gly Gly Arg Leu Asp Tyr
 1   5   10

<210> 1067
<211> 5
<212> PRT
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<220>
<223> Made in lab

<400> 1067
His Tyr Trp Met Lys
 1   5

<210> 1068
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1068
Gly Ile Ser Ser Ser Gly Gly Gln Thr Asp Tyr Ala Asp Ser Val Lys
 1   5   10   15
Gly

<210> 1069
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1069
Ser Pro Arg Leu Arg Phe Leu Glu Trp Pro Arg Asn Tyr Tyr Gly Met

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 1               5                  10                  15
Asp Val


<210> 1070
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1070
Leu Tyr Met Met Val
 1               5

<210> 1071
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1071
Tyr Ile Gly Pro Ser Gly Gly Ala Tyr Ala Asp Ser Val Lys Gly
 1               5                  10                  15

<210> 1072
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1072
Ser Val Arg Gly Leu Thr Phe Asp Tyr
 1               5

<210> 1073
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1073
Pro Tyr Glu Met Gly
 1               5

<210> 1074
<211> 17
<212> PRT
<213> Artificial Sequence
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<220>
<223> Made in lab

<400> 1074
Arg Ile Ser Pro Ser Gly Gly Met Thr Leu Tyr Ala Asp Ser Val Lys
 1   5   10   15
Gly

<210> 1075
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1075
Met Gly Arg Gly Gly Trp Trp Ala Phe Asp Ala Phe Asp Ile
 1   5   10

<210> 1076
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1076
Trp Tyr Lys Met Val
 1   5

<210> 1077
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1077
Gly Ile Tyr Pro Ser Gly Gly Thr Thr His Tyr Ala Asp Ser Val Lys
 1   5   10   15
Gly

<210> 1078
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1078
Gly Gly Gly Asp Phe Trp Ser Gly Tyr Tyr Pro Phe Asp Tyr

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 1               5                  10

<210> 1079
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1079
Gln Ser Ala Leu Thr Gln Asp Pro Ala Val Ser Val Ala Leu Gly Gln
 1               5                  10                  15
Thr Val Arg Phe Thr Cys Gln Gly Asp Ser Leu Arg Asn Tyr His Pro
            20                  25                  30
Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
        35                  40                  45
Gly Lys Asn Asn Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser
    50                  55                  60
Thr Ser Gly Asp Thr Ala Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu
65                  70                  75                  80
Asp Glu Ala Asp Tyr Tyr Cys Asn Ser Arg Asp Ser Ser Gly Asn Leu
                85                  90                  95
Val Phe Phe Ala Gly Gly Thr Lys Leu Thr Val Leu
            100                 105

<210> 1080
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1080
Gln Tyr Glu Leu Thr Gln Pro Pro Ser Val Ser Val Ser Pro Gly Gln
 1               5                  10                  15
Thr Ala Ser Ile Thr Cys Ser Gly Asp Lys Leu Gly Asp Lys Tyr Ala
            20                  25                  30
Ser Trp Tyr Gln Gln Lys Pro Asp Gln Ser Pro Val Leu Val Ile Tyr
        35                  40                  45
Gln Asp Arg Lys Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
    50                  55                  60
Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr Gln Ala Met
65                  70                  75                  80
Asp Glu Ala Asp Tyr Tyr Cys Gln Ala Trp Asp Ser Asn Thr Val Val
                85                  90                  95
Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100                 105

<210> 1081
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab
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<400> 1081
Gln Ser Ala Leu Thr Gln Ser Pro Ser Ala Ser Gly Thr Pro Gly Gln
 1   5   10   15
Thr Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ser Asp
            20   25   30
Tyr Val His Trp Tyr Gln His Leu Pro Gly Thr Ala Pro Lys Leu Leu
        35   40   45
Ile Tyr Arg Asn Asn Lys Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
    50   55   60
Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Arg
65   70   75   80
Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu
                85   90   95
Asn Gly Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100   105   110

<210> 1082
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1082
Gln Tyr Glu Leu Thr Gln Pro Pro Ser Val Ser Val Ser Pro Gly Gln
 1   5   10   15
Thr Ala Ser Ile Thr Cys Ser Gly Asp Lys Leu Gly Asp Lys Tyr Ala
            20   25   30
Ser Trp Tyr Gln Gln Arg Pro Gly Gln Ser Pro Val Val Ile Ile Tyr
        35   40   45
Glu Asp Asn Lys Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
    50   55   60
Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr Gln Thr Met
65   70   75   80
Asp Glu Ala Asp Tyr Tyr Cys Gln Thr Trp Ala Ser Gly Thr Val Leu
                85   90   95
Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100   105

<210> 1083
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1083
Gln Tyr Glu Leu Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln
 1   5   10   15
Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn
            20   25   30
Thr Val Asn Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
        35   40   45
Ile Tyr Ala Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser

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    50                  55                  60
Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln
65                  70                  75                  80
Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Val Trp Asp Asp Ser Leu
                85                  90                  95
Asn Ala Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100                 105                 110

<210> 1084
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1084
Gln Tyr Glu Leu Thr Gln Pro Pro Ser Val Ser Val Ser Pro Gly Gln
 1               5                  10                  15
Thr Ala Arg Ile Thr Cys Ser Gly Asp Lys Leu Glu Asn Lys Tyr Thr
            20                  25                  30
Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Val Leu Val Ile Tyr
        35                  40                  45
Glu Asp Ile Glu Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
    50                  55                  60
Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr Gln Ala Met
65                  70                  75                  80
Asp Glu Ala Asp Tyr Tyr Cys Gln Ala Trp Asp Ser Asn Ile Ala Val
                85                  90                  95
Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100                 105

<210> 1085
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1085
Gln Ser Ala Leu Thr Gln Pro Pro Ser Ala Ser Glu Thr Pro Gly Gln
 1               5                  10                  15
Arg Val Thr Ile Ser Cys Ser Gly Gly Asn Ser Asn Ile Gly Ser His
            20                  25                  30
Tyr Val Tyr Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
        35                  40                  45
Ile Tyr Arg Asp Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
    50                  55                  60
Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Phe Ser Gly Leu Arg
65                  70                  75                  80
Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu
                85                  90                  95
Gly Gly Pro Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100                 105                 110

<210> 1086
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<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1086
Gln Ser Val Leu Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln
 1   5   10   15
Arg Val Thr Ile Ser Ser Ser Gly Ser Ser Ser Asn Ile Gly Arg Asn
            20   25   30
Ala Val Asn Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
        35   40   45
Ile Tyr Asn Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
    50   55   60
Ala Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln
65   70   75   80
Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu
                85   90   95
Asn Gly Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100   105   110

<210> 1087
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1087
Gln Tyr Glu Leu Thr Gln Ala Pro Ser Val Ser Val Ala Pro Gly Gln
 1   5   10   15
Thr Ala Thr Ile Ser Cys Gly Gly Asn Asn Ile Gly Asp Lys Ser Val
            20   25   30
His Trp Tyr Arg Gln Arg Pro Gly Gln Ala Pro Met Val Val Ile Tyr
        35   40   45
Glu Asp Lys Asn Arg Pro Ala Gly Ile Pro Glu Arg Leu Ser Gly Ser
    50   55   60
Asn Ser Glu Asn Thr Ala Thr Leu Thr Ile Asn Arg Val Glu Ala Glu
65   70   75   80
Asp Glu Ala Asp Tyr Phe Cys Gln Val Trp Asp Ser Ser Thr Asp His
                85   90   95
His Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100   105

<210> 1088
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1088
Gln Tyr Glu Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Lys

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 1               5                  10                  15
Thr Ala Thr Ile Thr Cys Gly Gly Asn Asn Ile Gly Thr Thr Ser Val
            20                  25                  30
Gln Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Ile Ile Tyr
        35                  40                  45
Tyr Gly Ser Asp Arg Pro Ser Arg Ile Pro Glu Arg Phe Ser Gly Ser
    50                  55                  60
Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Ala Gln Pro Val
65                  70                  75                  80
Asp Glu Ala Asp Tyr Ile Cys Gln Thr Trp Val Lys Gly Ala Gly Ile
                85                  90                  95
Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100                 105

<210> 1089
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1089
Gln Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
 1               5                  10                  15
Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Arg Asn
            20                  25                  30
Tyr Leu Asn Trp Tyr Gln Gln Glu Pro Gly Lys Ala Pro Lys Leu Leu
        35                  40                  45
Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser
    50                  55                  60
Gly Ser Gly Ser Gly Thr Asp Phe Ile Leu Thr Ile Ser Ser Leu Gln
65                  70                  75                  80
Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Val Thr Pro
                85                  90                  95
Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100                 105

<210> 1090
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1090
Gln Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu
 1               5                  10                  15
Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Val Asn Ser
            20                  25                  30
Leu Asn Trp Tyr Gln Gln Arg Arg Gly Glu Ala Pro Lys Leu Leu Ile
        35                  40                  45
Ser Gly Ile Ser Ser Leu Arg Arg Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60
Ser Arg Ser Gly Thr Asp Phe Ile Leu Thr Ile Ser Ser Leu Glu Pro
65                  70                  75                  80
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Glu Asp Phe Ala Thr Tyr Phe Cys Gln Gln Ser His Ser Val Pro Leu
                85                  90                  95
Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100                 105

<210> 1091
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1091
Gln Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
 1               5                  10                  15
Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Arg Asn
            20                  25                  30
Asp Leu Gly Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu
        35                  40                  45
Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser
    50                  55                  60
Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln
65                  70                  75                  80
Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro
                85                  90                  95
Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100                 105

<210> 1092
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1092
Gln Asp Ile Gln Met Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro
 1               5                  10                  15
Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser
            20                  25                  30
Asp Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
        35                  40                  45
Ile Tyr Asp Ala Phe Lys Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser
    50                  55                  60
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu
65                  70                  75                  80
Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asn Trp Pro
                85                  90                  95
Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100                 105

<210> 1093
<211> 108
<212> PRT
<213> Artificial Sequence
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<220>
<223> Made in lab

<400> 1093
Gln Asp Ile Gln Met Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro
 1   5   10   15
Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val 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 Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser
    50   55   60
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu
65   70   75   80
Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asn Trp Pro
                85   90   95
Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100   105

<210> 1094
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1094
Gln Asp Ile Gln Met Thr Gln Ser Pro Leu Ser Leu Pro Val Ile Pro
 1   5   10   15
Gly Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu Tyr
            20   25   30
Ser Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln
        35   40   45
Ser Pro Gln Leu Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val
    50   55   60
Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys
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 Ser Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile
            100   105   110
Lys

<210> 1095
<211> 105
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1095
Gln Asp Ile Gln Met Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro
 1   5   10   15

Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser
            20   25   30
Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu
        35   40   45
Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe
    50   55   60
Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu
65   70   75   80
Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Ile Phe
                85   90   95
Gly Gly Gly Thr Lys Val Glu Ile Lys
            100   105

<210> 1096
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1096
Gln Asp Ile Gln Met Thr Gln Ser Pro Ala Thr Leu Ser Val Ser Pro
 1   5   10   15
Gly Glu Arg Val Thr Leu Ser Cys Arg Thr Ser Gln Tyr Ile Arg Thr
            20   25   30
Asn Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Arg Leu Leu
        35   40   45
Ile Arg Asp Gly Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Thr
    50   55   60
Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Glu
65   70   75   80
Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asn Trp Pro
                85   90   95
Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100   105

<210> 1097
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1097
Gln Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
 1   5   10   15
Gly Asp Arg Val Thr Ile Thr Cys Arg Thr Ser Gln Gln Ile Met Thr
            20   25   30
Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu
        35   40   45
Ile Tyr Val Ala Ser Arg Leu Gln Gly Gly Val Pro Ser Arg Phe Ser
    50   55   60
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln
65   70   75   80
Pro Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Phe Trp Thr Pro

```
                85                  90                  95
Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Arg
            100                 105

<210> 1098
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1098
Gln Asp Ile Gln Met Thr Gln Ser Pro Asp Ser Leu Ser Ala Ser Val
 1               5                  10                  15
Gly Asp Thr Ile Thr Ile Ser Cys Gln Ala Ser Gln Asp Ile Asp Asn
            20                  25                  30
Tyr Leu Asn Trp Tyr Gln Gln Arg Ser Gly Lys Ala Pro Lys Leu Leu
        35                  40                  45
Ile Tyr Asp Ala Tyr Asn Leu Lys Ala Gly Val Pro Ser Arg Phe Arg
    50                  55                  60
Gly Ser Arg Ser Gly Thr Asp Phe Phe Leu Thr Ile Ser Ser Leu Gln
65                  70                  75                  80
Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Val Phe Asp Asp Leu Ser
                85                  90                  95
Val Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Arg
            100                 105

<210> 1099
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1099
Gln Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Val Ser Val
 1               5                  10                  15
Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Lys Asn
            20                  25                  30
Asp Leu Gly Trp Tyr Gln Gln Arg Pro Gly Lys Ala Pro Lys Leu Leu
        35                  40                  45
Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser
    50                  55                  60
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln
65                  70                  75                  80
Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Asn Ser Phe Pro
                85                  90                  95
Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Val Lys
            100                 105

<210> 1100
<211> 108
<212> PRT
<213> Artificial Sequence
```

<220>
<223> Made in lab

<400> 1100
Gln Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
 1   5   10   15
Gly Asp Arg Val Thr Ile Thr Cys Gln Ala Ser His Asp Ile Asn Asn
            20   25   30
Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Asn Val Leu
        35   40   45
Ile Tyr Asp Ala Ser Asn Leu Gln Ser Gly Val Pro Ser Arg Phe Ser
    50   55   60
Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln
65   70   75   80
Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asp Thr Leu Pro
                85   90   95
Val Thr Phe Gly Gly Gly Thr Lys Val Gln Thr Lys
            100   105

