# ORAL PEPTIDE INHIBITORS OF INTERLEUKIN-23 RECEPTOR AND THEIR USE TO TREAT INFLAMMATORY BOWEL DISEASES

## CROSS REFERENCE TO RELATED APPLICATIONS

**[0001]** This application claims priority to U.S. Provisional Application No. 62/025,899, filed on July 17, 2014, U.S. Provisional Application No. 62/119,685, filed on February 23, 2015, and U.S. Provisional Application No. 62/119,688, filed on February 23, 2015, each of which is incorporated by reference herein in its entirety.

## SEQUENCE LISTING

The instant application contains a Sequence Listing which has been submitted electronically in ASCII format and is hereby incorporated by reference in its entirety. Said ASCII copy, created on October 8, 2015, is named PRTH-002-02WO_SL.txt and is 516,536 bytes in size.

## FIELD OF THE INVENTION

**[0002]** The present invention relates to novel peptide inhibitors of the interleukin-23 receptor, and their use to treat or prevent a variety of diseases and disorders, including inflammatory bowel disease, Crohn's disease and psoriasis.

## BACKGROUND

**[0003]** The interleukin-23 (IL-23) cytokine has been implicated as playing a crucial role in the pathogenesis of autoimmune inflammation and related diseases and disorders, such as multiple sclerosis, asthma, rheumatoid arthritis, psoriasis, and inflammatory bowel diseases (IBDs), e.g., ulcerative colitis and Crohn's disease. Studies in acute and chronic mouse models of IBD revealed a primary role of IL-23R and downstream effector cytokines in disease pathogenesis. IL-23R is expressed on various adaptive and innate immune cells including Th17 cells, γδ T cells, natural killer (NK) cells, dendritic cells, macrophages, and innate lymphoid cells, which are found abundantly in the intestine. At the intestine mucosal surface, the gene expression and protein levels of IL-23R are found to be elevated in IBD patients. It is believed that IL-23 mediates this effect by promoting the development of a pathogenic $CD4^+$ T cell population that produces IL-6, IL-17, and tumor necrosis factor (TNF).

**[0004]** Production of IL-23 is enriched in the intestine, where it is believed to play a key role in regulating the balance between tolerance and immunity through T-cell-dependent and T-cell-independent pathways of intestinal inflammation through effects on T-helper 1 (Th1) and Th17-associated cytokines, as well as restraining regulatory T-cell responses in the gut, favoring

form of any of the foregoing; and X17 is Leu, Lys, Arg, Glu, Ser, Gly, Gln or absent, or a corresponding α-methyl amino acid form of any of the foregoing.

**[0020]** In certain embodiments of peptide inhibitors of Xa, the bond is a disulfide bond, a thioether bond, a lactam bond, a triazole ring, a selenoether bond, a diselenide bond, or an olefin bond.

**[0021]** In particular embodiments of peptide inhibitors of Xa, X4 is Cys and X9 is Cys, and the bond is a disulfide bond. In particular embodiments, X4 is Pen and X9 is Pen, and the bond is a disulfide bond. In certain embodiments: X7 is Trp; X10 is Phe, Tyr, a Phe analog, or a Tyr analog; X11 is Trp, 1-Nal or 2-Nal; and X12 is Aib, α-Me-Lys, a-Me-Leu, Achc, Acvc, Acpc, Acbc or THP. In certain embodiments: X7 is Trp; X10 is Phe, Tyr, a Phe analog, or a Tyr analog; X11 is Trp, 1-Nal or 2-Nal; and X12 is Aib, α-Me-Lys or a-Me-Leu. In particular embodiments, the peptide inhibitor comprises any of the following the amino acid sequences: Pen-Q-T-W-Q-Pen-[Phe(4-OMe)]-[2-Nal]-[α-Me-Lys]-E-N-G (SEQ ID NO: 254); Pen-N-T-W-Q-[Pen]-[Phe[4-(2-aminoethoxy)]-[2-Nal]-[Aib]-[Lys(Ac)]-N-N (SEQ ID NO: 255); Pen-Q-T-W-Q-[Pen]-[Phe[4-(2-aminoethoxy)]-[2-Nal]-[α-MeLeu]-[Lys(Ac)]-N-N (SEQ ID NO: 256); or Pen-Q-T-W-Q-[Pen]-[Phe(4-$CONH_2$)]-[2-Nal]-[α-MeLys]-[Lys(Ac)]-N-N (SEQ ID NO: 257), wherein the peptide inhibitor comprises a disulfide bond between the two Pen amino acids.

**[0022]** In particular embodiments of peptide inhibitors of Xa, X4 is an amino acid, aliphatic acid, alicyclic acid or modified 2- methyl aromatic acid having a carbon side chain capable of forming a thioether bind with X9; X9 is a sulfur-containing amino acid capable of forming a thioether bond with X4, and the bond between X4 and X9 is a thioether bond. In certain embodiments, X4 is Abu, 2-chloromethylbenzoic acid, mercapto-propanoic acid, mercapto-butyric acid, 2-chloro-acetic acid, 3-chloro-propanoic acid, 4-chloro-butyric acid, 3-chloro-isobutyric acid; and X9 is Abu, Cys, Pen, hCys, D-Pen, D-Cys, or D-hCys.In certain embodiments, X4 is Abu; and X9 is Cys. In certain embodiments, X7 is Trp; X10 is Phe, Tyr, a Phe analog, or a Tyr analog; X11 is Trp, 1-Nal or 2-Nal; and X12 is α-Me-Lys, α-Me-Leu, α-Me-Ser, α-Me-Val, Achc, Acvc, Acpc, Acbc, or [4-amino-4-carboxy-tetrahydropyran]. In certain embodiments, X7 is Trp; X10 is Phe, Tyr, a Phe analog, or a Tyr analog; X11 is Trp, 1-Nal or 2-Nal; and X12 is α-Me-Lys or [4-amino-4-carboxy-tetrahydropyran]. In particular

embodiments, the peptide inhibitor comprises any of the following amino acid sequences: [Abu]-Q-T-W-Q-C-[Phe(4-OMe)]-[2-Nal]-[α-MeLys]-E-N-G (SEQ ID NO: 258); [Abu]-Q-T-W-Q-C-[Phe(4-(2-aminoethoxy))]-W-[α-MeLys]-E-N-G (SEQ ID NO: 259); or [Abu]-Q-T-W-Q-C-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[4-amino-4-carboxy-tetrahydropyran]-E-N-N (SEQ ID NO: 260), wherein the peptide inhibitor comprises a thioether bond between the Abu and the C.

**[0023]** In certain embodiments of peptide inhibitors of Xa: X4 is Pen, Cys or hCys; X5 is any amino acid; X6 is any amino acid; X7 is Trp, Bip, Gln, His, Glu(Bzl), 4-Phenylbenzylalanine, Tic, Phe[4-(2-aminoethoxy)], Phe(3,4-$Cl_2$), Phe(4-OMe), 5-Hydroxy-Trp, 6-Chloro-Trp, N-MeTrp, α-Me-Trp, 1,2,3,4 -tetrahydro-norharman, Phe(4-$CO_2H$), Phe(4-$CONH_2$), Phe(3,4-Dimethoxy), Phe(4-$CF_3$), Phe(4-tBu), ββ-diPheAla, Glu, Gly, Ile, Asn, Pro, Arg, Thr or Octgly, or a corresponding α-methyl amino acid form of any of the foregoing; X8 is any amino acid; X9 is Pen, Cys or hCys; X10 is 1-Nal, 2-Nal, Aic, Bip, (D)Cys, Cha, DMT, (D)Tyr, Glu, Phe, His, Trp, Thr, Tic, Tyr, 4-pyridylAla, Octgly, a Phe analog or a Tyr analog (optionally, Phe(3,4-$F_2$), Phe(3,4-$Cl_2$), F(3-Me), Phe[4-(2-aminoethoxy)], Phe[4-(2-(acetyl-aminoethoxy)], Phe(4-Br), Phe(4-$CONH_2$), Phe(4-Cl), Phe(4-CN), Phe(4-guanidino), Phe(4-Me), Phe(4-$NH_2$), Phe(4-$N_3$), Phe(4-OMe), or Phe(4-OBzl)), or a corresponding α-methyl amino acid form of any of the foregoing; X11 is 2-Nal, 1-Nal, 2,4-dimethylPhe, Bip, Phe(3,4-$Cl_2$), Phe (3,4-$F_2$), Phe(4-$CO_2H$), βhPhe(4-F), α-Me-Trp, 4-phenylcyclohexyl, Phe(4-$CF_3$), α-MePhe, βhNal, βhPhe, βhTyr, βhTrp, Nva(5-phenyl), Phe, His, hPhe, Tic, Tqa, Trp, Tyr, Phe(4-OMe), Phe(4-Me), Trp(2,5,7-tri-tert-Butyl), Phe(4-Oallyl), Tyr(3-tBu), Phe(4-tBu), Phe(4-guanidino, Phe(4-OBzl), Octgly, Glu(Bzl), 4-Phenylbenzylalanine, Phe[4-(2-aminoethoxy)], 5-Hydroxy-Trp, 6-Chloro-Trp, N-MeTrp, 1,2,3,4-tetrahydro-norharman, Phe(4-$CONH_2$), Phe(3,4-$OMe_2$) Phe(2,3-$Cl_2$), Phe(2,3-$F_2$), Phe(4-F), 4-phenylcyclohexylalanine or Bip, or a corresponding α-methyl amino acid form of any of the foregoing; X12 is α-MeLys, α-MeOrn, α-MeLeu, α-MeVal, 4-amino-4-carboxy-tetrahydropyran, Achc, Acpc, Acbc, Acvc, MeLeu, Aib, (D)Ala, (D)Asn, (D)Leu, (D)Asp, (D)Phe, (D)Thr, 3-Pal, Aib, β-Ala, βhGlu, βhAla, βhLeu, βhVal, β-spiro-pip, Cha, Chg, Asp, Dab, Dap, α-DiethylGly, Glu, Phe, hLeu, hArg, hLeu, Ile, Lys, Leu, Asn, N-MeLeu, N-MeArg, Ogl, Orn, Pro, Gln, Arg, Ser, Thr or Tle, or a corresponding α-methyl amino acid form of any of the foregoing; X13 is Lys(Ac), (D)Asn, (D)Leu, (D)Thr, (D)Phe, Ala, Aib, α-MeLeu, β-Ala, βhGlu, βhAla, βhLeu, βhVal, β-spiro-pip, Cha, Chg, Asp, Lys, Arg, Orn, Dab, Dap, α-

**[0031]** In a related aspect, the present invention includes a peptide dimer inhibitor of an interleukin-23 receptor, wherein the peptide dimer inhibitor comprises two peptide monomer subunits connected via one or more linker moieties, wherein each peptide monomer subunit has a sequence or structure set forth herein.In certain embodiments, one or both peptide monomer subunit is cyclized via an intramolecular bond between X4 and X9. In certain embodiments, one or both intramolecular bond is a disulfide bond, a thioether bond, a lactam bond, a selenoether, diselenide, or an olefin bond. In certain embodiments, the linker is any of those shown in Table 2. In certain embodiments, the linker moiety is a diethylene glycol linker, an iminodiacetic acid (IDA) linker, a β-Ala-iminodiaceticacid (β-Ala-IDA) linker, or a PEG linker. In particular embodiments, the N-terminus of each peptide monomer subunit is connected by the linker moiety. In particular embodiments, the C-terminus of each peptide monomer subunit is connected by the linker moiety. In certain embodiments, the linker connects an internal amino acid residue of at least one of the peptide monomer subunits to the N-terminus, C-terminus, or an internal amino acid residue of the other peptide monomer subunit.

**[0032]** In a further related aspect, the present invention includes a polynucleotide comprising a sequence encoding a peptide inhibitor of the present invnetion or one or both peptide monomer subunit of a peptide dimer inhibitor of the present invention. The present invention also included a vector comprising the polynucleotide.

**[0033]** In another aspect, the present invention includes a pharmaceutical composition comprising a peptide inhibitor or a peptide dimer inhibitor of the present invention, and a pharmaceutically acceptable carrier, excipient, or diluent.In particular embodiments, the pharmaceutical composition comprises an enteric coating.In certain embodiments, the enteric coating protects and releases the pharmaceutical composition within a subject's lower gastrointestinal system.

In another aspect, the present invention includes a use of an effective amount of the pharmaceutical composition as described herein in the manufacture of a medicament for treating an Inflammatory Bowel Disease (IBD), ulcerative colitis, Crohn's disease, Celiac disease (nontropical Sprue), enteropathy associated with seronegative arthropathies, microscopic colitis, collagenous colitis, eosinophilic gastroenteritis, colitis associated with radio- or chemo-therapy,

colitis associated with disorders of innate immunity as in leukocyte adhesion deficiency-1, chronic granulomatous disease, glycogen storage disease type 1b, Hermansky-Pudlak syndrome, Chediak-Higashi syndrome, and Wiskott-Aldrich Syndrome, pouchitis resulting after proctocolectomy and ileoanal anastomosis, gastrointestinal cancer, pancreatitis, insulin-dependent diabetes mellitus, mastitis, cholecystitis, cholangitis, pericholangitis, chronic bronchitis, chronic sinusitis, asthma, psoriasis, psoriatic arthritis, or graft versus host disease in a subject. Also is a method for treating or preventing a disease associated with IL-23 signalling, including but not limited to an Inflammatory Bowel Disease (IBD), ulcerative colitis, Crohn's disease, Celiac disease (*nontropical Sprue)*, enteropathy associated with seronegative arthropathies, microscopic colitis, collagenous colitis, eosinophilic gastroenteritis, colitis associated with radio- or chemo-therapy, colitis associated with disorders

of innate immunity as in leukocyte adhesion deficiency-1, chronic granulomatous disease, glycogen storage disease type 1b, Hermansky-Pudlak syndrome, Chediak-Higashi syndrome, and Wiskott-Aldrich Syndrome, pouchitis resulting after proctocolectomy and ileoanal anastomosis, gastrointestinal cancer, pancreatitis, insulin-dependent diabetes mellitus, mastitis, cholecystitis, cholangitis, pericholangitis, chronic bronchitis, chronic sinusitis, asthma, psoriasis, or graft versus host disease in a subject, comprising providing to the subject an effective amount of the pharmaceutical composition of the present invention.In certain embodiments, the inflammatory bowel disease is ulcerative colitis or Crohn's disease. In particular embodimnts, the peptide inhibitor or the peptide dimer inhibitor inhibits binding of an interleukin-23 (IL-23) to the interleukin-23 receptor (IL-23R). In certain embodiments, the pharmaceutical composition is provided to the subject by an oral, intravenous, peritoneal, intradermal, subcutaneous, intramuscular, intrathecal, inhalation, vaporization, nebulization, sublingual, buccal, parenteral, rectal, intraocular, inhalation, vaginal, or topical route of administration. In particular embodiments, the pharmaceutical composition is provided orally for treating Inflammatory Bowel Disease (IBD), ulcerative colitis, Crohn's disease. In certain embodiments, the pharmaceutical composition is provided to the subject topically, parenterally, intravenously, subcutaneously, peritonealy, or intravenously for treating psoriasis.

***BRIEF DESCRIPTION OF THE DRAWINGS***

**[0034] Figure 1** provides an example of a rat IL-23 dose-response curve as measured by levels of IL-17A in the rat splenoctye assay.

**[0035] Figure 2** is a graph showing IL-12-dependent production of IFNγ from human PBMCs treated with the indicated amounts of Compound A or Compound B.

**[0036] Figure 3** shows results for DAI values from Day 7. Statistical analysis for significance was determined using Student's t-test (GraphPad Prism). Differences were noted as signficant *$p<0.05$, **$p<0.01$, ***$p<0.001$, ****$p<0.0001$.

**[0037] Figure 4** shows an alignment of the amino acid sequences of human IL23R (SEQ ID NO: 760), mouse IL-23R (SEQ ID NO: 761), rat IL23R (SEQ ID NO: 762), chimp IL-23R (SEQ ID NO: 763), dog IL-23R (SEQ ID NO: 764) and cow IL-23R (SEQ ID NO: 765), with highly conserved amino acid

and IL-23R. In certain embodiments, the peptide inhibitors bind and/or inhibit human IL-23R. In certain embodiments, the peptide inhibitors bind and/or inhibit both human and rodent IL-23R. In certain embodiments, the peptide inhibitors bind and/or inhibit both human and rat IL-23R. In particular embodiments, the peptide inhibitors inhibit rat IL-23R at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, or at least 95% as well as they bind or inhibit human IL-23R, e.g., as determined by an assay described herein. In certain embodiments, the peptide inhibitors preferentially bind and/or inhibit human and/or rat IL-23R as compared to mouse IL-23R. In particular embodiments, the peptide inhibitors preferentially bind to rat IL-23R as compared to mouse IL-23R. In particular embodiments, the peptide inhibitors preferentially bind to human IL-23R as compared to mouse IL-23R. In certain embodiments, binding of a peptide inhibitor to mouse IL-23R is less than 75%, less than 50%, less than 40%, less than 30%, less than 20%, or less than 10% of binding of the same peptide inhibitor to human IL-23R and/or rat IL-23R. In certain embodiments of peptide inhibitors that preferentially bind and/or inhibit human IL-23R and/or rat IL-23R as compared to mouse IL-23R, the peptide inhibitor binds to a region of IL-23R that is disrupted by the presence of additional amino acids present in mouse IL-23R but not human IL-23R or rat IL-23. In one embodiment, the additional amino acids present in the mouse IL-23R are in the region corresponding to about amino acid residue 315 to about amino acid residue 340 of the mouse IL23R protein, e.g., amino acid region NWQPWSSPFVHQTSQETGKR (SEQ ID NO: 261). In particular embodiments, the peptide inhibitors bind to a region of human IL-23R from about amino acid 230 to about amino acid residue 370.