<210> 1101
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1101
Gln Ser Ala Leu Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln
 1   5   10   15
Arg Val Thr Ile Ser Cys Ala Gly Ser Ser Ser Asn Ile Gly Ser Asn
            20   25   30
Ser Val Tyr Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Arg Leu Leu
        35   40   45
Leu Tyr Ser Asn Asn Lys Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
    50   55   60
Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Arg
65   70   75   80
Ser Glu Asp Asp Gly Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu
                85   90   95
Arg Ser Val Val Phe Gly Gly Gly Thr Gln Leu Thr Val Leu
            100   105   110

<210> 1102
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1102
Gln Ser Ala Leu Thr Gln Pro Pro Ser Val Ser Gly Thr Pro Gly Gln
 1   5   10   15
Lys Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Thr Ile Gly Ser Asn
            20   25   30
Phe Val Asn Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu

```
        35                  40                  45
Ile Tyr Thr Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
    50                  55                  60
Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln
65                  70                  75                  80
Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Thr Trp Asp Asp Asn Leu
                85                  90                  95
Leu Gly Pro Val Phe Gly Gly Gly Thr Arg Leu Ala Val Leu
            100                 105                 110
```

<210> 1103
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1103

```
Gln Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val
 1               5                  10                  15
Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Glu Gly Ile Ser Ser
            20                  25                  30
Arg Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Val Leu
        35                  40                  45
Ile Tyr Ala Thr Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser
    50                  55                  60
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Gly Leu Gln
65                  70                  75                  80
Pro Glu Asp Phe Ala Ser Tyr Tyr Cys Leu Gln Ala Asn Thr Leu Pro
                85                  90                  95
Leu Thr Phe Gly Gly Gly Thr Arg Val Glu Ile Lys
            100                 105
```

<210> 1104
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1104

```
Gln Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
 1               5                  10                  15
Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Leu Gly Val Ser Asn
            20                  25                  30
Tyr Leu Ala Trp Leu Gln Gln Lys Pro Gly Lys Ala Pro Lys Ser Leu
        35                  40                  45
Ile Tyr Ala Ala Ser Ile Leu Gln Thr Gly Val Pro Ser Lys Phe Ser
    50                  55                  60
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Asn Leu Gln
65                  70                  75                  80
Pro Asp Asp Ser Ala Thr Tyr Tyr Cys Gln His Tyr Gln Gly Tyr Pro
                85                  90                  95
Tyr Thr Phe Gly Asn Gly Thr Lys Leu Glu Ile Arg
            100                 105
```

<210> 1105
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1105
Gln Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
 1   5   10   15
Gly Asp Arg Val Ala Ile Thr Cys Arg Ala Ser Gln Ser Ile Asp Thr
            20   25   30
Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu
        35   40   45
Ile Tyr Ala Ala Ser Lys Leu Glu Asp Gly Val Pro Ser Arg Phe Ser
    50   55   60
Gly Ser Gly Thr Gly Thr Asp Phe Thr Leu Thr Ile Arg Ser Leu Gln
65   70   75   80
Pro Glu Asp Phe Ala Ser Tyr Phe Cys Gln Gln Ser Tyr Ser Ser Pro
                85   90   95
Gly Ile Thr Phe Gly Pro Gly Thr Lys Val Glu Ile Lys
            100   105

<210> 1106
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1106
Gln Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
 1   5   10   15
Gly Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Asp Ile Ser Asp
            20   25   30
Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu
        35   40   45
Ile Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val Thr Ser Arg Phe Ser
    50   55   60
Gly Ser Gly Tyr Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln
65   70   75   80
Pro Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Asn Asp Asn Leu Pro
                85   90   95
Phe Thr Phe Gly Pro Gly Thr Lys Val His Ile Lys
            100   105

<210> 1107
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1107
Gln Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
 1   5   10   15
Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser
            20   25   30
Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu
        35   40   45
Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser
    50   55   60
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln
65   70   75   80
Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro
                85   90   95
Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100   105

<210> 1108
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1108
Gln Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
 1   5   10   15
Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Gly Gln Ala Ile Arg Asn
            20   25   30
Asn Leu Gly Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Asn Arg Leu
        35   40   45
Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser
    50   55   60
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln
65   70   75   80
Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln His Asn Ser Phe Pro
                85   90   95
Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100   105

<210> 1109
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1109
Gln Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
 1   5   10   15
Gly Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Asp Ile Ile Asn
            20   25   30
Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu
        35   40   45
Ile Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser
    50   55   60

```
Gly Gly Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln
65                  70                  75                  80
Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asp Asn Leu Pro
                85                  90                  95
Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100                 105

<210> 1110
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1110
Gln Asp Ile Gln Met Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro
 1               5                  10                  15
Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Thr Gln Ser Val Arg His
            20                  25                  30
Asn Tyr Leu Ala Trp Tyr Gln Gln Arg Pro Gly Gln Ala Pro Arg Leu
        35                  40                  45
Leu Ile Phe Gly Ala Phe Phe Arg Ala Thr Gly Ile Pro Asp Arg Phe
    50                  55                  60
Ser Gly Arg Gly Ser Glu Thr Asp Phe Thr Leu Thr Ile Asp Arg Leu
65                  70                  75                  80
Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser
                85                  90                  95
Pro Val Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100                 105

<210> 1111
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1111
Gln Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
 1               5                  10                  15
Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser
            20                  25                  30
Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu
        35                  40                  45
Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser
    50                  55                  60
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln
65                  70                  75                  80
Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Ser
                85                  90                  95
Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100                 105

<210> 1112
<211> 110
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<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1112
Gln Asp Ile Gln Met Thr Gln Ser Pro Gly Thr Leu Ser Leu Phe Pro
 1   5   10   15
Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser
            20   25   30
Arg Tyr Leu Ala Trp Tyr Gln Gln Arg Phe Gly Gln Ala Pro Arg Leu
        35   40   45
Leu Ile Tyr Ala Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe
    50   55   60
Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu
65   70   75   80
Glu Pro Glu Asp Ser Ala Phe Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser
                85   90   95
Pro Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100   105   110

<210> 1113
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1113
Gln Asp Ile Gln Met Thr Gln Ser Pro Gly Thr Leu Ser Val Ser Pro
 1   5   10   15
Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Phe
            20   25   30
Ser Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
        35   40   45
Ile Tyr Asp Thr Ser Asn Arg Val Ala Gly Ile Pro Ala Arg Phe Ser
    50   55   60
Gly Ser Gly Ala Gly Thr Asp Phe Thr Leu Ser Ile Ser Thr Leu Glu
65   70   75   80
Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln His Arg Ser Asn Trp Pro
                85   90   95
Gly Phe Gly Gln Gly Thr Lys Leu Glu Leu Lys
            100   105

<210> 1114
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1114
Gln Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
 1   5   10   15

```
Gly Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Asp Ile Ile Asn
            20                  25                  30
Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu
        35                  40                  45
Ile Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser
    50                  55                  60
Gly Gly Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln
65                  70                  75                  80
Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asp Asn Leu Pro
                85                  90                  95
Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Asn Lys
            100                 105

<210> 1115
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1115
Gln Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
 1               5                  10                  15
Gly Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln His Ile Ser Lys
            20                  25                  30
Tyr Leu Asn Trp Tyr Gln Gln Gln Pro Gly Lys Ala Pro Lys Leu Leu
        35                  40                  45
Ile Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser
    50                  55                  60
Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln
65                  70                  75                  80
Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asp Asn Leu Pro
                85                  90                  95
Leu Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
            100                 105

<210> 1116
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1116
Gln Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
 1               5                  10                  15
Gly Asp Thr Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Gly Ser
            20                  25                  30
Tyr Leu Asn Trp Tyr Gln Glu Lys Ser Gly Lys Ala Pro Lys Leu Leu
        35                  40                  45
Ile Tyr Ala Ala Thr Ser Leu His Thr Gly Val Pro Ser Arg Phe Ser
    50                  55                  60
Gly Ser Gly Ser Gly Ala Glu Phe Thr Leu Thr Ile Asn Gly Leu Gln
65                  70                  75                  80
Pro Glu Asp Ser Ala Thr Tyr Tyr Cys Gln Gln Tyr Asp Asn Tyr Pro
```

```
                85                  90                  95
Leu Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
            100                 105

<210> 1117
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1117
Gln Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
 1               5                  10                  15
Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Arg Asn
            20                  25                  30
Asp Leu Gly Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu
        35                  40                  45
Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser
    50                  55                  60
Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln
65                  70                  75                  80
Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro
                85                  90                  95
Arg Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
            100                 105

<210> 1118
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1118
Gln Asp Ile Gln Met Thr Gln Ser Pro Ala Thr Leu Ser Val Ser Pro
 1               5                  10                  15
Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser
            20                  25                  30
Asn Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
        35                  40                  45
Ile Tyr Gly Ala Ser Thr Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser
    50                  55                  60
Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln
65                  70                  75                  80
Ser Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Asn Asn Trp Pro
                85                  90                  95
Arg Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
            100                 105

<210> 1119
<211> 108
<212> PRT
<213> Artificial Sequence
```

<220>
<223> Made in lab

<400> 1119
Gln Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
 1   5   10   15
Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Arg Ile Ile Asn
            20   25   30
Tyr Val Ser Trp Phe Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu
        35   40   45
Ile Tyr Gly Ala Ser Thr Leu Gln Thr Gly Val Pro Ser Arg Phe Thr
    50   55   60
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Thr Ser Leu Gln
65   70   75   80
Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Arg Gln Ser Tyr Ser Ser Pro
                85   90   95
Leu Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Arg
            100   105

<210> 1120
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1120
Gln Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
 1   5   10   15
Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Thr Ile Thr Thr
            20   25   30
Ser Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu
        35   40   45
Ile Asp Ala Ala Ser Arg Leu Gln Asn Gly Val Pro Ser Arg Phe Ser
    50   55   60
Gly Thr Gly Ser Gly Thr His Phe Thr Leu Thr Val Ser Ser Leu Gln
65   70   75   80
Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Asn Ile Pro
                85   90   95
Tyr Thr Phe Gly Gln Gly Thr Asn Leu Asp Met Lys
            100   105

<210> 1121
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1121
Gln Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
 1   5   10   15
Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Gly Ser
            20   25   30
Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu

```
        35                  40                  45
Ile Ser Asp Ala Ser Asn Leu Gln Ser Gly Val Pro Ser Arg Phe Ser
    50                  55                  60
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ala Ser Leu Gln
65                  70                  75                  80
Pro Asp Asp Phe Ala Thr Tyr His Cys Gln Gln Ser Tyr Arg Leu Phe
                85                  90                  95
Pro Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
            100                 105

<210> 1122
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1122
Gln Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val
 1               5                  10                  15
Gly Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Gly Ile Tyr Asn
            20                  25                  30
Tyr Val Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu
        35                  40                  45
Ile Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val Pro Pro Arg Phe Ser
    50                  55                  60
Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Thr Ser Leu Gln
65                  70                  75                  80
Pro Glu Asp Thr Ala Thr Tyr Tyr Cys Gln Gln Tyr Asp Asp Val Pro
                85                  90                  95
Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
            100                 105

<210> 1123
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1123
Gln Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val
 1               5                  10                  15
Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Ser
            20                  25                  30
Trp Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu
        35                  40                  45
Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser
    50                  55                  60
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln
65                  70                  75                  80
Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ala Asn Ser Phe Pro
                85                  90                  95
Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
            100                 105
```

<210> 1124
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1124
Gln Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
 1   5   10   15
Gly Asp Arg Val Thr Ile Ser Cys Arg Ser Ser Gln Ser Ile Ala Lys
            20   25   30
Tyr Leu Thr Trp Tyr Gln Gln Lys Ala Gly Lys Ala Pro Lys Leu Leu
        35   40   45
Ile Phe Ala Ala Ser Glu Leu Gln Ser Gly Val Pro Ser Arg Phe Ser
    50   55   60
Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Thr Ser Leu Gln
65   70   75   80
Pro Glu Asp Phe Val Thr Tyr Tyr Cys Gln Gln Thr Tyr Ser Phe Pro
                85   90   95
His Thr Phe Gly Gln Gly Thr Ser Leu Arg Ile Lys
            100   105

<210> 1125
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1125
Gln Tyr Glu Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Gln
 1   5   10   15
Thr Ala Lys Ile Thr Cys Ala Gly Asn Asn Ile Gly Ser Lys Ser Val
            20   25   30
His Trp Tyr Gln Gln Arg Pro Gly Gln Ala Pro Val Leu Val Val Tyr
        35   40   45
Asp Asp Ser Asp Arg Pro Pro Gly Ile Pro Glu Arg Leu Ser Gly Ser
    50   55   60
Asn Ser Glu Asn Thr Ala Thr Leu Thr Ile Ser Arg Val Glu Ala Gly
65   70   75   80
Asp Glu Ala Asp Tyr Tyr Cys Gln Val Trp Asp Ser Asp Ser Asp His
                85   90   95
Tyr Val Phe Gly Ser Gly Thr Lys Val Thr Val Leu
            100   105

<210> 1126
<211> 105
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1126
Gln Tyr Glu Leu Thr Gln Pro Pro Ser Val Ser Val Ser Pro Gly Gln
 1   5   10   15
Thr Ala Ser Ile Thr Cys Ser Gly Asp Arg Leu Gly Asp Lys Tyr Ala
            20   25   30
Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Val Tyr
        35   40   45
Asp Asp Ser Glu Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
    50   55   60
Asn Ser Gly Asn Thr Ala Ala Leu Thr Ile Gly Arg Val Glu Ala Gly
65   70   75   80
Asp Glu Ala Asp Tyr Tyr Cys Gln Val Trp Asp Ser Ser Ile Val Phe
                85   90   95
Gly Ser Gly Thr Lys Val Thr Val Leu
            100   105

<210> 1127
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1127
Gln Ser Val Leu Thr Gln Pro Arg Ser Val Ser Gly Ser Leu Gly Gln
 1   5   10   15
Ser Val Thr Ile Ser Cys Thr Gly Ser Thr Ser Asp Val Gly Gly Tyr
            20   25   30
Thr Tyr Val Ser Trp Tyr Gln Gln Glu Pro Gly Lys Ala Pro Lys Leu
        35   40   45
Met Ile His Asp Val Ser Lys Arg Pro Ser Gly Val Pro Asp Arg Phe
    50   55   60
Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Ile Ile Ser Gly Leu
65   70   75   80
Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Cys Ser Tyr Ala Gly Ser
                85   90   95
Tyr Ser Tyr Val Phe Gly Thr Gly Thr Lys Val Thr Val Leu
            100   105   110

<210> 1128
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1128
Gln Tyr Glu Leu Thr Gln Pro Pro Ser Val Ser Val Ser Pro Gly Gln
 1   5   10   15
Thr Ala Ser Ile Thr Cys Ser Gly Asp Lys Leu Gly Asp Lys Tyr Ala
            20   25   30
Cys Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Val Leu Val Ile Tyr
        35   40   45
Gln Asp Ser Lys Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
    50   55   60

Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr Gln Ala Met
65 70 75 80
Asp Glu Ala Asp Tyr Tyr Cys Gln Ala Trp Asp Ser Ser Thr Tyr Val
85 90 95
Phe Gly Thr Gly Thr Lys Val Thr Val Leu
100 105

<210> 1129
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1129
Gln Ser Ala Leu Thr Gln Pro Arg Ser Val Ser Gly Ser Pro Gly Gln
1 5 10 15
Ser Val Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp Val Gly Gly His
20 25 30
Asn Tyr Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Leu
35 40 45
Met Ile Tyr Asp Val Ser Lys Arg Pro Ser Gly Val Pro Asp Arg Phe
50 55 60
Ser Gly Ser Lys Tyr Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu
65 70 75 80
Gln Ala Glu Asp Glu Ala Asp Phe Tyr Cys Cys Ser Tyr Ala Gly Arg
85 90 95
Tyr Thr Tyr Val Phe Gly Thr Gly Thr Lys Val Thr Val Leu
100 105 110

<210> 1130
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1130
Gln Tyr Glu Leu Thr Gln Pro Pro Ser Val Ser Val Ser Pro Gly Gln
1 5 10 15
Thr Ala Ser Ile Thr Cys Ser Gly Asp Arg Leu Glu Asp Lys Tyr Thr
20 25 30
Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Leu Leu Val Ile Tyr
35 40 45
Gln Asp Asn Lys Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
50 55 60
Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr Gln Ala Met
65 70 75 80
Asp Glu Ala Asp Tyr Phe Cys Gln Ala Trp Asp Ser Ser Ser Ala Tyr
85 90 95
Val Phe Gly Thr Gly Thr Lys Val Thr Val Leu
100 105

<210> 1131
<211> 108

<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1131
Gln Ser Ala Leu Thr Gln Gln Pro Ser Val Ser Val Ala Pro Gly Lys
 1   5   10   15
Thr Ala Thr Ile Thr Cys Gly Gly Asn Asn Ile Gly Ser Lys Ser Val
            20   25   30
His Trp Tyr Gln Gln Arg Pro Gly Gln Ala Pro Val Val Val Met Phe
        35   40   45
Phe Asp Tyr Asp Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser
    50   55   60
Asn Ser Gly Asp Thr Ala Thr Leu Thr Ile Ser Arg Val Glu Ala Gly
65   70   75   80
Asp Glu Ala Asp Tyr Tyr Cys Gln Val Trp Asp Ser Arg Thr Asp Arg
                85   90   95
Tyr Val Phe Gly Thr Gly Thr Thr Val Thr Val Leu
            100   105

<210> 1132
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1132
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ile Tyr
            20   25   30
Asp Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45
Ser Trp Ile Ser Pro Ser Gly Gly Arg Thr Leu 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 Thr Trp Asp Tyr Tyr Asp Ser Ser Gly Tyr Phe Asn Asp Ala
            100   105   110
Phe Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
        115   120   125

<210> 1133
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1133

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ala Tyr
            20   25   30
Asn Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45
Ser Ser Ile Val Ser Ser Gly Gly Thr Thr Thr 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 Gly Val Gly Trp Leu Leu Asp Tyr Trp Gly Gln Gly Thr
            100   105   110
Leu Val Thr Val Ser Ser
        115

<210> 1134
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1134
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ala Tyr
            20   25   30
Gln Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45
Ser Ser Ile Ser Ser Ser Gly Gly Tyr Thr Ser 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 Ser Arg Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu
            100   105   110
Val Thr Val Ser Ser
        115

<210> 1135
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1135
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Glu Tyr
            20   25   30
Pro Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

```
        35                  40                  45
Ser Gly Ile Gly Ser Ser Gly Gly Ser Thr Thr Tyr Ala Asp Ser Val
    50                  55                  60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
Ala Arg Ala Pro Leu Tyr Ser Ser Thr Ser Tyr Ala Phe Asp Ile Trp
            100                 105                 110
Gly Gln Gly Thr Met Val Thr Val Ser Ser
        115                 120
```

<210> 1136
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1136

```
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1               5                  10                  15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Phe Tyr
            20                  25                  30
Trp Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
Ser Gly Ile Gly Pro Ser Gly Gly Thr Thr Phe 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 Gly Ser Tyr Phe Asp Leu Trp Gly Arg Gly Thr Leu Val
            100                 105                 110
Thr Val Ser Ser
        115
```

<210> 1137
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1137

```
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1               5                  10                  15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Gly Tyr
            20                  25                  30
Gly Met Val Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
Ser Ser Ile Ser Pro Ser Gly Gly Glu Thr Leu 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 Gln Met Trp Pro Gly Val Ala Phe Glu Met Trp Gly Gln
            100                 105                 110
Gly Thr Met Val Thr Val Ser Ser
        115                 120

<210> 1138
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1138
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1               5                  10                  15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Leu Tyr
            20                  25                  30
Phe Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
Ser Ser Ile Gly Ser Ser Asp Gly Tyr Thr Arg 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 Leu Ser Trp Trp Pro Asp Ala Phe Asp Ile Trp Gly Gln
            100                 105                 110
Gly Thr Met Val Thr Val Ser Ser
        115                 120

<210> 1139
<211> 104
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1139
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1               5                  10                  15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Pro Tyr
            20                  25                  30
Arg Met Glu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
Ser Trp Ile Tyr Ser Ser Gly Gly Ile Thr Asn 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 Thr Tyr Tyr Cys
                85                  90                  95
Ala Arg Leu Val Thr Val Ser Ser
            100
```

<210> 1140
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1140
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Val Tyr
            20   25   30
Asp Met Val Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45
Ser Ser Ile Gly Pro Ser Gly Gly Trp Thr Gly 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 Ser Gly Gly Trp Glu Ala Leu Tyr Tyr Tyr Tyr Tyr Met
            100   105   110
Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
        115   120   125

<210> 1141
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1141
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Val Tyr
            20   25   30
Phe Met Asp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45
Ser Gly Ile Gly Pro Ser Gly Gly Val Thr Ser 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 Ala Gly Gln Leu Ala Gln Gly His Tyr Tyr Met Asp Val Trp Gly
            100   105   110
Lys Gly Thr Thr Val Thr Val Ser Ser
        115   120

<210> 1142
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1142
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Lys Tyr
            20   25   30
Asp Met Leu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45
Ser Tyr Ile Tyr Pro Ser Gly Gly Leu Thr Glu 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 Ala Pro Arg Ser Leu Ser Phe Asp Ile Trp Gly Gln Gly
            100   105   110
Thr Met Val Thr Val Ser Ser
        115

<210> 1143
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1143
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Tyr
            20   25   30
Met Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45
Ser Ser Ile Tyr Pro Ser Gly Gly Val Thr Glu 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 Gly Trp Tyr Gly Tyr Pro Thr Trp Gly Gln Gly Thr Leu
            100   105   110
Val Thr Val Ser Ser
        115

<210> 1144
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1144
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

```
 1               5                  10                  15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Tyr
            20                  25                  30
Met Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
Ser Val Ile Val Pro Ser Gly Gly Phe Thr Met Tyr Ala Asp Ser Val
    50                  55                  60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
Ala Arg Ser Ser Arg Leu Trp Ser Gly Tyr Tyr Pro Phe Asp Tyr Trp
            100                 105                 110
Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120
```

<210> 1145
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1145

```
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1               5                  10                  15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Tyr
            20                  25                  30
Ser Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
Ser Ser Ile Tyr Ser Ser Gly Gly Glu Thr Gly 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 Met Ala Val Tyr Tyr Cys
                85                  90                  95
Ala Arg Glu Arg Tyr Asn Ser Phe Thr Ser Trp Gly Gln Gly Thr Met
            100                 105                 110
Val Thr Val Ser Ser
        115
```

<210> 1146
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1146

```
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1               5                  10                  15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30
Val Met Val Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
```

```
Ser Val Ile Ser Pro Ser Gly Gly Val Thr Phe Tyr Ala Asp Ser Val
    50                  55                  60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
Ala Arg Asp Arg Arg Ser Asn Ser Leu Phe Asp Pro Trp Gly Gln Gly
            100                 105                 110
Thr Leu Val Thr Val Ser Ser
        115
```

<210> 1147
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1147

```
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1               5                  10                  15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr
            20                  25                  30
Gly Met Val Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
Ser Tyr Ile Trp Pro Ser Gly Gly Leu Thr Trp Tyr Ala Asp Ser Val
    50                  55                  60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
Ala Arg Ser Gly Tyr Ser Tyr Gly Arg Phe Asp Tyr Trp Gly Gln Gly
            100                 105                 110
Thr Leu Val Thr Val Ser Ser
        115
```

<210> 1148
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1148

```
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1               5                  10                  15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Tyr Tyr
            20                  25                  30
Asp Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
Ser Trp Ile Ser Pro Ser Gly Gly Ser Thr Leu 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 Ser Ser Gly Leu Tyr Gly Ser Gly Ser Tyr Ala Ala Phe Asp Val
            100                 105                 110
Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
        115                 120

<210> 1149
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1149
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1               5                  10                  15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Tyr Tyr
            20                  25                  30
His Met Val Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
Ser Tyr Ile Ser Pro Ser Gly Gly Asp Thr His Tyr Ala Asp Ser Val
    50                  55                  60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
Ala Arg Gly Arg Tyr Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr
            100                 105                 110
Val Thr Val Ser Ser
        115

<210> 1150
<211> 129
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1150
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1               5                  10                  15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Gly Tyr
            20                  25                  30
Ile Met Met Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
Ser Gly Ile Tyr Pro Ser Gly Gly Gly Thr Asp 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 Arg Pro Gly Tyr Tyr Asp Ser Thr Asp Asp Asp Tyr Tyr
            100                 105                 110
Tyr Tyr Pro Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser
        115                 120                 125
```

Ser

<210> 1151
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1151
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Val Tyr
            20   25   30
Trp Met Glu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45
Ser Ser Ile Ser Ser Ser Gly Gly Leu Thr Ser 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
Thr Thr Asp Leu Val Ser Asn Trp Pro Trp Gly Gly Tyr Trp Gly Gln
            100   105   110
Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 1152
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1152
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser His Tyr
            20   25   30
Lys Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45
Ser Ser Ile Ser Ser Ser Gly Gly Asp Thr Ala Tyr Ala Asp Ser Val
    50   55   60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65   70   75   80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95
Ala Arg Asp Arg Ala Pro Tyr Tyr Tyr Asp Ser Ser Gly Tyr Tyr Ser
            100   105   110
Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115   120   125

<210> 1153
<211> 119

<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1153
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser His Tyr
            20   25   30
Ala Met Tyr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45
Ser Ser Ile Ser Pro Ser Gly Gly Tyr Thr Tyr Tyr Ala Asp Ser Val
    50   55   60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65   70   75   80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95
Ala Arg Glu Ser Gly Thr Thr Asn Ala Phe Asp Ile Trp Gly Gln Gly
            100   105   110
Thr Met Val Thr Val Ser Ser
        115

<210> 1154
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1154
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Tyr
            20   25   30
His Met Glu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45
Ser Tyr Ile Ser Pro Ser Gly Gly Ser Thr His 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 Trp Thr Val Pro Arg Asp Trp Gly Gln Gly Thr Leu
            100   105   110
Val Thr Val Ser Ser
        115

<210> 1155
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1155
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Tyr
            20   25   30
Trp Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45
Ser Ser Ile Val Ser Ser Gly Gly Met Thr Asp 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 His Arg Gly Asp Ser Gly Leu Asp Tyr Trp Gly Gln Gly Thr
            100   105   110
Leu Val Thr Val Ser Ser
        115

<210> 1156
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1156
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser His Tyr
            20   25   30
Pro Met Leu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45
Ser Gly Ile Ser Ser Ser Gly Gly Trp Thr Asp Tyr Ala Asp Ser Val
    50   55   60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65   70   75   80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95
Ala Arg Asp Arg Ala Leu Gly Met Asp Val Trp Gly Gln Gly Thr Thr
            100   105   110
Val Thr Val Ser Ser
        115

<210> 1157
<211> 115
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1157
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Leu Tyr