**[0095]** In certain embodiments, peptide inhibitors show GI-restricted localization following oral administration. In particular embodiments, greater than 50%, greater than 60%, greater than 70%, greater than 80%, or greater than 90% of orally administered peptide inhibitor is localized to gastrointestinal organs and tissues. In particular embodiments, blood plasma levels of orally administered peptide inhibitor are less than 20%, less than 10%, less than 5%, less than 2%, less than 1% or less than 0.5% the levels of peptide inhibitor found in the small intestine mucosa, colon mucosa, or proximal colon.

**[0096]** The various peptide inhibitors of the invention may be constructed solely of natural amino acids. Alternatively, the peptide inhibitors may include non-natural amino acids including, but not limited to, modified amino acids. In certain embodiments, modified amino

X9 is Cys, Pen, hCys, D-Pen, D-Cys, D-hCys, Glu, Lys, Orn, Dap, Dab, D-Dap, D-Dab, D-Asp, D-Glu, D-Lys, Asp, Leu, Val, Phe, Ser, Sec, Abu, β-azido-Ala-OH, propargylglycine, 2-2-allylglycine, 2-(3'-butenyl)glycine, 2-(4'-pentenyl)glycine, or 2-(5'-hexenyl)glycine;

X10 is Tyr, Phe, Phe(3,4-$F_2$), Phe(3,4-$Cl_2$), F(3-Me), Phe[4-(2-aminoethoxy)], Phe[4-(2-(acetyl-aminoethoxy)], Phe(4-Br), Phe(4-$CONH_2$), Phe(4-Cl), Phe(4-CN), Phe(4-guanidino), Phe(4-Me), Phe(4-$NH_2$), Phe(4-$N_3$), Phe(4-OMe), Phe(4-OBzl) or Tyr;

X11 is Trp, 1-Nal, 2-Nal, Phe(3,4-$OMe_2$) 5-Hydroxy-Trp, Phe(3,4-$Cl_2$) or Tyr(3-t-Bu)

X12 is His, Phe, Arg, N-Me-His, or Val, Cav, Cpa, Leu, Cit, hLeu, 3-Pal, t-butyl-Ala, t-butyl-Gly 4-amino-4-carboxy-tetrahydropyran, Achc Acpc, Acbc, Acvc, Agp, Aib, α-DiethylGly, α-MeLys, α-MeLys(Ac), α-Me-Leu, α-MeOrn, α-MeSer, α-MeVal, Cha, Cit, Cpa, (D)Asn, Glu, hArg, or Lys;

X13 is Thr, Sarc, Glu, Phe, Arg, Leu, Lys, Val, βhAla, Aib, Lys(Ac), Cit, Asp, Dab, Dap, Glu, hArg, Lys, Asn, Orn, or Gln;

X14 is Phe, Tyr βhPhe, Asn, Arg, GQln, Lys(Ac), His; Dap(Ac), Dab(Ac), or Asp;

X15 is Gly, Ser, Thr, Gln, Ala, Sarc, β-Ala, Glu, Arg or Asn;

X16 is any amino acid or absent;

X17 is any amino acid or absent;

X18 is any amino acid or absent;

X19 is any amino acid or absent; and

X20 is any amino acid or absent.

In particular embodiments of Ia: X5 is Ala, Arg, Glu, Phe, Leu, Thr, Ser, Aib, Sarc, D-Ala, D-Arg, D-Glu, D-Phe, D-Leu, D-Thr, D-Ser, D-Aib or D-Sarc; X10 is Tyr or Phe; X11 is Trp, 1-Nal or 2-Nal; X12 is His, Phe, Arg, N-Me-His, or Val, Cav, Cpa, Leu, Cit, hLeu, 3-Pal, t-butyl-Ala or t-butyl-Gly; X13 is Thr, Sarc, Glu, Phe, Arg, Leu, Lys, Val, βhAla, or Aib; X14 is Phe,

X9 is Cys, Pen, hCys, D-Pen, D-Cys, D-hCys, Glu, Lys, Orn, Dap, Dab, D-Dap, D-Dab, D-Asp, D-Glu, D-Lys, Asp, Sec, Abu, β-azido-Ala-OH, propargylglycine, 2-allylglycine, 2-(3'-butenyl)glycine, 2-(4'-pentenyl)glycine, or 2-(5'-hexenyl)glycine;

X10 is Tyr, Phe, Phe(3,4-$F_2$), Phe(3,4-$Cl_2$), F(3-Me), Phe[4-(2-aminoethoxy)], Phe[4-(2-(acetyl-aminoethoxy)], Phe(4-Br), Phe(4-$CONH_2$), Phe(4-Cl), Phe(4-CN), Phe(4-guanidino), Phe(4-Me), Phe(4-$NH_2$), Phe(4-$N_3$), Phe(4-OMe), Phe(4-OBzl) or Tyr

X11 is Trp, 1-Nal, 2-Nal, Phe(3,4-$OMe_2$) 5-Hydroxy-Trp, Phe(3,4-$Cl_2$), Tyr(3-t-Bu)

X12 is His, Phe, Arg, N-Me-His, Val, Cav, Cpa, Leu, Cit, hLeu, 3-Pal, t-butyl-Ala, t-butyl-Gly4-amino-4-carboxy-tetrahydropyran, Achc Acpc, Acbc, Acvc, Agp, Aib, α-DiethylGly, α-MeLys, α-MeLys(Ac), α-Me-Leu, α-MeOrn, α-MeSer, α-MeVal, Cha, Cit, Cpa, (D)Asn, Glu, hArg, or Lys

X13 is Thr, Sarc, Glu, Phe, Arg, Leu, Lys, Val, βhAlaAib, Lys(Ac), Cit, Asp, Dab, Dap, Glu, hArg, Lys, Asn, Orn, or Gln

X14 is Phe, Tyr, or βhPhe, Asn, Arg, ~~Q~~Gln, Lys(Ac), His; Dap(Ac), Dab(Ac) or Asp;

X15 is Gly, Ser, Thr, Gln, Ala, or Sarc, β-Ala, Glu, Arg or Asn;

X16 is any amino acid or absent;

X17 is any amino acid, or absent;

X18 is any amino acid or absent;

X19 is any amino acid or absent; and

X20 is any amino acid or absent.

**[00133]** In particular embodiments of Ib: X5 is Ala, Arg, Glu, Phe, Leu, Thr, Ser, Aib, Sarc, D-Ala, D-Arg, D-Glu, D-Phe, D-Leu, D-Thr, D-Ser, D-Aib or D-Sarc; X10 is Tyr or Phe; X11 is Trp, 1-Nal or 2-Nal; X12 is His, Phe, Arg, N-Me-His, Val, Cav, Cpa, Leu, Cit, hLeu, 3-Pal, t-butyl-Ala or t-butyl-Gly; X13 is Thr, Sarc, Glu, Phe, Arg, Leu, Lys, Val, βhAla or Aib; X14 is

X8 is Val, Gln, Glu, or Lys;

X9 is Cys, Pen, hCys, D-Pen, D-Cys, D-hCys, Glu, Lys, Orn, Dap, Dab, D-Dap, D-Dab, D-Asp, D-Glu, D-Lys, Asp, Sec, Abu, β-azido-Ala-OH, propargylglycine, 2-allylglycine, 2-(3'-butenyl)glycine, 2-(4'-pentenyl)glycine, or 2-(5'-hexenyl)glycine;

X11 is Trp, 1-Nal, 2-Nal Phe(3,4-$OMe_2$) 5-Hydroxy-Trp, Phe(3,4-$Cl_2$) or Tyr(3-t-Bu)

X12 is His, Phe, Arg, N-Me-His, Val, Cav, Cpa, Leu, Cit, hLeu, 3-Pal, t-butyl-Ala t-butyl-Gly; 4-amino-4-carboxy-tetrahydropyran, Achc Acpc, Acbc, Acvc, Agp, Aib, α-DiethylGly, α-MeLys, α-MeLys(Ac), α-Me-Leu, α-MeOrn, α-MeSer, α-MeVal, Cha, Cit, Cpa, (D)Asn, Glu, hArg, or Lys

X13 is Thr, Sarc, Glu, Phe, Arg, Leu, Lys, Val, βhAla, or Aib, Lys(Ac), Cit, Asp, Dab, Dap, Glu, hArg, Lys, Asn, Orn, or Gln

X14 is Phe, Tyr, βhPhe, Asn, Arg, ~~Q~~Gln, Lys(Ac), His; Dap(Ac), Dab(Ac) or Asp;

X15 is Gly, Ser, Thr, Gln, Ala, Sarc, β-Ala, Glu, Arg or Asn;

X16 is any amino acid or absent;

X17 is any amino acid or absent;

X18 is any amino acid or absent;

X19 is any amino acid or absent; and

X20 is any amino acid or absent.

**[00140]** In particular embodiments of Ic, X5 is Ala, Arg, Glu, Phe, Leu, Thr, Ser, Aib, Sarc, D-Ala, D-Arg, D-Glu, D-Phe, D-Leu, D-Thr, D-Ser, D-Aib, or D-Sarc; X11 is Trp, 1-Nal, or 2-Nal; X12 is His, Phe, Arg, N-Me-His, Val, Cav, Cpa, Leu, Cit, hLeu, 3-Pal, t-butyl-Ala or t-butyl-Gly; X13 is Thr, Sarc, Glu, Phe, Arg, Leu, Lys, Val, βhAla, or Aib; X14 is Phe, Tyr, or βhPhe; X15 is Gly, Ser, Thr, Gln, Ala, or Sarc; X16 is Asp, Glu, Ala, AEA, AEP, βhAla, Gaba, or absent; and X17 is Leu, Lys, Arg, or absent.

X12 is His, Phe, Arg, N-Me-His, Val, Cav, Cpa, Leu, Cit, hLeu, 3-Pal, t-butyl-Ala, t-butyl-Gly, 4-amino-4-carboxy-tetrahydropyran, Achc Acpc, Acbc, Acvc, Agp, Aib, α-DiethylGly, α-MeLys, α-MeLys(Ac), α-Me-Leu, α-MeOrn, α-MeSer, α-MeVal, Cha, Cit, Cpa, (D)Asn, Glu, hArg, or Lys

X13 is Thr, Sarc, Glu, Phe, Arg, Leu, Lys, Val, βhAla, Aib, Lys(Ac), Cit, Asp, Dab, Dap, Glu, hArg, Lys, Asn, Orn, or Gln

X14 is Phe, Tyr, βhPhe, Asn, Arg, QGln, Lys(Ac), His, Dap(Ac), Dab(Ac) or Asp;

X15 is Gly, Ser, Thr, Gln, Ala, Sarc, β-Ala, Glu, Arg or Asn;

X16 is any amino acid or absent;

X17 is any amino acid or absent;

X18 is any amino acid or absent;

X19 is any amino acid or absent; and

X20 is any amino acid or absent,

**[00147]** wherein X4 and X9 are optionally linked by a intramolecular disulphide bridge.

**[00148]** In certain embodiments of Id: X5 is Ala, Arg, Glu, Phe, Leu, Thr, Ser, Aib, Sarc, D-Ala, D-Arg, D-Glu, D-Phe, D-Leu, D-Thr, D-Ser, D-Aib, or D-Sarc; X10 is Tyr or Phe; X11 is Trp, 1-Nal, or 2-Nal; X12 is His, Phe, Arg, N-Me-His, Val, Cav, Cpa, Leu, Cit, hLeu, 3-Pal, t-butyl-Ala, or t-butyl-Gly; X13 is Thr, Sarc, Glu, Phe, Arg, Leu, Lys, Val, βhAla, or Aib; X14 is Phe, Tyr, or βhPhe; X15 is Gly, Ser, Thr, Gln, Ala, or Sarc; X16 is Asp, Glu, Ala, AEA, AEP, βhAla, Gaba, or absent; and X17 is Leu, Lys, Arg, or absent.

**[00149]** In certain embodiments of Formula I, X comprises the sequence of Formula Ie:

X1-X2-X3-X4-X5-X6-W-X8-X9-X10-X11-X12-X13-X14-X15-X16-X17-X18-X19-X20

(Ie)

**[00150]** wherein

X1 is any amino acid or absent;

X2 is any amino acid or absent;

X3 is any amino acid or absent;

X4 is Pen, hCys, D-Pen, D-Cys, or D-hCys;

X5 is Ala, Arg, Glu, Phe, Leu, Thr, Ser, Aib, Sarc, D-Ala, D-Arg, D-Glu, D-Phe, D-Leu, D-Thr, D-Ser, α-MeOrn, α-MeSer, CitDap, Dab, Dap (Ac), Gly, Lys, Asn, N-Me-Gln, N-Me-Arg, Orn or Gln;

X6 is Asp, Thr, Asn, Phe, D-Asp, D-Thr, D-Asn, or D-Phe;

X8 is Val, Gln, Glu, or Lys;

X9 is Pen, hCys, D-Pen, D-Cys, D-hCys;

X10 is Tyr, Phe Phe(3,4-$F_2$), Phe(3,4-$Cl_2$), F(3-Me), Phe[4-(2-aminoethoxy)], Phe[4-(2-(acetyl-aminoethoxy)], Phe(4-Br), Phe(4-$CONH_2$), Phe(4-Cl), Phe(4-CN), Phe(4-guanidino), Phe(4-Me), Phe(4-$NH_2$), Phe(4-$N_3$), Phe(4-OMe), Phe(4-OBzl) or Tyr;

X11 is Trp, 1-Nal, 2-Nal, Phe(3,4-$OMe_2$) 5-Hydroxy-Trp, Phe(3,4-$Cl_2$) or Tyr(3-t-Bu);

X12 is His, Phe, Arg, N-Me-His, Val, Cav, Cpa, Leu, Cit, hLeu, 3-Pal, t-butyl-Ala, t-butyl-Gly, 4-amino-4-carboxy-tetrahydropyran, Achc Acpc, Acbc, Acvc, Agp, Aib, α-DiethylGly, α-MeLys, α-MeLys(Ac), α-Me-Leu, α-MeOrn, α-MeSer, α-MeVal, Cha, Cit, Cpa, (D)Asn, Glu, hArg, or Lys;

X13 is Thr, Sarc, Glu, Phe, Arg, Leu, Lys, Val, βhAla, Aib, Lys(Ac), Cit, Asp, Dab, Dap, Glu, hArg, Lys, Asn, Orn, or Gln;

X14 is Phe, Tyr, βhPhe, Asn, Arg, GQln, Lys(Ac), His; Dap(Ac), Dab(Ac) or Asp;

X15 is Gly, Ser, Thr, Gln, Ala, Sarc, β-Ala, Glu, Arg or Asn;

X1 is any amino acid or absent;

X2 is any amino acid or absent;

X3 is any amino acid or absent;

X4 is Glu, Lys, Orn, Dap, Dab, D-Dap, D-Dab, D-Asp, D-Glu, D-Lys, or Asp;

X5 is Ala, Arg, Glu, Phe, Leu, Thr, Ser, Aib, Sarc, D-Ala, D-Arg, D-Glu, D-Phe, D-Leu, D-Thr, D-Ser, α-MeOrn, α-MeSer, Cit, Dap, Dab, Dap (Ac), Gly, Lys, Asn, N-Me-Gln, N-Me-Arg, Orn or Gln;

X6 is Asp, Thr, Asn, Phe, D-Asp, D-Thr, D-Asn, or D-Phe;

X8 is Val, Gln, Glu, or Lys;

X9 is Glu, Lys, Orn, Dap, Dab, D-Dap, D-Dab, D-Asp, D-Glu, D-Lys, or Asp;

X10 is Tyr, Phe, Phe(3,4-F2), Phe(3,4-Cl2), F(3-Me), Phe[4-(2-aminoethoxy)], Phe[4-(2-(acetyl-aminoethoxy)], Phe(4-Br), Phe(4-CONH2), Phe(4-Cl), Phe(4-CN), Phe(4-guanidino), Phe(4-Me), Phe(4-NH2), Phe(4-$N_3$), Phe(4-OMe), Phe(4-OBzl) or Tyr;

X11 is Trp, 1-Nal, 2-Nal, Phe(3,4-$OMe_2$) 5-Hydroxy-Trp, Phe(3,4-$Cl_2$) or Tyr(3-t-Bu);