```
            20                  25                  30
Ser Met Val Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
Ser Arg Ile Arg Pro Ser Gly Gly Gln Thr Met Tyr Ala Asp Ser Val
    50                  55                  60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
Ala Thr Gly Tyr Ala Phe Asp Ile Trp Gly Gln Gly Thr Met Val Thr
            100                 105                 110
Val Ser Ser
        115
```

<210> 1158
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1158

```
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1               5                  10                  15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Phe Tyr
            20                  25                  30
Asp Met Leu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
Ser Ser Ile Trp Ser Ser Gly Gly Gln Thr Gly 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 Met Tyr Tyr Cys
                85                  90                  95
Ala Arg Glu Lys Ala Ser Asp Leu Ser Gly Ser Tyr Ser Glu Ala Leu
            100                 105                 110
Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120                 125
```

<210> 1159
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1159

```
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1               5                  10                  15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Tyr
            20                  25                  30
His Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
Ser Tyr Ile Tyr Pro Ser Gly Gly Val Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60
```

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Thr Thr Gly Ile Ala Ala Ala Gly Asn Tyr Tyr Tyr Tyr Tyr Gly Met
100 105 110
Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120 125

<210> 1160
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1160
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Lys Tyr
20 25 30
Gly Met Val Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
Ser Ser Ile Ser Ser Ser Gly Gly Asn Thr Ala 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 Glu Leu Glu Arg Arg Arg Arg Asn Tyr Tyr Gly Met Asp
100 105 110
Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 1161
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1161
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Tyr
20 25 30
Ala Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
Ser Ser Ile Tyr Ser Ser Gly Gly Asp Thr Ala Tyr Ala Asp Tyr 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 Tyr Tyr Thr Gly Trp Asn Phe Asp Tyr Trp Gly Gln Gly

```
            100                 105                 110
Thr Leu Val Thr Val Ser Ser
        115

<210> 1162
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1162
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1               5                  10                  15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Gln Tyr
            20                  25                  30
Asp Met Val Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
Ser Tyr Ile Tyr Ser Ser Gly Gly His Thr Leu Tyr Val 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 Thr Tyr Tyr Cys
                85                  90                  95
Ala Arg Ile Arg Ser Ser Gly Tyr Tyr His Glu Val Leu Asp Tyr Trp
            100                 105                 110
Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120

<210> 1163
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1163
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1               5                  10                  15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr
            20                  25                  30
Met Met Tyr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
Ser Val Ile Gly Pro Ser Gly Gly Ala Thr Gly 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 Ile Arg Lys Ala Phe Gly Tyr Gly Ser Gly Ser Leu Asp Tyr
            100                 105                 110
Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120

<210> 1164
```

<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1164
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Tyr Tyr
            20   25   30
Asp Met Gln Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45
Ser Tyr Ile Gly Pro Ser Gly Gly Asp Thr Asp 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 Ser Ser Ser Tyr Tyr Tyr Asp Ser Ser Gly Tyr Tyr His Glu Ala
            100   105   110
Phe Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
        115   120   125

<210> 1165
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1165
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Tyr Tyr
            20   25   30
Met Met Arg Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45
Ser Tyr Ile Gly Pro Ser Gly Gly Ala Thr Thr Tyr Ala Asp Ser Val
    50   55   60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65   70   75   80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95
Ala Arg Gly Arg Ser Val Lys Tyr Tyr Tyr Asp Ser Ser Gly Tyr Leu
            100   105   110
Leu Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115   120   125

<210> 1166
<211> 122
<212> PRT
<213> Artificial Sequence

<220>

<223> Made in lab

<400> 1166
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser His Tyr
            20   25   30
Ser Met Tyr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45
Ser Gly Ile Tyr Ser Ser Gly Gly Pro Thr Ile 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 Leu Gln Ile Glu Met Ala Thr Ile Gly His Phe Asp Tyr Trp
            100   105   110
Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 1167
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1167
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Gln Tyr
            20   25   30
Asp Met Val Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45
Ser Tyr Ile Tyr Ser Ser Gly Gly His Thr Leu Tyr Val 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 Thr Tyr Tyr Cys
                85   90   95
Ala Arg Ile Arg Ser Ser Gly Tyr Tyr His Glu Val Leu Asp Tyr Trp
            100   105   110
Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 1168
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1168
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1   5   10   15

```
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser His Tyr
            20                  25                  30
Trp Met Met Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
Ser Ser Ile Val Pro Ser Gly Gly Asp Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
Thr Thr Asp Pro Val Met Thr Pro Val Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110
Leu Val Thr Val Ser Ser
        115

<210> 1169
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1169
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1               5                  10                  15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Pro Tyr
            20                  25                  30
Phe Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
Ser Ser Ile Tyr Pro Ser Gly Gly Ile Thr Lys 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 Thr Tyr Tyr Cys
                85                  90                  95
Ala Lys Glu Thr Tyr Tyr Tyr Gly Ser Gly Ser Tyr Ala Phe Asp Ile
            100                 105                 110
Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
        115                 120

<210> 1170
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1170
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1               5                  10                  15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Gln Tyr
            20                  25                  30
Tyr Met Tyr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
Ser Arg Ile Ser Pro Ser Gly Gly Met Thr Ser 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 Met Tyr Tyr Cys
                85                  90                  95
Ala Arg His Lys Tyr Gly Gly Pro Asp Phe Trp Gly Gln Gly Thr Leu
            100                 105                 110
Val Thr Val Ser Ser
        115
```

<210> 1171
<211> 115
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1171

```
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1               5                  10                  15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Tyr
            20                  25                  30
Gln Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
Ser Ser Ile Arg Ser Ser Gly Gly Val Thr Lys 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 Met Tyr Tyr Cys
                85                  90                  95
Ala Arg Gly Arg Gly Leu Ser Ser Trp Gly Gln Gly Thr Leu Val Thr
            100                 105                 110
Val Ser Ser
        115
```

<210> 1172
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1172

```
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1               5                  10                  15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Leu Tyr
            20                  25                  30
Thr Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
Ser Tyr Ile Ser Pro Ser Gly Gly Phe Thr Gly Tyr Ala Asp Ser Val
    50                  55                  60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
```

```
Ala Thr Trp Gly Asp Pro Trp Gly Gln Gly Thr Leu Val Thr Val Ser
            100                 105                 110
Ser


<210> 1173
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1173
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1               5                  10                  15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
            20                  25                  30
Phe Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
Ser Arg Ile Ser Ser Ser Gly Gly His Thr Met 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 Asp Tyr Tyr Asp Ser Ser Gly Tyr Tyr Pro Pro Ala
            100                 105                 110
Phe Asp Ile Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
        115                 120                 125

<210> 1174
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1174
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1               5                  10                  15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ile Tyr
            20                  25                  30
Trp Met Tyr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
Ser Gly Ile Gly Pro Ser Gly Gly Tyr Thr Ser 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 Asn Gly Gly Phe Asp Ser Trp Gly Gln Gly Thr Leu Val
            100                 105                 110
Thr Val Ser Ser
        115
```

<210> 1175
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1175
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Pro Tyr
            20   25   30
His Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45
Ser Ser Ile Tyr Pro Ser Gly Gly Phe Thr Ala 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 Ser Ala Tyr Tyr Tyr Asp Ser Ser Pro Pro Ala Phe Asp
            100   105   110
Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
        115   120

<210> 1176
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1176
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr
            20   25   30
Ala Met Tyr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45
Ser Ser Ile Tyr Ser Ser Gly Gly Ala Thr Trp Tyr Ala Asp Ser Val
    50   55   60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65   70   75   80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95
Ala Arg Ser Thr Phe Asp Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu
            100   105   110
Val Thr Val Ser Ser
        115

<210> 1177
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1177
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Lys Tyr
            20   25   30
Arg Met Met Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45
Ser Tyr Ile Ser Ser Ser Gly Gly Ala Thr Ile 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 His Gly Pro Gln Ile Ala Ala Trp Tyr Phe Asp Leu Trp Gly
            100   105   110
Arg Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 1178
<211> 128
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1178
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Pro Tyr
            20   25   30
Ser Met Asp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45
Ser Gly Ile Ser Ser Ser Gly Gly Arg Thr Val 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 Thr Tyr Tyr Cys
                85   90   95
Ala Arg Gly Pro Tyr Tyr Asp Phe Trp Ser Gly Tyr Tyr Ile Asp Arg
            100   105   110
Gly Pro Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115   120   125

<210> 1179
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1179
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

```
 1               5                  10                  15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Trp Tyr
            20                  25                  30
Met Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
Ser Trp Ile Ser Ser Ser Gly Gly Phe Thr Pro 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 Gln Gln Trp Pro Gly Val Ala Phe Asp Ile Trp Gly Gln
            100                 105                 110
Gly Thr Met Val Thr Val Ser Ser
        115                 120
```

<210> 1180
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1180

```
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1               5                  10                  15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Phe Tyr
            20                  25                  30
Pro Met Met Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
Ser Tyr Ile Gly Pro Ser Gly Gly Asn Asn Ala Asp Ser Val Lys Gly
    50                  55                  60
Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln
65                  70                  75                  80
Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Thr Tyr Tyr Cys Ala Arg
                85                  90                  95
Gly Leu Trp Phe Gly Gly Arg Leu Asp Tyr Trp Gly Gln Gly Thr Leu
            100                 105                 110
Val Thr Val Ser Ser
        115
```

<210> 1181
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1181

```
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1               5                  10                  15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser His Tyr
            20                  25                  30
Trp Met Lys Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
```

```
Ser Gly Ile Ser Ser Ser Gly Gly Gln Thr Asp Tyr Ala Asp Ser Val
    50                  55                  60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
Ala Arg Ser Pro Arg Leu Arg Phe Leu Glu Trp Pro Arg Asn Tyr Tyr
            100                 105                 110
Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
        115                 120                 125
```

<210> 1182
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1182

```
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1               5                  10                  15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Leu Tyr
            20                  25                  30
Met Met Val Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
Ser Tyr Ile Gly Pro Ser Gly Gly Ala Tyr Ala Asp Ser Val Lys Gly
    50                  55                  60
Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln
65                  70                  75                  80
Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
                85                  90                  95
Ser Val Arg Gly Leu Thr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110
Thr Val Ser Ser
        115
```

<210> 1183
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1183

```
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1               5                  10                  15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Pro Tyr
            20                  25                  30
Glu Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
Ser Arg Ile Ser Pro Ser Gly Gly Met Thr Leu 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 Met Gly Arg Gly Gly Trp Trp Ala Phe Asp Ala Phe Asp Ile
            100                 105                 110
Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
        115                 120

<210> 1184
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1184
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1               5                  10                  15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Trp Tyr
            20                  25                  30
Lys Met Val Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
Ser Gly Ile Tyr Pro Ser Gly Gly Thr Thr His Tyr Ala Asp Ser Val
    50                  55                  60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
Ala Lys Gly Gly Gly Asp Phe Trp Ser Gly Tyr Tyr Pro Phe Asp Tyr
            100                 105                 110
Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120

<210> 1185
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1185
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1               5                  10                  15
Val Ile Met Ser Arg Gly Xaa
            20

<210> 1186
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1186
Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
 1               5                  10                  15
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Asp Thr Thr Gly
20

<210> 1187
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 1187
Arg Ala Ser Glu Ser Val His Asn Phe Gly Ile Ser Phe Met Asn
1 5 10 15

<210> 1188
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 1188
Thr Ala Ser Asn Gln Gly Ser
1 5

<210> 1189
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 1189
His Gln Gly Lys Glu Val Pro Trp Thr
1 5

<210> 1190
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 1190
Arg Ala Ser Glu Ser Val Gly Asn Phe Gly Ile Ser Phe Val Asn
1 5 10 15

<210> 1191
<211> 7
<212> PRT
<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 1191
Ala Ala Ser Asn Gln Gly Ser
 1   5

<210> 1192
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 1192
Gln Gln Ser Lys Glu Val Pro Tyr Thr
 1   5

<210> 1193
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 1193
Asn Thr Tyr Ala Met Asn
 1   5

<210> 1194
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 1194
Arg Thr Val Thr Lys Ser Asn Lys Tyr Ala Thr Tyr Tyr Ala Asp Ser
 1   5   10   15
Val Ser Asp

<210> 1195
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 1195
Glu Asp Tyr Tyr Gly Thr Leu Asp Tyr
 1   5

<210> 1196

<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 1196
Ser Tyr Trp Met His
 1   5

<210> 1197
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 1197
Glu Ile Asn Pro Ser Asn Gly Arg Thr Asn Tyr Asn Glu Arg Phe Lys
 1   5   10   15
Ser

<210> 1198
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 1198
Ser Asp Thr Lys Ala Thr Cys Asp Tyr
 1   5

<210> 1199
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 1199
Glu Ile Val Leu Thr Gln Ser Pro Pro Ser Leu Ala Val Ser Leu Gly
 1   5   10   15
Gln Arg Ala Thr Ile Ser Cys Arg Ala Ser Glu Ser Val His Asn Phe
            20   25   30
Gly Ile Ser Phe Met Asn Trp Phe Gln Gln Lys Ser Gly Gln Pro Pro
        35   40   45
Lys Leu Leu Ile Tyr Thr Ala Ser Asn Gln Gly Ser Gly Val Pro Ala
    50   55   60
Arg Phe Ser Gly Arg Gly Ser Gly Thr Asp Phe Ser Leu Ile Ile His
65   70   75   80
Pro Val Glu Glu Asp Asp Thr Ala Met Tyr Phe Cys His Gln Gly Lys