X12 is His, Phe, Arg, N-Me-His, Val, Cav, Cpa, Leu, Cit, hLeu, 3-Pal, t-butyl-Ala, or t-butyl-Gly, 4-amino-4-carboxy-tetrahydropyran, Achc Acpc, Acbc, Acvc, Agp, Aib, α-DiethylGly, α-MeLys, α-MeLys(Ac), α-Me-Leu, α-MeOrn, α-MeSer, α-MeVal, Cha, Cit, Cpa, (D)Asn, Glu, hArg, or Lys;

X13 is Thr, Sarc, Glu, Phe, Arg, Leu, Lys, Val, βhAla, Aib, Lys(Ac), Cit, Asp, Dab, Dap, Glu, hArg, Lys, Asn, Orn, or Gln;

X14 is Phe, Tyr, βhPhe, Asn, Arg, QGln, Lys(Ac), His; Dap(Ac), Dab(Ac) or Asp;

X15 is Gly, Ser, Thr, Gln, Ala, Sarc, β-Ala, Glu, Arg or Asn;

X16 is any amino acid or absent;

X5 is Ala, Arg, Glu, Phe, Leu, Thr, Ser, Aib, Sarc, D-Ala, D-Arg, D-Glu, D-Phe, D-Leu, D-Thr, D-Ser, α-MeOrn, α-MeSer, Cit, Dap, Dab, Dap(Ac), Gly, Lys, Asn, N-MeGln, N-MeArg, Orn or Gln;

X6 is Asp, Thr, Asn, Phe, D-Asp, D-Thr, D-Asn, or D-Phe;

X8 is Val, Gln, Glu, or Lys;

X9 is β-azido-Ala-OH or propargylglycine, ;

X10 is Tyr, Phe, Phe(3,4-$F_2$), Phe(3,4-$Cl_2$), F(3-Me), Phe[4-(2-aminoethoxy)], Phe[4-(2-(acetyl-aminoethoxy)], Phe(4-Br), Phe(4-$CONH_2$), Phe(4-Cl), Phe(4-CN), Phe(4-guanidino), Phe(4-Me), Phe(4-$NH_2$), Phe(4-$N_3$), Phe(4-OMe), Phe(4-OBzl) or Tyr;

X11 is Trp, 1-Nal, 2-Nal, Phe(3,4-$OMe_2$) 5-Hydroxy-Trp, Phe(3,4-$Cl_2$) or Tyr(3-t-Bu)

X12 is His, Phe, Arg, N-Me-His, Val, Cav, Cpa, Leu, Cit, hLeu, 3-Pal, t-butyl-Ala, or t-butyl-Gly, 4-amino-4-carboxy-tetrahydropyran, Achc Acpc, Acbc, Acvc, Agp, Aib, α-DiethylGly, α-MeLys, α-MeLys(Ac), α-Me-Leu, α-MeOrn, α-MeSer, α-MeVal, Cha, Cit, Cpa, (D)Asn, Glu, hArg, or Lys;

X13 is Thr, Sarc, Glu, Phe, Arg, Leu, Lys, Val, βhAla, Aib, Lys(Ac), Cit, Asp, Dab, Dap, Glu, hArg, Lys, Asn, Orn, or Gln;

X14 is Phe, Tyr, βhPhe, Asn, Arg, ⊖Gln, Lys(Ac), His; Dap(Ac), Dab(Ac) or Asp;

X15 is Gly, Ser, Thr, Gln, Ala, or Sarc, β-Ala, Glu, Arg or Asn;

X16 is any amino acid or absent;

X17 is any amino acid or absent;

X18 is any amino acid or absent;

X19 is any amino acid or absent; and

X20 is any amino acid or absent,

**[00165]** wherein X4 and X9 are optionally cyclized through an intramolecular triazole ring.

**[00166]** In particular embodiments of Ig: X5 is Ala, Arg, Glu, Phe, Leu, Thr, Ser, Aib, Sarc, D-Ala, D-Arg, D-Glu, D-Phe, D-Leu, D-Thr, D-Ser, D-Aib, or D-Sarc; X6 is Asp, Thr, Asn, Phe, D-Asp, D-Thr, D-Asn, or D-Phe; X8 is Val, Gln, Glu, or Lys; X9 is β-azido-Ala-OH or propargylglycine; X10 is Tyr or Phe; X11 is Trp, 1-Nal, or 2-Nal; X12 is His, Phe, Arg, N-Me-His, Val, Cav, Cpa, Leu, Cit, hLeu, 3-Pal, t-butyl-Ala, or t-butyl-Gly; X13 is Thr, Sarc, Glu, Phe, Arg, Leu, Lys, Val, βhAla, or Aib; X14 is Phe, Tyr, or βhPhe; X15 is Gly, Ser, Thr, Gln, Ala, or Sarc; X16 is Asp, Glu, Ala, AEA, AEP, βhAla, Gaba, or absent; and X17 is Leu, Lys, Arg, or absent.

**[00167]** In certain embodiments of Formula I, X comprises the sequence of Formula Ih:

X1-X2-X3-~~C~~X4-X5-X6-W-X8-~~C~~X9-Y-X11-H-X13-F-X15-X16-X17-X18-X19-X20 (SEQ ID NO: 1111)

(Ih)

**[00168]** wherein

X1 is any amino acid or absent;

X2 is any amino acid or absent;

X3 is any amino acid or absent;

X4 is 2-allylglycine, 2-(3'-butenyl)glycine, 2-(4'-pentenyl)glycine, or 2-(5'-hexenyl)glycine;

X5 is Ala, Arg, Sarc, α-MeOrn, α-MeSer, Cit, Dap, Dab, Dap(Ac), Gly, Lys, Asn, N-MeGln, N-MeArg, Orn or Gln;

X6 is Asp, Thr, or Asn;

X8 is Val, Gln, or Glu;

X9 is 2-allylglycine, 2-(3'-butenyl)glycine, 2-(4'-pentenyl)glycine, or 2-(5'-hexenyl)glycine;

X11 is Trp, 1-Nal, 2-Nal, Phe(3,4-$OMe_2$) 5-Hydroxy-Trp, Phe(3,4-$Cl_2$) or Tyr(3-t-Bu)

X4 is Cys, Pen, hCys, D-Pen, D-Cys, D-hCys, 2-chloromethylbenzoic acid, mercapto-propanoic acid, mercapto-butyric acid, 2-chloro-acetic acid, 3-choro-propanoic acid, 4-chloro-butyric acid, or 3-chloro-isobutyric acid;

X5 is Ala, Arg, Glu, Phe, Leu, Thr, Ser, Aib, Sarc, D-Ala, D-Arg, D-Glu, D-Phe, D-Leu, D-Thr, D-Ser, D-Aib, or D-Sarc, α-MeOrn, α-MeSer, Cit, Dap, Dab, Dap(Ac), Gly, Lys, Asn, N-MeGln, N-MeArg, Orn or Gln;

X6 is Asp, Thr, Asn, Phe, D-Asp, D-Thr, D-Asn, or D-Phe;

X8 is Val, Gln, Glu, or Lys;

X9 is Cys, Pen, hCys, D-Pen, D-Cys, D-hCys, or Abu;

X10 is Tyr, Phe, Phe(3,4-$F_2$), Phe(3,4-$Cl_2$), F(3-Me), Phe[4-(2-aminoethoxy)], Phe[4-(2-(acetyl-aminoethoxy)], Phe(4-Br), Phe(4-$CONH_2$), Phe(4-Cl), Phe(4-CN), Phe(4-guanidino), Phe(4-Me), Phe(4-$NH_2$), Phe(4-$N_3$), Phe(4-OMe), Phe(4-OBzl) or Tyr;

X11 is Trp, 1-Nal, 2-Nal, Phe(3,4-$OMe_2$) 5-Hydroxy-Trp, Phe(3,4-$Cl_2$) or Tyr(3-t-Bu)

X12 is His, Phe, Arg, N-Me-His, Val, Cav, Cpa, Leu, Cit, hLeu, 3-Pal, t-butyl-Ala, t-butyl-Gly, 4-amino-4-carboxy-tetrahydropyran, Achc Acpc, Acbc, Acvc, Agp, Aib, α-DiethylGly, α-MeLys, α-MeLys(Ac), α-Me-Leu, α-MeOrn, α-MeSer, α-MeVal, Cha, Cit, Cpa, (D)Asn, Glu, hArg, or Lys;

X13 is Thr, Sarc, Glu, Phe, Arg, Leu, Lys, Val, βhAla, Aib, Lys(Ac), Cit, Asp, Dab, Dap, Glu, hArg, Lys, Asn, Orn, or Gln;

X14 is Phe, Tyr, βhPhe, Asn, Arg, ~~Q~~Gln, Lys(Ac), His; Dap(Ac), Dab(Ac) or Asp;