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                85                  90                  95
Glu Val Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
            100                 105                 110

<210> 1200
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 1200
Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
 1               5                  10                  15
Gln Arg Ala Thr Ile Ser Cys Arg Ala Ser Glu Ser Val Gly Asn Phe
            20                  25                  30
Gly Ile Ser Phe Val Asn Trp Phe Gln Gln Lys Pro Gly Gln Pro Pro
        35                  40                  45
Lys Leu Leu Ile Tyr Ala Ala Ser Asn Gln Gly Ser Gly Val Pro Ala
    50                  55                  60
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Ser Leu Asn Ile His
65                  70                  75                  80
Pro Met Glu Glu Asp Asp Thr Ala Met Tyr Phe Cys Gln Gln Ser Lys
                85                  90                  95
Glu Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
            100                 105                 110

<210> 1201
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 1201
Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
 1               5                  10                  15
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Glu Ser Val His Asn Phe
            20                  25                  30
Gly Ile Ser Phe Met Asn Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
        35                  40                  45
Arg Leu Leu Ile Tyr Thr Ala Ser Asn Gln Gly Ser Gly Ile Pro Ala
    50                  55                  60
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65                  70                  75                  80
Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys His Gln Gly Lys
                85                  90                  95
Glu Val Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
            100                 105                 110

<210> 1202
<211> 111
<212> PRT
<213> Artificial Sequence
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<220>
<223> Made in a lab

<400> 1202
Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Pro Gly
 1   5   10   15
Gln Arg Ala Thr Ile Thr Cys Arg Ala Ser Glu Ser Val His Asn Phe
            20   25   30
Gly Ile Ser Phe Met Asn Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
        35   40   45
Lys Leu Leu Ile Tyr Thr Ala Ser Asn Gln Gly Ser Gly Val Pro Ala
    50   55   60
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn
65   70   75   80
Pro Val Glu Ala Asn Asp Thr Ala Asn Tyr Tyr Cys His Gln Gly Lys
                85   90   95
Glu Val Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
            100   105   110

<210> 1203
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 1203
Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
 1   5   10   15
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Glu Ser Val Gly Asn Phe
            20   25   30
Gly Ile Ser Phe Val Asn Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
        35   40   45
Arg Leu Leu Ile Tyr Ala Ala Ser Asn Gln Gly Ser Gly Ile Pro Ala
    50   55   60
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65   70   75   80
Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Ser Lys
                85   90   95
Glu Val Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100   105   110

<210> 1204
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 1204
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1   5   10   15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Glu Ser Val Gly Asn Phe
            20   25   30
Gly Ile Ser Phe Val Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro

```
        35                  40                  45
Lys Leu Leu Ile Tyr Ala Ala Ser Asn Gln Gly Ser Gly Val Pro Ser
    50                  55                  60
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65                  70                  75                  80
Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Lys
                85                  90                  95
Glu Val Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100                 105                 110

<210> 1205
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 1205
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Lys Gly
 1               5                  10                  15
Thr Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Asn Thr Tyr
            20                  25                  30
Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Ser Leu Glu Trp Val
        35                  40                  45
Ala Arg Thr Val Thr Lys Ser Asn Lys Tyr Ala Thr Tyr Tyr Ala Asp
    50                  55                  60
Ser Val Ser Asp Arg Val Thr Ile Ser Arg Glu Asp Ser Gln Ser Met
65                  70                  75                  80
Leu Tyr Leu Gln Met Thr Asn Leu Lys Thr Glu Asp Thr Ala Met Tyr
                85                  90                  95
Tyr Cys Val Arg Glu Asp Tyr Tyr Gly Thr Leu Asp Tyr Trp Gly Gln
            100                 105                 110
Gly Thr Ser Val Thr Val Ser Ser
        115                 120

<210> 1206
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 1206
Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Lys Pro Gly Ala
 1               5                  10                  15
Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Ile Phe Thr Ser Tyr
            20                  25                  30
Trp Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
        35                  40                  45
Gly Glu Ile Asn Pro Ser Asn Gly Arg Thr Asn Tyr Asn Glu Arg Phe
    50                  55                  60
Lys Ser Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65                  70                  75                  80
Ile Gln Leu Ser Ser Leu Thr Ser Asp Asp Ser Ala Val Tyr Tyr Cys
                85                  90                  95
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Ser Arg Ser Asp Thr Lys Ala Thr Cys Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110
Thr Leu Thr Val Ser Ser
        115

<210> 1207
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 1207
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 Asn Thr Tyr
            20                  25                  30
Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
Gly Arg Thr Val Thr Lys Ser Asn Lys Tyr Ala Thr Tyr Tyr Ala Asp
    50                  55                  60
Ser Val Ser Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Ser
65                  70                  75                  80
Leu Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr
                85                  90                  95
Tyr Cys Ala Arg Glu Asp Tyr Tyr Gly Thr Leu Asp Tyr Trp Gly Gln
            100                 105                 110
Gly Thr Leu Val Thr Val Ser Ser
        115                 120

<210> 1208
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 1208
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 Asn Thr Tyr
            20                  25                  30
Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
Gly Arg Thr Val Thr Lys Ser Asn Lys Tyr Ala Thr Tyr Tyr Ala Asp
    50                  55                  60
Ser Val Ser Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Ser
65                  70                  75                  80
Leu Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr
                85                  90                  95
Tyr Cys Ala Arg Glu Asp Tyr Tyr Gly Thr Leu Asp Tyr Trp Gly Gln
            100                 105                 110
Gly Thr Leu Val Thr Val Ser Ser
        115                 120
```

<210> 1209
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 1209
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1   5   10   15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ile Phe Thr Ser Tyr
            20   25   30
Trp Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35   40   45
Gly Glu Ile Asn Pro Ser Asn Gly Arg Thr Asn Tyr Asn Glu Arg Phe
    50   55   60
Lys Ser Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
65   70   75   80
Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
                85   90   95
Ala Arg Ser Asp Thr Lys Ala Thr Cys Asp Tyr Trp Gly Gln Gly Thr
            100   105   110
Thr Val Thr Val Ser Ser
        115

<210> 1210
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 1210
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1   5   10   15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ile Phe Thr Ser Tyr
            20   25   30
Trp Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35   40   45
Gly Glu Ile Asn Pro Ser Asn Gly Arg Thr Asn Tyr Asn Glu Arg Phe
    50   55   60
Lys Ser Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
65   70   75   80
Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
                85   90   95
Ala Arg Ser Asp Thr Lys Ala Thr Cys Asp Tyr Trp Gly Gln Gly Thr
            100   105   110
Thr Val Thr Val Ser Ser
        115

<210> 1211
<211> 333
<212> DNA
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 1211
gagattgtgc tgacccaatc tccaccttct ttggctgtgt ctctggggca gagggccacc 60
atctcctgca gagccagcga aagtgttcat aattttggca ttagttttat gaactggttt 120
caacagaaat caggacagcc acccaaactc ctcatctata ctgcatccaa ccaaggatcc 180
ggggtccctg ccaggtttag tggcagaggg tctgggacag acttcagtct catcatccac 240
cctgtggagg aagatgatac tgcaatgtat ttctgtcacc aaggtaagga ggttccgtgg 300
acgttcggtg gaggcaccaa gctagaaatc aaa 333

<210> 1212
<211> 333
<212> DNA
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 1212
gacattgtgc tgacccaatc tccagcttct ttggctgtgt ctctagggca gagggccacc 60
atctcctgca gagccagcga aagtgttggt aattttggca ttagttttgt gaactggttc 120
caacagaaac caggacagcc acccaaactc ctcatctatg ctgcctccaa ccaaggatcc 180
ggggtccctg ccaggtttag tggcagtggg tctgggacag acttcagcct caacatccat 240
cctatggagg aggatgatac tgcaatgtat ttctgtcagc aaagtaagga ggttccgtac 300
acgttcggag gggggaccaa gctggaaata aaa 333

<210> 1213
<211> 333
<212> DNA
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 1213
gaaattgtgt tgacacagtc tccagccacc ctgtctttgt ctccagggga aagagccacc 60
ctctcctgca gagccagcga aagtgttcat aattttggca ttagttttat gaactggtac 120
caacagaaac ctggccaggc tcccaggctc ctcatctata ctgcatccaa ccaaggatcc 180
ggcatcccag ccaggttcag tggcagtggg tctgggacag acttcactct caccatcagc 240
agcctagagc ctgaagattt tgcagtttat tactgtcacc aaggtaagga ggttccgtgg 300
acgttcggcc aagggaccaa ggtggaaatc aaa 333

<210> 1214
<211> 333
<212> DNA
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 1214
gacattgtgc tgacccagtc tccagcctcc ttggccgtgt ctccaggaca gagggccacc 60
atcacctgca gagccagcga aagtgttcat aattttggca ttagttttat gaactggtat 120
cagcagaaac caggacaacc tcctaaactc ctgatttaca ctgcatccaa ccaaggatcc 180
ggggtcccag ccaggttcag cggcagtggg tctgggaccg atttcaccct cacaattaat 240
cctgtggaag ctaatgatac tgcaaattat tactgtcacc aaggtaagga ggttccgtgg 300

acgttcggcc aagggaccaa ggtggaaatc aaa 333

<210> 1215
<211> 333
<212> DNA
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 1215
gaaattgtgt tgacacagtc tccagccacc ctgtctttgt ctccagggga aagagccacc 60
ctctcctgca gagccagcga aagtgttggt aattttggca ttagttttgt gaactggtac 120
caacagaaac ctggccaggc tcccaggctc ctcatctatg ctgcctccaa ccaaggatcc 180
ggcatcccag ccaggttcag tggcagtggg tctgggacag acttcactct caccatcagc 240
agcctagagc ctgaagattt tgcagtttat tactgtcagc aaagtaagga ggttccgtac 300
acttttggcc aggggaccaa gctggagatc aag 333

<210> 1216
<211> 334
<212> DNA
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 1216
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgca gagccagcga aagtgttggt aattttggca ttagttttgt gaactggtat 120
cagcagaaac cagggaaagc ccctaagctc ctgatctatg ctgcctccaa ccaaggatcc 180
ggggtcccat caaggttcag tggcagtgga tctgggacag atttcactct caccatcagc 240
agtctgcaac ctgaagattt tgcaacttac tactgtcagc aaagtaagga ggttccgtac 300
acttttggcc aggggaccaa gctggagatc aagt 334

<210> 1217
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 1217
gaggtgcagc ttgttgagtc tggtggagga ttggtacagc ctaaagggac attgagactc 60
tcatgtgccg cctctggatt cagcttcaat acctatgcca tgaactgggt ccgccaggct 120
ccaggaaaga gtttggagtg ggttgctcgc acagtgacta aaagtaataa gtatgcaaca 180
tattatgcag attcagtgag tgacagagtc accatctcca gagaggattc acaaagcatg 240
ctttatctgc aaatgaccaa cttgaaaact gaggacacag ccatgtatta ctgtgtgaga 300
gaagattact acggcactct ggactactgg ggtcaaggaa cctcagtcac cgtctcctca 360

<210> 1218
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 1218
caggtccaac tgcagcagcc tggggctgaa ctggtgaagc ctggggcttc tgtgaagctg 60
tcctgcaagg cttctggcta catcttcacc agctactgga tgcactgggt gaagcagagg 120
cctggacaag gccttgagtg gattggagag attaatccta gcaacggtcg tactaactac 180
aatgagaggt tcaagagcaa ggccacactg actgtagaca aatcctccag cacagcctac 240
attcaactca gcagcctgac atctgatgac tctgcggtct attactgttc aagatcggat 300
actaaggcta cgtgtgacta ctggggccaa ggcaccactc tcacagtctc ctca 354

<210> 1219
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 1219
gaggtgcagc tggtggagtc tgggggaggc ttggtccagc ctggagggtc cctgagactc 60
tcctgtgcag cctctggatt caccttcaat acctatgcca tgaactgggt ccgccaggct 120
ccagggaagg ggctggagtg ggttggccgc acagtgacta aaagtaataa gtatgcaaca 180
tattatgcag attcagtgag tgacagattc accatctcaa gagatgattc aaagaactca 240
ctgtatctgc aaatgaacag cctgaaaacc gaggacacgg ccgtgtatta ctgtgctaga 300
gaagattact acggcactct ggactactgg ggccaaggaa ccctggtcac cgtctcctca 360

<210> 1220
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 1220
gaggtgcagc tggtggagtc tgggggaggc ttggtccagc ctggagggtc cctgagactc 60
tcctgtgcag cctctggatt caccttcaat acctatgcca tgaactgggt ccgccaggct 120
ccagggaagg ggctggagtg ggttggccgc acagtgacta aaagtaataa gtatgcaaca 180
tattatgcag attcagtgag tgacagattc accatctcaa gagatgattc aaagaactca 240
ctgtatctgc aaatgaacag cctgaaaacc gaggacacgg ccgtgtatta ctgtgctaga 300
gaagattact acggcactct ggactactgg ggccaaggaa ccctggtcac cgtctcctca 360