X15 is Gly, Ser, Thr, Gln, Ala, Sarc, β-Ala, Glu, Arg or Asn;

X16 is any amino acid or absent;

X17 is any amino acid or absent;

X8 is Val, Gln, Glu, or Lys;

X9 is Sec or Abu;

X10 is Tyr, Phe, Phe(3,4-$F_2$), Phe(3,4-$Cl_2$), F(3-Me), Phe[4-(2-aminoethoxy)], Phe[4-(2-aminoethoxy), Phe[4-(2-(acetyl-aminoethoxy)], Phe(4-Br), Phe(4-$CONH_2$), Phe(4-Cl), Phe(4-CN), Phe(4-guanidino), Phe(4-Me), Phe(4-$NH_2$), Phe(4-$N_3$), Phe(4-OMe), Phe(4-OBzl) or Tyr;

X11 is Trp, 1-Nal, 2-Nal, Phe(3,4-$OMe_2$) 5-Hydroxy-Trp, Phe(3,4-$Cl_2$) or Tyr(3-t-Bu);

X12 is His, Phe, Arg, N-Me-His, Val, Cav, Cpa, Leu, Cit, hLeu, 3-Pal, t-butyl-Ala, t-butyl-Gly, 4-amino-4-carboxy-tetrahydropyran, Achc, Acpc, Acbc, Agp, Aib, α-DiethylGly, α-MeLys, α-MeLys(Ac), α-Me-Leu, α-MeOrn, α-MeSer, α-MeVal, Cha, Cit, Cpa, (D)Asn, Glu, hArg, or Lys;

X13 is Thr, Sarc, Glu, Phe, Arg, Leu, Lys, Val, βhAla, Aib, Lys(Ac), Cit, Asp, Dab, Dap, Glu, hArg, Lys, Asn, Orn, or Gln;

X14 is Phe, Tyr, βhPhe, Asn, Arg, QGln, Lys(Ac), His; Dap(Ac), Dab(Ac) or Asp;

X15 is Gly, Ser, Thr, Gln, Ala, Sarc, β-Ala, Glu, Arg or Asn;

X16 is any amino acid or absent;

X17 is any amino acid or absent;

X18 is any amino acid or absent;

X19 is any amino acid or absent; and

X20 is any amino acid or absent,

**[00177]** wherein X4 and X9 are optionally cyclized via an intramolecular thioseleno or diselenide bond.

**[00178]** In particular embodiments of Ij: X5 is Ala, Arg, Glu, Phe, Leu, Thr, Ser, Aib, Sarc, D-Ala, D-Arg, D-Glu, D-Phe, D-Leu, D-Thr, D-Ser, D-Aib, or D-Sarc; X10 is Tyr or Phe; X11 is

X12 is His, Phe, Arg, N-Me-His, Val, D-His, Cav, Cpa, Leu, Cit, hLeu, 3-Pal, t-butyl-Ala, t-butyl-Gly,4-amino-4-carboxy-tetrahydropyran, Achc Acpc, Acbc, Acvc, Agp, Aib, α-DiethylGly, α-MeLys, α-MeLys(Ac), α-Me-Leu, α-MeOrn, α-MeSer, α-MeVal, Cha, Cit, Cpa, (D)Asn, Glu, hArg, or Lys;

X13 is Thr, Sarc, Glu, Phe, Arg, Leu, Lys, Val, βhAla, Aib, Lys(Ac), Cit, Asp, Dab, Dap, Glu, hArg, Lys, Asn, Orn, or Gln;

X14 is Phe, Tyr, βhPhe, Asn, Arg, QGln, Lys(Ac), His; Dap(Ac), Dab(Ac) or Asp or absent;

X15 is Gly, Ser, Thr, Gln, Ala, Sarc, β-Ala, Glu, Arg or Asn or absent;

X16 is any amino acid or absent;

X17 is any amino acid or absent;

X18 is any amino acid or absent;

X19 is any amino acid or absent; and

X20 is any amino acid or absent.

**[00181]** In particular embodiments of Ik: X5 is Ala, Arg, Glu, Phe, Leu, Thr, Ser, Aib, Sarc, D-Ala, D-Arg, D-Glu, D-Phe, D-Leu, D-Thr, D-Ser, D-Aib, or D-Sarc; X10 is Tyr or Phe; X11 is Trp, 1-Nal, or 2-Nal; X12 is His, Phe, Arg, N-Me-His, Val, D-His, Cav, Cpa, Leu, Cit, hLeu, 3-Pal, t-butyl-Ala, or t-butyl-Gly; X13 is Thr, Sarc, Glu, Phe, Arg, Leu, Lys, Val, βhAla, Aib or absent; X14 is Phe, Tyr, βhPhe or absent; X15 is Gly, Ser, Thr, Gln, Ala, Sarc or absent; X16 is Asp, Glu, Ala, AEA, AEP, βhAla, Gaba, Leu, or absent; and X17 is Leu, Lys, Arg, or absent.

In certain embodiments of Formula I, X comprises or consists of the sequence of Formula II:

X1-X2-X3-X4-X5-X6-W-X8-X9-X10-X11-X12-X13-X14-X15-X16-X17-X18-X19-X20 (II),

**[00182]** wherein

X1 is any amino acid or absent;

X2 is any amino acid or absent;

X3 is any amino acid or absent;

X4 is Cys, Pen, hCys, D-Pen, D-Cys, D-hCys, Met, Glu, Asp, Lys, Orn, Dap, Dab, D-Dap, D-Dab, D-Asp, D-Glu, D-Lys or absent;

X5 is Ala, Arg, Glu, Phe, Leu, Thr, Ser, Aib, Sarc, α-MeOrn, α-MeSer, Cit, Dap, Dab, Dap(Ac), Gly, Lys, Asn, N-MeGln, N-MeArg, Orn or Gln;

X6 is Asp, Thr, Asn, or Phe;

X8 is Val, Gln, Glu, or Lys;

X9 is Cys, Pen, hCys, D-Pen, D-Cys, D-hCys, Glu, Lys, Orn, Dap, Dab, D-Dap, D-Dab, D-Asp, D-Glu, D-Lys, Asp, Leu, Val, Phe, or Ser;

X10 is Tyr, Phe, Phe(3,4-$F_2$), Phe(3,4-$Cl_2$), F(3-Me), Phe[4-(2-aminoethoxy)], Phe[4-(2-(acetyl-aminoethoxy)], Phe(4-Br), Phe(4-$CONH_2$), Phe(4-Cl), Phe(4-CN), Phe(4-guanidino), Phe(4-Me), Phe(4-$NH_2$), Phe(4-$N_3$), Phe(4-OMe), Phe(4-OBzl) or Tyr;

X11 is Trp, 1-Nal, 2-Nal, , Phe(3,4-$OMe_2$) 5-Hydroxy-Trp, Phe(3,4-$Cl_2$) or Tyr(3-t-Bu);

X12 is His, Phe, Arg, N-Me-His, Val, D-His, Cav, Cpa, Leu, Cit, hLeu, 3-Pal, t-butyl-Ala, t-butyl-Gly, 4-amino-4-carboxy-tetrahydropyran, Achc Acpc, Acbc, Acvc, Agp, Aib, α-DiethylGly, α-MeLys, α-MeLys(Ac), α-Me-Leu, α-MeOrn, α-MeSer, α-MeVal, Cha, Cit, Cpa, (D)Asn, Glu, hArg, or Lys;

X13 is Thr, Sarc, Glu, Phe, Arg, Leu, Lys, Val, βhAla, Aib, Lys(Ac), Cit, Asp, Dab, Dap, Glu, hArg, Lys, Asn, Orn, or Gln or absent;

X14 is Phe, Tyr, βhPhe, Asn, Arg, ~~Q~~Gln, Lys(Ac), His; Dap(Ac), Dab(Ac) or Asp or absent;

X15 is Gly, Ser, Thr, Gln, Ala, Sarc, β-Ala, Glu, Arg or Asn or absent;

X16 is any amino acid or absent;

X17 is any amino acid or absent;

X18 is any amino acid or absent;

X19 is any amino acid or absent; and

X20 is any amino acid or absent.

**[00183]** In particular embodiments of II: X5 is Ala, Arg, Glu, Phe, Leu, Thr, Ser, Aib, or Sarc; X10 is Tyr or Phe; X11 is Trp, 1-Nal, or 2-Nal; X12 is His, Phe, Arg, N-Me-His, Val, D-His, Cav, Cpa, Leu, Cit, hLeu, 3-Pal, t-butyl-Ala, or t-butyl-Gly; X13 is Thr, Sarc, Glu, Phe, Arg, Leu, Lys, Val, βhAla, Aib or absent; X14 is Phe, Tyr, βhPhe or absent; X15 is Gly, Ser, Thr, Gln, Ala, Sarc or absent; X16 is Asp, Glu, Ala, AEA, AEP, βhAla, Gaba, Leu, or absent; and X17 is Leu, Lys, Arg, or absent.