<210> 1221
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 1221
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60
tcctgcaagg cttctggcta catcttcacc agctactgga tgcactgggt gcgacaggcc 120
cctggacaag ggcttgagtg gatgggagag attaatccta gcaacggtcg tactaactac 180
aatgagaggt tcaagagcag ggtcaccatg accagggaca cgtccatcag cacagcctac 240
atggagctga gcaggctgag atctgacgac acggccgtgt attactgtgc gagatcggat 300
actaaggcta cgtgtgacta ctggggccaa gggaccacgg tcaccgtctc ctct 354

<210> 1222
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 1222
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60
tcctgcaagg cttctggcta catcttcacc agctactgga tgcactgggt gcgacaggcc 120
cctggacaag ggcttgagtg gatgggagag attaatccta gcaacggtcg tactaactac 180
aatgagaggt tcaagagcag ggtcaccatg accagggaca cgtccatcag cacagcctac 240
atggagctga gcaggctgag atctgacgac acggccgtgt attactgtgc gagatcggat 300
actaaggcta cgtgtgacta ctggggccaa gggaccacgg tcaccgtctc ctct 354

<210> 1223
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 1223
Gln Arg His Asn Asn Ser Ser Leu Asn Thr Gly Thr Gln Met Ala Gly
1 5 10 15
His Ser Pro Asn Ser
20

<210> 1224
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 1224
Gln Arg His Asn Asn Ser Ser Leu Asn Thr Gly Thr Gln Lys Ala Arg
1 5 10 15
His Ser Pro Asn Ser
20

<210> 1225
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 1225
Gln Arg His Asn Asn Ser Ser Leu Asn Thr Gly Thr Gln Met Ala Arg
1 5 10 15
His Ser Pro Asn Ser
20

<210> 1226
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 1226
Gln Arg His Asn Asn Ser Ser Leu Asn Thr Arg Thr Gln Lys Ala Gly
 1   5   10   15
His Ser Pro Asn Ser
            20

<210> 1227
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 1227
Gln Arg His Asn Asn Ser Ser Leu Asn Thr Arg Thr Gln Met Ala Gly
 1   5   10   15
His Ser Pro Asn Ser
            20

<210> 1228
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 1228
Gln Arg His Asn Asn Ser Ser Leu Asn Thr Arg Thr Gln Met Ala Arg
 1   5   10   15
His Ser Pro Asn Ser
            20

<210> 1229
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in lab

<400> 1229
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1   5   10   15
Val Ile Met Ser Arg Gly
            20

<210> 1230
<211> 723
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 1230
Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr Ala Pro Glu Pro Gly Ser
 1   5   10   15
Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln Thr Ala Gln Met Cys Cys
            20   25   30
Ser Lys Cys Ser Pro Gly Gln His Ala Lys Val Phe Cys Thr Lys Thr
        35   40   45
Ser Asp Thr Val Cys Asp Ser Cys Glu Asp Ser Thr Tyr Thr Gln Leu
    50   55   60
Trp Asn Trp Val Pro Glu Cys Leu Ser Cys Gly Ser Arg Cys Ser Ser
65   70   75   80
Asp Gln Val Glu Thr Gln Ala Cys Thr Arg Glu Gln Asn Arg Ile Cys
                85   90   95
Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu Ser Lys Gln Glu Gly Cys
            100   105   110
Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg Pro Gly Phe Gly Val Ala
        115   120   125
Arg Pro Gly Thr Glu Thr Ser Asp Val Val Cys Lys Pro Cys Ala Pro
    130   135   140
Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr Asp Ile Cys Arg Pro His
145   150   155   160
Gln Ile Cys Asn Val Val Ala Ile Pro Gly Asn Ala Ser Met Asp Ala
                165   170   175
Val Cys Thr Ser Thr Ser Pro Thr Arg Ser Met Ala Pro Gly Ala Val
            180   185   190
His Leu Pro Gln Pro Val Ser Thr Arg Ser Gln His Thr Gln Pro Thr
        195   200   205
Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser Phe Leu Leu Pro Met Gly
    210   215   220
Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly Asp Thr Gly Glu Pro Lys
225   230   235   240
Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala
                245   250   255
Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
            260   265   270
Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
        275   280   285
Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
    290   295   300
Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
305   310   315   320
Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
                325   330   335
Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala Leu Pro Ala
            340   345   350
Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
        355   360   365
Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln
    370   375   380

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Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
385                 390                 395                 400
Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
                405                 410                 415
Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
            420                 425                 430
Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
        435                 440                 445
Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
    450                 455                 460
Leu Ser Pro Gly Gln Arg His Asn Asn Ser Ser Leu Asn Thr Gly Thr
465                 470                 475                 480
Gln Met Ala Gly His Ser Pro Asn Ser Ala Pro Trp Gln Cys Ala Pro
                485                 490                 495
Cys Ser Ala Glu Lys Leu Ala Leu Cys Pro Pro Val Ser Ala Ser Cys
            500                 505                 510
Ser Glu Val Thr Arg Ser Ala Gly Cys Gly Cys Cys Pro Met Cys Ala
        515                 520                 525
Leu Pro Leu Gly Ala Ala Cys Gly Val Ala Thr Ala Arg Cys Ala Arg
    530                 535                 540
Gly Leu Ser Cys Arg Ala Leu Pro Gly Glu Gln Gln Pro Leu His Ala
545                 550                 555                 560
Leu Thr Arg Gly Gln Gly Ala Cys Val Gln Glu Ser Asp Ala Ser Ala
                565                 570                 575
Pro His Ala Ala Glu Ala Gly Ser Pro Glu Ser Pro Glu Ser Thr Glu
            580                 585                 590
Ile Thr Glu Glu Glu Leu Leu Asp Asn Phe His Leu Met Ala Pro Ser
        595                 600                 605
Glu Glu Asp His Ser Ile Leu Trp Asp Ala Ile Ser Thr Tyr Asp Gly
    610                 615                 620
Ser Lys Ala Leu His Val Thr Asn Ile Lys Lys Trp Lys Glu Pro Cys
625                 630                 635                 640
Arg Ile Glu Leu Tyr Arg Val Val Glu Ser Leu Ala Lys Ala Gln Glu
                645                 650                 655
Thr Ser Gly Glu Glu Ile Ser Lys Phe Tyr Leu Pro Asn Cys Asn Lys
            660                 665                 670
Asn Gly Phe Tyr His Ser Arg Gln Cys Glu Thr Ser Met Asp Gly Glu
        675                 680                 685
Ala Gly Leu Cys Trp Cys Val Tyr Pro Trp Asn Gly Lys Arg Ile Pro
    690                 695                 700
Gly Ser Pro Glu Ile Arg Gly Asp Pro Asn Cys Gln Ile Tyr Phe Asn
705                 710                 715                 720
Val Gln Asn
```

<210> 1231
<211> 2235
<212> DNA
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 1231
atggattttc aagtgcagat tttcagcttc ctgctaatca gtgcttcagt cataatgtcg 60
cgaggattgc ccgcccaggt ggcatttaca ccctacgccc cggagcccgg gagcacatgc 120
cggctcagag aatactatga ccagacagct cagatgtgct gcagcaaatg ctcgccgggc 180

```
caacatgcaa aagtcttctg taccaagacc tcggacaccg tgtgtgactc ctgtgaggac     240
agcacataca cccagctctg gaactgggtt cccgagtgct tgagctgtgg ctcccgctgt     300
agctctgacc aggtggaaac tcaagcctgc actcgggaac agaaccgcat ctgcacctgc     360
aggcccggct ggtactgcgc gctgagcaag caggaggggt gccggctgtg cgcgccgctg     420
cgcaagtgcc gcccgggctt cggcgtggcc agaccaggaa ctgaaacatc agacgtggtg     480
tgcaagccct gtgccccggg gacgttctcc aacacgactt catccacgga tatttgcagg     540
ccccaccaga tctgtaacgt ggtggccatc cctgggaatg caagcatgga tgcagtctgc     600
acgtccacgt cccccacccg gagtatggcc ccaggggcag tacacttacc ccagccagtg     660
tccacacgat cccaacacac gcagccaact ccagaaccca gcactgctcc aagcacctcc     720
ttcctgctcc caatgggccc cagcccccca gctgaaggga gcactggcga caccggtgag     780
cccaaatctt ctgacaaaac tcacacatgc ccaccgtgcc cagcacctga agccgcgggt     840
gcaccgtcag tcttcctctt ccccccaaaa cccaaggaca ccctcatgat ctcccggacc     900
cctgaggtca catgcgtggt ggtggacgtg agccacgaag accctgaggt caagttcaac     960
tggtacgtgg acggcgtgga ggtgcataat gccaagacaa agccgcggga ggagcagtac    1020
aacagcacgt accgtgtggt cagcgtcctc accgtcctgc accaggactg gctgaatggc    1080
aaggcgtacg cgtgcgcggt ctccaacaaa gccctcccag cccccatcga gaaaaccatc    1140
tccaaagcca aagggcagcc ccgagaacca caggtgtaca ccctgccccc atcccgggat    1200
gagctgacca agaaccaggt cagcctgacc tgcctggtca aaggcttcta tccaagcgac    1260
atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cacgcctccc    1320
gtgctggact ccgacggctc cttcttcctc tacagcaagc tcaccgtgga caagagcagg    1380
tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac    1440
acgcagaaga gcctctccct gtctccgggt cagaggcaca acaattcttc cctgaataca    1500
ggaactcaga tggcaggtca ttctccgaat tctgctccgt ggcagtgcgc gccctgctcc    1560
gccgagaagc tcgcgctctg cccgccggtg tccgcctcgt gctcggaggt cacccggtcc    1620
gccggctgcg gctgttgccc gatgtgcgcc ctgcctctgg gcgccgcgtg cggcgtggcg    1680
actgcacgct gcgcccgggg actcagttgc cgcgcgctgc cgggggagca gcaacctctg    1740
cacgccctca cccgcggcca aggcgcctgc gtgcaggagt ctgacgcctc cgctccccat    1800
gctgcagagg cagggagccc tgaaagccca gagagcacgg agataactga ggaggagctc    1860
ctggataatt tccatctgat ggccccttct gaagaggatc attccatcct ttgggacgcc    1920
atcagtacct atgatggctc gaaggctctc catgtcacca acatcaaaaa atggaaggag    1980
ccctgccgaa tagaactcta cagagtcgta gagagtttag ccaaggcaca ggagacatca    2040
ggagaagaaa tttccaaatt ttacctgcca aactgcaaca agaatggatt ttatcacagc    2100
agacagtgtg agacatccat ggatggagag gcgggactct gctggtgcgt ctacccttgg    2160
aatgggaaga ggatccctgg gtctccagag atcaggggag accccaactg ccagatatat    2220
tttaatgtac aaaac                                                     2235

<210> 1232
<211> 1156
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 1232
Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
 1               5                  10                  15
Asp Thr Thr Gly Glu Ile Cys Gly Pro Gly Ile Asp Ile Arg Asn Asp
            20                  25                  30
Tyr Gln Gln Leu Lys Arg Leu Glu Asn Cys Thr Val Ile Glu Gly Tyr
        35                  40                  45
Leu His Ile Leu Leu Ile Ser Lys Ala Glu Asp Tyr Arg Ser Tyr Arg
    50                  55                  60
Phe Pro Lys Leu Thr Val Ile Thr Glu Tyr Leu Leu Leu Phe Arg Val
65                  70                  75                  80
Ala Gly Leu Glu Ser Leu Gly Asp Leu Phe Pro Asn Leu Thr Val Ile
                85                  90                  95
```

```
Arg Gly Trp Lys Leu Phe Tyr Asn Tyr Ala Leu Val Ile Phe Glu Met
            100                 105                 110
Thr Asn Leu Lys Asp Ile Gly Leu Tyr Asn Leu Arg Asn Ile Thr Arg
        115                 120                 125
Gly Ala Ile Arg Ile Glu Lys Asn Ala Asp Leu Cys Tyr Leu Ser Thr
    130                 135                 140
Val Asp Trp Ser Leu Ile Leu Asp Ala Val Ser Asn Asn Tyr Ile Val
145                 150                 155                 160
Gly Asn Lys Pro Pro Lys Glu Cys Gly Asp Leu Cys Pro Gly Thr Met
                165                 170                 175
Glu Glu Lys Pro Met Cys Glu Lys Thr Thr Ile Asn Asn Glu Tyr Asn
            180                 185                 190
Tyr Arg Cys Trp Thr Thr Asn Arg Cys Gln Lys Met Cys Pro Ser Thr
        195                 200                 205
Cys Gly Lys Arg Ala Cys Thr Glu Asn Asn Glu Cys Cys His Pro Glu
    210                 215                 220
Cys Leu Gly Ser Cys Ser Ala Pro Asp Asn Asp Thr Ala Cys Val Ala
225                 230                 235                 240
Cys Arg His Tyr Tyr Tyr Ala Gly Val Cys Val Pro Ala Cys Pro Pro
                245                 250                 255
Asn Thr Tyr Arg Phe Glu Gly Trp Arg Cys Val Asp Arg Asp Phe Cys
            260                 265                 270
Ala Asn Ile Leu Ser Ala Glu Ser Ser Asp Ser Glu Gly Phe Val Ile
        275                 280                 285
His Asp Gly Glu Cys Met Gln Glu Cys Pro Ser Gly Phe Ile Arg Asn
    290                 295                 300
Gly Ser Gln Ser Met Tyr Cys Ile Pro Cys Glu Gly Pro Cys Pro Lys
305                 310                 315                 320
Val Cys Glu Glu Glu Lys Lys Thr Lys Thr Ile Asp Ser Val Thr Ser
                325                 330                 335
Ala Gln Met Leu Gln Gly Cys Thr Ile Phe Lys Gly Asn Leu Leu Ile
            340                 345                 350
Asn Ile Arg Arg Gly Asn Asn Ile Ala Ser Glu Leu Glu Asn Phe Met
        355                 360                 365
Gly Leu Ile Glu Val Val Thr Gly Tyr Val Lys Ile Arg His Ser His
    370                 375                 380
Ala Leu Val Ser Leu Ser Phe Leu Lys Asn Leu Arg Leu Ile Leu Gly
385                 390                 395                 400
Glu Glu Gln Leu Glu Gly Asn Tyr Ser Phe Tyr Val Leu Asp Asn Gln
                405                 410                 415
Asn Leu Gln Gln Leu Trp Asp Trp Asp His Arg Asn Leu Thr Ile Lys
            420                 425                 430
Ala Gly Lys Met Tyr Phe Ala Phe Asn Pro Lys Leu Cys Val Ser Glu
        435                 440                 445
Ile Tyr Arg Met Glu Glu Val Thr Gly Thr Lys Gly Arg Gln Ser Lys
    450                 455                 460
Gly Asp Ile Asn Thr Arg Asn Asn Gly Glu Arg Ala Ser Cys Glu Ser
465                 470                 475                 480
Asp Val Leu His Phe Thr Ser Thr Thr Thr Ser Lys Asn Arg Ile Ile
                485                 490                 495
Ile Thr Trp His Arg Tyr Arg Pro Pro Asp Tyr Arg Asp Leu Ile Ser
            500                 505                 510
Phe Thr Val Tyr Tyr Lys Glu Ala Pro Phe Lys Asn Val Thr Glu Tyr
        515                 520                 525
Asp Gly Gln Asp Ala Cys Gly Ser Asn Ser Trp Asn Met Val Asp Val
    530                 535                 540
Asp Leu Pro Pro Asn Lys Asp Val Glu Pro Gly Ile Leu Leu His Gly
```

```
545                 550                 555                 560
Leu Lys Pro Trp Thr Gln Tyr Ala Val Tyr Val Lys Ala Val Thr Leu
                565                 570                 575
Thr Met Val Glu Asn Asp His Ile Arg Gly Ala Lys Ser Glu Ile Leu
            580                 585                 590
Tyr Ile Arg Thr Asn Ala Ser Val Pro Ser Ile Pro Leu Asp Val Leu
        595                 600                 605
Ser Ala Ser Asn Ser Ser Ser Gln Leu Ile Val Lys Trp Asn Pro Pro
    610                 615                 620
Ser Leu Pro Asn Gly Asn Leu Ser Tyr Tyr Ile Val Arg Trp Gln Arg
625                 630                 635                 640
Gln Pro Gln Asp Gly Tyr Leu Tyr Arg His Asn Tyr Cys Ser Lys Asp
                645                 650                 655
Lys Ile Pro Ile Arg Lys Tyr Ala Asp Gly Thr Ile Asp Ile Glu Glu
            660                 665                 670
Val Thr Glu Asn Pro Lys Thr Glu Val Cys Gly Gly Glu Lys Gly Pro
        675                 680                 685
Cys Cys Ala Cys Pro Lys Thr Glu Ala Glu Lys Gln Ala Glu Lys Glu
    690                 695                 700
Glu Ala Glu Tyr Arg Lys Val Phe Glu Asn Phe Leu His Asn Ser Ile
705                 710                 715                 720
Phe Val Pro Arg Pro Glu Arg Lys Arg Arg Asp Val Met Gln Val Ala
                725                 730                 735
Asn Thr Thr Met Ser Ser Arg Ser Arg Asn Thr Thr Ala Ala Asp Thr
            740                 745                 750
Tyr Asn Ile Thr Asp Pro Glu Glu Leu Glu Thr Glu Tyr Pro Phe Phe
        755                 760                 765
Glu Ser Arg Val Asp Asn Lys Glu Arg Thr Val Ile Ser Asn Leu Arg
    770                 775                 780
Pro Phe Thr Leu Tyr Arg Ile Asp Ile His Ser Cys Asn His Glu Ala
785                 790                 795                 800
Glu Lys Leu Gly Cys Ser Ala Ser Asn Phe Val Phe Ala Arg Thr Met
                805                 810                 815
Pro Ala Glu Gly Ala Asp Asp Ile Pro Gly Pro Val Thr Trp Glu Pro
            820                 825                 830
Arg Pro Glu Asn Ser Ile Phe Leu Lys Trp Pro Glu Pro Glu Asn Pro
        835                 840                 845
Asn Gly Leu Ile Leu Met Tyr Glu Ile Lys Tyr Gly Ser Gln Val Glu
    850                 855                 860
Asp Gln Arg Glu Cys Val Ser Arg Gln Glu Tyr Arg Lys Tyr Gly Gly
865                 870                 875                 880
Ala Lys Leu Asn Arg Leu Asn Pro Gly Asn Tyr Thr Ala Arg Ile Gln
                885                 890                 895
Ala Thr Ser Leu Ser Gly Asn Gly Ser Trp Thr Asp Pro Val Phe Phe
            900                 905                 910
Tyr Val Gln Ala Lys Thr Gly Tyr Glu Asn Ser Ser Glu Pro Lys Ser
        915                 920                 925
Ser Asp Lys Thr His Thr Ser Pro Pro Ser Ser Ala Pro Glu Leu Leu
    930                 935                 940
Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
945                 950                 955                 960
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
                965                 970                 975
His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
            980                 985                 990
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
        995                 1000                1005
```

```
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
    1010                1015                1020
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
1025                1030                1035                1040
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
                1045                1050                1055
Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
            1060                1065                1070
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
        1075                1080                1085
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
    1090                1095                1100
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
1105                1110                1115                1120
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
                1125                1130                1135
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
            1140                1145                1150
Ser Pro Gly Lys
        1155

<210> 1233
<211> 961
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 1233
Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
 1               5                  10                  15
Asp Thr Thr Gly Glu Ile Cys Gly Pro Gly Ile Asp Ile Arg Asn Asp
            20                  25                  30
Tyr Gln Gln Leu Lys Arg Leu Glu Asn Cys Thr Val Ile Glu Gly Tyr
        35                  40                  45
Leu His Ile Leu Leu Ile Ser Lys Ala Glu Asp Tyr Arg Ser Tyr Arg
    50                  55                  60
Phe Pro Lys Leu Thr Val Ile Thr Glu Tyr Leu Leu Leu Phe Arg Val
65                  70                  75                  80
Ala Gly Leu Glu Ser Leu Gly Asp Leu Phe Pro Asn Leu Thr Val Ile
                85                  90                  95
Arg Gly Trp Lys Leu Phe Tyr Asn Tyr Ala Leu Val Ile Phe Glu Met
            100                 105                 110
Thr Asn Leu Lys Asp Ile Gly Leu Tyr Asn Leu Arg Asn Ile Thr Arg
        115                 120                 125
Gly Ala Ile Arg Ile Glu Lys Asn Ala Asp Leu Cys Tyr Leu Ser Thr
    130                 135                 140
Val Asp Trp Ser Leu Ile Leu Asp Ala Val Ser Asn Asn Tyr Ile Val
145                 150                 155                 160
Gly Asn Lys Pro Pro Lys Glu Cys Gly Asp Leu Cys Pro Gly Thr Met
                165                 170                 175
Glu Glu Lys Pro Met Cys Glu Lys Thr Thr Ile Asn Asn Glu Tyr Asn
            180                 185                 190
Tyr Arg Cys Trp Thr Thr Asn Arg Cys Gln Lys Met Cys Pro Ser Thr
        195                 200                 205
Cys Gly Lys Arg Ala Cys Thr Glu Asn Asn Glu Cys Cys His Pro Glu
```

```
    210                 215                 220
Cys Leu Gly Ser Cys Ser Ala Pro Asp Asn Asp Thr Ala Cys Val Ala
225                 230                 235                 240
Cys Arg His Tyr Tyr Tyr Ala Gly Val Cys Val Pro Ala Cys Pro Pro
                245                 250                 255
Asn Thr Tyr Arg Phe Glu Gly Trp Arg Cys Val Asp Arg Asp Phe Cys
            260                 265                 270
Ala Asn Ile Leu Ser Ala Glu Ser Ser Asp Ser Glu Gly Phe Val Ile
        275                 280                 285
His Asp Gly Glu Cys Met Gln Glu Cys Pro Ser Gly Phe Ile Arg Asn
    290                 295                 300
Gly Ser Gln Ser Met Tyr Cys Ile Pro Cys Glu Gly Pro Cys Pro Lys
305                 310                 315                 320
Val Cys Glu Glu Glu Lys Lys Thr Lys Thr Ile Asp Ser Val Thr Ser
                325                 330                 335
Ala Gln Met Leu Gln Gly Cys Thr Ile Phe Lys Gly Asn Leu Leu Ile
            340                 345                 350
Asn Ile Arg Arg Gly Asn Asn Ile Ala Ser Glu Leu Glu Asn Phe Met
        355                 360                 365
Gly Leu Ile Glu Val Val Thr Gly Tyr Val Lys Ile Arg His Ser His
    370                 375                 380
Ala Leu Val Ser Leu Ser Phe Leu Lys Asn Leu Arg Leu Ile Leu Gly
385                 390                 395                 400
Glu Glu Gln Leu Glu Gly Asn Tyr Ser Phe Tyr Val Leu Asp Asn Gln
                405                 410                 415
Asn Leu Gln Gln Leu Trp Asp Trp Asp His Arg Asn Leu Thr Ile Lys
            420                 425                 430
Ala Gly Lys Met Tyr Phe Ala Phe Asn Pro Lys Leu Cys Val Ser Glu
        435                 440                 445
Ile Tyr Arg Met Glu Glu Val Thr Gly Thr Lys Gly Arg Gln Ser Lys
    450                 455                 460
Gly Asp Ile Asn Thr Arg Asn Asn Gly Glu Arg Ala Ser Cys Glu Ser
465                 470                 475                 480
Asp Val Leu His Phe Thr Ser Thr Thr Thr Ser Lys Asn Arg Ile Ile
                485                 490                 495
Ile Thr Trp His Arg Tyr Arg Pro Pro Asp Tyr Arg Asp Leu Ile Ser
            500                 505                 510
Phe Thr Val Tyr Tyr Lys Glu Ala Pro Phe Lys Asn Val Thr Glu Tyr
        515                 520                 525
Asp Gly Gln Asp Ala Cys Gly Ser Asn Ser Trp Asn Met Val Asp Val
    530                 535                 540
Asp Leu Pro Pro Asn Lys Asp Val Glu Pro Gly Ile Leu Leu His Gly
545                 550                 555                 560
Leu Lys Pro Trp Thr Gln Tyr Ala Val Tyr Val Lys Ala Val Thr Leu
                565                 570                 575
Thr Met Val Glu Asn Asp His Ile Arg Gly Ala Lys Ser Glu Ile Leu
            580                 585                 590
Tyr Ile Arg Thr Asn Ala Ser Val Pro Ser Ile Pro Leu Asp Val Leu
        595                 600                 605
Ser Ala Ser Asn Ser Ser Ser Gln Leu Ile Val Lys Trp Asn Pro Pro
    610                 615                 620
Ser Leu Pro Asn Gly Asn Leu Ser Tyr Tyr Ile Val Arg Trp Gln Arg
625                 630                 635                 640
Gln Pro Gln Asp Gly Tyr Leu Tyr Arg His Asn Tyr Cys Ser Lys Asp
                645                 650                 655
Lys Ile Pro Ile Arg Lys Tyr Ala Asp Gly Thr Ile Asp Ile Glu Glu
            660                 665                 670
```