**[00184]** In certain embodiments, X13 is Thr, Sarc, Glu, Phe, Arg, Leu, Lys, βhAla, Aib, Lys(Ac), Cit, Asp, Dab, Dap, Glu, hArg, Lys, Asn, Orn, or Gln. In certain embodiments, X13 is Thr, Sarc, Glu, Phe, Arg, Leu, Lys, βhAla, or Aib.

**[00185]** In certain embodiments, X14 is Phe, Tyr, βhPhe, Asn, Arg, QGln, Lys(Ac), His; Dap(Ac), Dab(Ac) or Asp. In certain embodiments, X14 is Phe, Tyr, or βhPhe.

**[00186]** In certain embodiments, X15 is Gly, Ser, Thr, Gln, Ala, Sarc, β-Ala, Glu, Arg or Asn. In certain embodiments, X15 is Gly, Ser, Thr, Gln, Ala, or Sarc.

**[00187]** In certain embodiments, X12 is alpha amino acid, e.g., 4-amino-4-carboxy-tetrahydropyran, Achc Acpc, Acbc, Aib, α-MeGly(diethyl), α-MeLys, α-MeLys(Ac), α-Me-Leu, α-MeOrn, α-MeSer, α-MeVal.

**[00188]** In certain embodiments, X13 is present.

**[00189]** In certain embodiments, X13 and X14 are present.

**[00190]** In certain embodiments, X13, X14 and X15 are present.

**[00191]** In particular embodiments, X4 is present.

MeLys, α-MeLys(Ac), α-Me-Leu, α-MeOrn, α-MeSer, α-MeVal, Cha, Cit, Cpa, (D)Asn, Glu, hArg, or Lys;

X13 is Thr, Sarc, Glu, Phe, Arg, Leu, Lys, βhAla, Val, Aib, Lys(Ac), Cit, Asp, Dab, Dap, Glu, hArg, Lys, Asn, Orn, or Gln or absent;

X14 is Phe, Tyr, βhPhe, Asn, Arg, QGln, Lys(Ac), His; Dap(Ac), Dab(Ac), or Asp or absent;

X15 is Gly, Ser, Thr, Gln, Ala, Sarc, β-Ala, Glu, Arg or Asn or absent;

X16 is any amino acid or absent;

X17 is any amino acid or absent;

X18 is any amino acid or absent;

X19 is any amino acid or absent; and

X20 is any amino acid or absent.

**[00197]** In certain embodiments of Im: X5 is Ala, Arg, Glu, Phe, Leu, Thr, Ser, Aib, or Sarc; X11 is Trp, 1-Nal, or 2-Nal; X12 is His, Phe, Arg, N-Me-His, Val, Cav, Cpa, Leu, Cit, hLeu, 3-Pal, t-butyl-Ala, or t-butyl-Gly; X13 is Thr, Sarc, Glu, Phe, Arg, Leu, Lys, βhAla, Val, Aib or absent; X14 is Phe, Tyr, βhPhe or absent; X15 is Gly, Ser, Thr, Gln, Ala, Sarc or absent; X16 is Asp, Glu, Ala, AEA, AEP, βhAla, Gaba, or absent; and X17 is Leu, Lys, Arg, or absent.

**[00198]** In certain embodiments, X13 is Thr, Sarc, Glu, Phe, Arg, Leu, Lys, βhAla, or Aib. In certain embodiments, X13 is Thr, Sarc, Glu, Phe, Arg, Leu, Lys, βhAla, Aib, Lys(Ac), Cit, Asp, Dab, Dap, Glu, hArg, Lys, Asn, Orn, or Gln.

**[00199]** In certain embodiments, X14 is Phe, Tyr, βhPhe, Asn, Arg, QGln, Lys(Ac), His; Dap(Ac), Dab(Ac) or Asp. In certain embodiments, X14 is Phe, Tyr, or βhPhe.

**[00200]** In certain embodiments, X15 is Gly, Ser, Thr, Gln, Ala, or Sarc, β-Ala, Glu, Arg or Asn. In certain embodiments, X15 is Gly, Ser, Thr, Gln, Ala, or Sarc.

X10 is Tyr Phe, Phe(3,4-$F_2$), Phe(3,4-$Cl_2$), F(3-Me), Phe[4-(2-aminoethoxy)], Phe[4-(2-(acetyl-aminoethoxy)], Phe(4-Br), Phe(4-$CONH_2$), Phe(4-Cl), Phe(4-CN), Phe(4-guanidino), Phe(4-Me), Phe(4-$NH_2$), Phe(4-$N_3$), Phe(4-OMe), Phe(4-OBzl) or Tyr;

X11 is Trp, 1-Nal, 2-Nal, Phe(3,4-$OMe_2$) 5-Hydroxy-Trp, Phe(3,4-$Cl_2$) or Tyr(3-t-Bu);

X12 is His, Phe, Arg, N-Me-His, Val, Cav, Cpa, Leu, Cit, hLeu, 3-Pal, t-butyl-Ala, or t-butyl-Gly, 4-amino-4-carboxy-tetrahydropyran, Achc Acpc, Acbc, Acvc, Agp, Aib, α-DiethylGly, α-MeLys, α-MeLys(Ac), α-Me-Leu, α-MeOrn, α-MeSer, α-MeVal, Cha, Cit, Cpa, (D)Asn, Glu, hArg, or Lys;

X13 is Thr, Sarc, Glu, Phe, Arg, Leu, Lys, βhAla, Val, Aib, Lys(Ac), Cit, Asp, Dab, Dap, Glu, hArg, Lys, Asn, Orn, or Gln or absent;

X14 is Phe, Tyr, βhPhe, Asn, Arg, QGln, Lys(Ac), His; Dap(Ac), Dab(Ac) or Asp or absent;

X15 is Gly, Ser, Thr, Gln, Ala, Sarc, β-Ala, Glu, Arg or Asn or absent;

X16 is any amino acid or absent;

X17 is any amino acid or absent;

X18 is any amino acid or absent;

X19 is any amino acid or absent; and

X20 is any amino acid or absent,

**[00211]** wherein the Cys at position X4 and and the Cys at position X9 are optionally linked by a disulphide bridge.

**[00212]** In certain embodiments of In: X5 is Ala, Arg, Glu, Phe, Leu, Thr, Ser, Aib, Sarc, α-MeOrn, α-MeSer, Cit, Dap, Dab, Dap(Ac), Gly, Lys, Asn, N-MeGln, N-MeArg, Orn or Gln; X10 is Tyr, Phe, Phe(3,4-$F_2$), Phe(3,4-$Cl_2$), F(3-Me), Phe[4-(2-aminoethoxy)], Phe[4-(2-(acetyl-aminoethoxy)], Phe(4-Br), Phe(4-$CONH_2$), Phe(4-Cl), Phe(4-CN), Phe(4-guanidino), Phe(4-Me), Phe(4-$NH_2$), Phe(4-$N_3$), Phe(4-OMe), Phe(4-OBzl) or Tyr; X11 is Trp, 1-Nal, 2-Nal, Phe(3,4-

$OMe_2$) 5-Hydroxy-Trp, Phe(3,4-$Cl_2$) or Tyr(3-t-Bu); X12 is His, Phe, Arg, N-Me-His, Val, Cav, Cpa, Leu, Cit, hLeu, 3-Pal, t-butyl-Ala, or t-butyl-Gly, 4-amino-4-carboxy-tetrahydropyran, Achc Acpc, Acbc, Acvc, Agp, Aib, α-DiethylGly, α-MeLys, α-MeLys(Ac), α-Me-Leu, α-MeOrn, α-MeSer, α-MeVal, Cha, Cit, Cpa, (D)Asn, Glu, hArg, or Lys; X13 is Thr, Sarc, Glu, Phe, Arg, Leu, Lys, βhAla, Val, Aib, Lys(Ac), Cit, Asp, Dab, Dap, Glu, hArg, Lys, Asn, Orn, or Gln or absent; X14 is Phe, Tyr, βhPhe, Asn, Arg, QGln, Lys(Ac), His; Dap(Ac), Dab(Ac) or Asp or absent; X15 is Gly, Ser, Thr, Gln, Ala, Sarc, β-Ala, Glu, Arg or Asn or absent; X16 is Asp, Glu, Ala, AEA, AEP, βhAla, Gaba, or absent; and X17 is Leu, Lys, Arg, or absent.