```
Val Thr Glu Asn Pro Lys Thr Glu Val Cys Gly Gly Glu Lys Gly Pro
        675                 680                 685
Cys Cys Ala Cys Pro Lys Thr Glu Ala Glu Lys Gln Ala Glu Lys Glu
    690                 695                 700
Glu Ala Glu Tyr Arg Lys Val Phe Glu Asn Phe Leu His Asn Ser Ile
705                 710                 715                 720
Phe Val Pro Arg Pro Glu Ser Asp Gln Glu Pro Lys Ser Cys Asp Lys
                725                 730                 735
Thr His Thr Ser Pro Pro Cys Ser Ala Pro Glu Leu Leu Gly Gly Pro
            740                 745                 750
Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
        755                 760                 765
Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
    770                 775                 780
Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
785                 790                 795                 800
Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
                805                 810                 815
Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
            820                 825                 830
Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
        835                 840                 845
Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
    850                 855                 860
Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
865                 870                 875                 880
Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
                885                 890                 895
Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
            900                 905                 910
Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
        915                 920                 925
Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
    930                 935                 940
Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
945                 950                 955                 960
Lys
```

<210> 1234
<211> 3468
<212> DNA
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 1234

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atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt      60
gaaatctgcg ggccaggcat cgacatccgc aacgactatc agcagctgaa gcgcctggag     120
aactgcacgg tgatcgaggg ctacctccac atcctgctca tctccaaggc cgaggactac     180
cgcagctacc gcttccccaa gctcacggtc attaccgagt acttgctgct gttccgagtg     240
gctggcctcg agagcctcgg agacctcttc cccaacctca cggtcatccg cggctggaaa     300
ctcttctaca actacgccct ggtcatcttc gagatgacca atctcaagga tattgggctt     360
tacaacctga ggaacattac tcgggggcc atcaggattg agaaaaatgc tgacctctgt     420
tacctctcca ctgtggactg gtccctgatc ctggatgcgg tgtccaataa ctacattgtg     480
gggaataagc ccccaaagga atgtggggac ctgtgtccag ggaccatgga ggagaagccg     540
```

atgtgtgaga agaccaccat caacaatgag tacaactacc gctgctggac cacaaaccgc 600
tgccagaaaa tgtgcccaag cacgtgtggg aagcgggcgt gcaccgagaa caatgagtgc 660
tgccaccccg agtgcctggg cagctgcagc gcgcctgaca acgacacggc ctgtgtagct 720
tgccgccact actactatgc cggtgtctgt gtgcctgcct gcccgcccaa cacctacagg 780
tttgagggct ggcgctgtgt ggaccgtgac ttctgcgcca acatcctcag cgccgagagc 840
agcgactccg aggggtttgt gatccacgac ggcgagtgca tgcaggagtg cccctcgggc 900
ttcatccgca acggcagcca gagcatgtac tgcatccctt gtgaaggtcc ttgcccgaag 960
gtctgtgagg aagaaaagaa aacaaagacc attgattctg ttacttctgc tcagatgctc 1020
caaggatgca ccatcttcaa gggcaatttg ctcattaaca tccgacgggg gaataacatt 1080
gcttcagagc tggagaactt catggggctc atcgaggtgg tgacgggcta cgtgaagatc 1140
cgccattctc atgccttggt ctccttgtcc ttcctaaaaa accttcgcct catcctagga 1200
gaggagcagc tagaagggaa ttactccttc tacgtcctcg acaaccagaa cttgcagcaa 1260
ctgtgggact gggaccaccg caacctgacc atcaaagcag ggaaaatgta ctttgctttc 1320
aatcccaaat tatgtgtttc cgaaatttac cgcatggagg aagtgacggg gactaaaggg 1380
cgccaaagca aaggggacat aaacaccagg aacaacgggg agagagcctc ctgtgaaagt 1440
gacgtcctgc atttcacctc caccaccacg tcgaagaatc gcatcatcat aacctggcac 1500
cggtaccggc cccctgacta cagggatctc atcagcttca ccgtttacta caaggaagca 1560
ccctttaaga atgtcacaga gtatgatggg caggatgcct gcggctccaa cagctggaac 1620
atggtggacg tggacctccc gcccaacaag gacgtggagc ccggcatctt actacatggg 1680
ctgaagccct ggactcagta cgccgtttac gtcaaggctg tgaccctcac catggtggag 1740
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<210> 1235
<211> 2883
<212> DNA
<213> Artificial Sequence

<220>
<223> Made in a lab

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aaa 2883

<210> 1236
<211> 633
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 1236
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Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln Thr Ala Gln Met Cys Cys
            20   25   30
Ser Lys Cys Ser Pro Gly Gln His Ala Lys Val Phe Cys Thr Lys Thr
        35   40   45
Ser Asp Thr Val Cys Asp Ser Cys Glu Asp Ser Thr Tyr Thr Gln Leu
    50   55   60
Trp Asn Trp Val Pro Glu Cys Leu Ser Cys Gly Ser Arg Cys Ser Ser
65   70   75   80
Asp Gln Val Glu Thr Gln Ala Cys Thr Arg Glu Gln Asn Arg Ile Cys
                85   90   95
Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu Ser Lys Gln Glu Gly Cys
            100   105   110
Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg Pro Gly Phe Gly Val Ala
        115   120   125
Arg Pro Gly Thr Glu Thr Ser Asp Val Val Cys Lys Pro Cys Ala Pro
    130   135   140
Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr Asp Ile Cys Arg Pro His
145   150   155   160
Gln Ile Cys Asn Val Val Ala Ile Pro Gly Asn Ala Ser Met Asp Ala
                165   170   175
Val Cys Thr Ser Thr Ser Pro Thr Arg Ser Met Ala Pro Gly Ala Val
            180   185   190
His Leu Pro Gln Pro Val Ser Thr Arg Ser Gln His Thr Gln Pro Thr
        195   200   205
Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser Phe Leu Leu Pro Met Gly
    210   215   220
Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly Asp Thr Gly Glu Pro Lys
225   230   235   240
Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala
                245   250   255
Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
            260   265   270
Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
        275   280   285
Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
    290   295   300
Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
305   310   315   320
Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
                325   330   335
Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala Leu Pro Ala
            340   345   350
Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
        355   360   365
Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln
    370   375   380
Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
385   390   395   400
Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
                405   410   415
Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu

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            420                 425                 430
Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
        435                 440                 445
Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
    450                 455                 460
Leu Ser Pro Gly Gln Arg His Asn Asn Ser Ser Leu Asn Thr Gly Thr
465                 470                 475                 480
Gln Met Ala Gly His Ser Pro Asn Ser Thr Ile Pro Pro His Val Gln
                485                 490                 495
Lys Ser Val Asn Asn Asp Met Ile Val Thr Asp Asn Asn Gly Ala Val
            500                 505                 510
Lys Phe Pro Gln Leu Cys Lys Phe Cys Asp Val Arg Phe Ser Thr Cys
        515                 520                 525
Asp Asn Gln Lys Ser Cys Met Ser Asn Cys Ser Ile Thr Ser Ile Cys
    530                 535                 540
Glu Lys Pro Gln Glu Val Cys Val Ala Val Trp Arg Lys Asn Asp Glu
545                 550                 555                 560
Asn Ile Thr Leu Glu Thr Val Cys His Asp Pro Lys Leu Pro Tyr His
                565                 570                 575
Asp Phe Ile Leu Glu Asp Ala Ala Ser Pro Lys Cys Ile Met Lys Glu
            580                 585                 590
Lys Lys Lys Pro Gly Glu Thr Phe Phe Met Cys Ser Cys Ser Ser Asp
        595                 600                 605
Glu Cys Asn Asp Asn Ile Ile Phe Ser Glu Glu Tyr Asn Thr Ser Asn
    610                 615                 620
Pro Asp Leu Leu Leu Val Ile Phe Gln
625                 630

<210> 1237
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 1237
Glu Gln Ala Pro Gly Thr Ala Pro Cys Ser Arg Gly Ser Ser Trp Ser
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Ala Asp Leu Asp Lys Cys Met Asp Cys Ala Ser Cys Arg Ala Arg Pro
            20                  25                  30
His Ser Asp Phe Cys Leu Gly Cys Ala Ala Ala Pro Pro Ala Pro Phe
        35                  40                  45
Arg Leu Leu Trp Thr Gly Glu Pro Lys Ser Ser Asp Lys Thr His Thr
    50                  55                  60
Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe
65                  70                  75                  80
Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
                85                  90                  95
Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
            100                 105                 110
Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
        115                 120                 125
Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
    130                 135                 140
Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys
145                 150                 155                 160
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Ala Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
                165                 170                 175
Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
            180                 185                 190
Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
        195                 200                 205
Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
    210                 215                 220
Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
225                 230                 235                 240
Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
                245                 250                 255
Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
            260                 265                 270
Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gln Arg His
        275                 280                 285
Asn Asn Ser Ser Leu Asn Thr Gly Thr Gln Met Ala Gly His Ser Pro
    290                 295                 300
Asn Ser Thr Ile Pro Pro His Val Gln Lys Ser Val Asn Asn Asp Met
305                 310                 315                 320
Ile Val Thr Asp Asn Asn Gly Ala Val Lys Phe Pro Gln Leu Cys Lys
                325                 330                 335
Phe Cys Asp Val Arg Phe Ser Thr Cys Asp Asn Gln Lys Ser Cys Met
            340                 345                 350
Ser Asn Cys Ser Ile Thr Ser Ile Cys Glu Lys Pro Gln Glu Val Cys
        355                 360                 365
Val Ala Val Trp Arg Lys Asn Asp Glu Asn Ile Thr Leu Glu Thr Val
    370                 375                 380
Cys His Asp Pro Lys Leu Pro Tyr His Asp Phe Ile Leu Glu Asp Ala
385                 390                 395                 400
Ala Ser Pro Lys Cys Ile Met Lys Glu Lys Lys Lys Pro Gly Glu Thr
                405                 410                 415
Phe Phe Met Cys Ser Cys Ser Ser Asp Glu Cys Asn Asp Asn Ile Ile
            420                 425                 430
Phe Ser Glu Glu Tyr Asn Thr Ser Asn Pro Asp Leu Leu Leu Val Ile
        435                 440                 445
Phe Gln
    450
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<210> 1238
<211> 1968
<212> DNA
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 1238

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cggctcagag aatactatga ccagacagct cagatgtgct gcagcaaatg ctcgccgggc     180
caacatgcaa aagtcttctg taccaagacc tcggacaccg tgtgtgactc ctgtgaggac     240
agcacataca cccagctctg gaactgggtt cccgagtgct tgagctgtgg ctcccgctgt     300
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aggcccggct ggtactgcgc gctgagcaag caggaggggt gccggctgtg cgcgccgctg     420
cgcaagtgcc gcccgggctt cggcgtggcc agaccaggaa ctgaaacatc agacgtggtg     480
tgcaagccct gtgccccggg gacgttctcc aacacgactt catccacgga tatttgcagg     540
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<210> 1239
<211> 1416
<212> DNA
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 1239
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<210> 1240
<211> 10
<212> PRT
<213> Human

<400> 1240
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 1 5 10

<210> 1241
<211> 7
<212> PRT
<213> Human

<400> 1241
Glu Arg Lys Cys Cys Val Glu
 1 5

<210> 1242
<211> 12
<212> PRT
<213> Human

<400> 1242
Glu Leu Lys Thr Pro Leu Gly Asp Thr Thr His Thr
 1 5 10

<210> 1243
<211> 10
<212> PRT
<213> Human

<400> 1243
Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro
 1 5 10

<210> 1244
<211> 7
<212> PRT
<213> Human

<400> 1244
Glu Ser Lys Tyr Gly Pro Pro
 1 5

<210> 1245
<211> 5
<212> PRT
<213> Human

<400> 1245
Cys Pro Pro Cys Pro
 1 5

<210> 1246

<211> 5
<212> PRT
<213> Human

<400> 1246
Cys Pro Arg Cys Pro
 1   5

<210> 1247
<211> 5
<212> PRT
<213> Human

<400> 1247
Cys Pro Ser Cys Pro
 1   5

<210> 1248
<211> 17
<212> PRT
<213> Human

<400> 1248
Glu Leu Lys Thr Pro Leu Gly Asp Thr Thr His Thr Cys Pro Arg Cys
 1   5   10   15
Pro

<210> 1249
<211> 15
<212> PRT
<213> Human

<400> 1249
Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro
 1   5   10   15

<210> 1250
<211> 34
<212> PRT
<213> Human

<400> 1250
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 1   5   10   15
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            20   25   30
Asn Thr

<210> 1251
<211> 24
<212> PRT
<213> Human

<400> 1251
Gly Arg Gly Gly Glu Glu Lys Lys Lys Glu Lys Glu Lys Glu Glu Gln

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<210> 1252
<211> 19
<212> PRT
<213> Human

<400> 1252

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Val Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Thr Pro Pro Thr Pro
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Ser Pro Ser
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<210> 1253
<211> 6
<212> PRT
<213> Human

<400> 1253

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Val Pro Pro Pro Pro Pro
 1               5
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<210> 1254
<211> 107
<212> PRT
<213> Human

<400> 1254

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Val Cys Ser Arg Asp Phe Thr Pro Pro Thr Val Lys Ile Leu Gln Ser
 1               5                  10                  15
Ser Ser Asp Gly Gly Gly His Phe Pro Pro Thr Ile Gln Leu Leu Cys
            20                  25                  30
Leu Val Ser Gly Tyr Thr Pro Gly Thr Ile Asn Ile Thr Trp Leu Glu
        35                  40                  45
Asp Gly Gln Val Met Asp Val Asp Leu Ser Thr Ala Ser Thr Thr Gln
    50                  55                  60
Glu Gly Glu Leu Ala Ser Thr Gln Ser Glu Leu Thr Leu Ser Gln Lys
65                  70                  75                  80
His Trp Leu Ser Asp Arg Thr Tyr Thr Cys Gln Val Thr Tyr Gln Gly
                85                  90                  95
His Thr Phe Glu Asp Ser Thr Lys Lys Cys Ala
            100                 105
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<210> 1255
<211> 112
<212> PRT
<213> Human

<400> 1255

```
Val Ile Ala Glu Leu Pro Pro Lys Val Ser Val Phe Val Pro Pro Arg
 1               5                  10                  15
Asp Gly Phe Phe Gly Asn Pro Arg Lys Ser Lys Leu Ile Cys Gln Ala
            20                  25                  30
Thr Gly Phe Ser Pro Arg Gln Ile Gln Val Ser Trp Leu Arg Glu Gly
        35                  40                  45
```

```
Lys Gln Val Gly Ser Gly Val Thr Thr Asp Gln Val Gln Ala Glu Ala
    50                  55                  60
Lys Glu Ser Gly Pro Thr Thr Tyr Lys Val Thr Ser Thr Leu Thr Ile
65                  70                  75                  80
Lys Glu Ser Asp Trp Leu Gly Gln Ser Met Phe Thr Cys Arg Val Asp
                85                  90                  95
His Arg Gly Leu Thr Phe Gln Gln Asn Ala Ser Ser Met Cys Val Pro
            100                 105                 110
```