**[00213]** In certain embodiments, X13 is Thr, Sarc, Glu, Phe, Arg, Leu, Lys, βhAla, Aib, Lys(Ac), Cit, Asp, Dab, Dap, Glu, hArg, Lys, Asn, Orn, or Gln. In certain embodiments, X13 is Thr, Sarc, Glu, Phe, Arg, Leu, Lys, βhAla, or Aib.

**[00214]** In certain embodiments, X14 is Phe, Tyr, βhPhe, Asn, Arg, QGln, Lys(Ac), His; Dap(Ac), Dab(Ac) or Asp. In certain embodiments, X14 is Phe, Tyr, or βhPhe.

**[00215]** In certain embodiments, X15 is Gly, Ser, Thr, Gln, Ala, Sarc, β-Ala, Glu, Arg or Asn. In certain embodiments, X15 is Gly, Ser, Thr, Gln, Ala, or Sarc.

**[00216]** In certain embodiments, X12 is an alpha amino acid, e.g., 4-amino-4-carboxy-tetrahydropyran, Achc Acpc, Acbc, Acvc, Aib, α-DiethylGly, α-MeLys, α-MeLys(Ac), α-Me-Leu, α-MeOrn, α-MeSer, α-MeVal.

**[00217]** In certain embodiments, X13 is present.

**[00218]** In certain embodiments, X13 and X14 are present.

**[00219]** In certain embodiments, X13, X14 and X15 are present.

**[00220]** In certain embodiments of the peptide inhibitor of Formula I, X comprises or consists of the sequence of Formula Io:

X1-X2-X3-C-X5-X6-W-X8-C-Y-X11-H-X13-X14-X15-X16-X17-X18-X19-X20 (Io) (SEQ ID NO: 1112)

**[00221]** wherein

X1 is any amino acid or absent;

X2 is any amino acid or absent;

X3 is any amino acid or absent;

X5 is Ala, Arg, Glu, Phe, Leu, Thr, Ser, Aib, Sarc, α-MeOrn, α-MeSer, Cit, Dap, Dab, Dap(Ac), Gly, Lys, Asn, N-MeGln, N-MeArg, Orn or Gln;

X6 is Asp, Thr, Asn, or Phe;

X8 is Val, Gln, Glu, or Lys;

X11 is Trp, 1-Nal, 2-Nal, Phe(3,4-$OMe_2$) 5-Hydroxy-Trp, Phe(3,4-$Cl_2$) or Tyr(3-t-Bu);

X13 is Thr, Sarc, Glu, Phe, Arg, Leu, Lys, βhAla, Val, Aib, Lys(Ac), Cit, Asp, Dab, Dap, Glu, hArg, Lys, Asn, Orn, or Gln or absent;

X14 is Phe, Tyr, Asn, Arg, QGln, Lys(Ac), His; Dap(Ac), Dab(Ac) or Asp or absent;

X15 is Gly, Ser, Thr, Gln, Ala, Sarc, β-Ala, Glu, Arg or Asn or absent;

X16 is any amino acid or absent;

X17 is any amino acid or absent;

X18 is any amino acid or absent;

X19 is any amino acid or absent; and

X20 is any amino acid or absent,

**[00222]** wherein the Cys at position X4 and and the Cys at position X9 are optionally linked by a disulphide bridge.

**[00223]** In certain embodiments of Io: X5 is Ala, Arg, Glu, Phe, Leu, Thr, Ser, Aib, Sarc, α-MeOrn, α-MeSer, Cit, Dap, Dab, Dap(Ac), Gly, Lys, Asn, N-MeGln, N-MeArg, Orn or Gln; X11 is Trp, 1-Nal, 2-Nal, Phe(3,4-$OMe_2$), 5-Hydroxy-Trp, Phe(3,4-$Cl_2$) or Tyr(3-t-Bu); X13 is

Thr, Sarc, Glu, Phe, Arg, Leu, Lys, βhAla, Val, Aib, Lys(Ac), Cit, Asp, Dab, Dap, Glu, hArg, Lys, Asn, Orn, Gln or absent; X14 is Phe, Tyr, Asn, Arg, QGln, Lys(Ac), His; Dap(Ac), Dab(Ac) Asp or absent; X15 is Gly, Ser, Thr, Gln, Ala, Sarc, β-Ala, Glu, Arg or Asn or absent; X16 is Asp, Glu, Glu, Ala, AEA, AEP, βhAla, Gaba, or absent; and X17 is Leu, Lys, Arg, or absent.

**[00224]** In certain embodiments, X12 is an alpha amino acid, e.g., 4-amino-4-carboxy-tetrahydropyran, Achc Acpc, Acbc, Acvc, Aib, α-DiethylGly, α-MeLys, α-MeLys(Ac), α-Me-Leu, α-MeOrn, α-MeSer, α-MeVal.

**[00225]** In certain embodiments, X13 is Thr, Sarc, Glu, Phe, Arg, Leu, Lys, βhAla, Aib, Lys(Ac), Cit, Asp, Dab, Dap, Glu, hArg, Lys, Asn, Orn, or Gln. In certain embodiments, X13 is Thr, Sarc, Glu, Phe, Arg, Leu, Lys, βhAla or Aib.

**[00226]** In certain embodiments, X14 is Phe, Tyr, Asn, Arg, QGln, Lys(Ac), His; Dap(Ac), Dab(Ac) or Asp. In certain embodiments, X14 is Phe or Tyr.

**[00227]** In certain embodiments, X15 is Gly, Ser, Thr, Gln, Ala, Sarc, β-Ala, Glu, Arg or Asn. In certain embodiments, X15 is Gly, Ser, Thr, Gln, Ala or Sarc.

**[00228]** In certain embodiments, X13 is present.

**[00229]** In certain embodiments, X13 and X14 are present.

**[00230]** In certain embodiments, X13, X14 and X15 are present.

**[00231]** In certain embodiments of the peptide inhibitor of Formula I, X comprises or consists of the sequence of Formula Ip:

X1-X2-X3-C-X5-X6-W-X8-C-Y-X11-H-X13-F-X15-X16-X17-X18-X19-X20 (Ip) (SEQ ID NO: 1113)

**[00232]** wherein

X1 is any amino acid or absent;

X2 is any amino acid or absent;

X12 is His, Phe, Arg, N-Me-His, Val, or D-His, Cav, Cpa, Leu, Cit, hLeu, 3-Pal, t-butyl-Ala, t-butyl-Gly, 4-amino-4-carboxy-tetrahydropyran, Achc Acpc, Acbc, Acvc, Agp, Aib, α-DiethylGly, α-MeLys, α-MeLys(Ac), α-Me-Leu, α-MeOrn, α-MeSer, α-MeVal, Cha, Cit, Cpa, (D)Asn, Glu, hArg, or Lys;

X13 is Thr, Sarc, Glu, Phe, Arg, Leu, Lys, βhAla, Val, Aib, Lys(Ac), Cit, Asp, Dab, Dap, Glu, hArg, Lys, Asn, Orn, Gln or absent;

X14 is Phe, Tyr, βhPhe, , Asn, Arg, QGln, Lys(Ac), His; Dap(Ac), Dab(Ac), Asp or absent;

X15 is Gly, Ser, Thr, Gln, Ala, Sarc, β-Ala, Glu, Arg, Asn or absent;

X16 is any amino acid or absent;

X17 is any amino acid or absent;

X18 is any amino acid or absent;

X19 is any amino acid or absent; and

X20 is any amino acid or absent,

**[00241]** wherein the Cys at position X4 and and the Cys at position X9 are optionally linked.

**[00242]** In certain embodiments of Iq: X5 is Ala, Arg, Glu, Phe, Leu, Thr, Ser, Aib, Sarc, D-Ala, D-Arg, D-Glu, D-Phe, D-Leu, D-Thr, D-Ser, D-Aib, or D-Sarc; X10 is Tyr or Phe; X11 is Trp, 1-Nal, or 2-Nal; X12 is His, Phe, Arg, N-Me-His, Val, or D-His, Cav, Cpa, Leu, Cit, hLeu, 3-Pal, t-butyl-Ala, or t-butyl-Gly; X13 is Thr, Sarc, Glu, Phe, Arg, Leu, Lys, βhAla, Val, Aib or absent; X14 is Phe, Tyr, βhPhe or absent; X15 is Gly, Ser, Thr, Gln, Ala, Sarc or absent; X16 is Asp, Glu, Ala, AEA, AEP, βhAla, Gaba, Leu, or absent; and X17 is Leu, Lys, Arg, or absent.

**[00243]** In certain embodiments, X12 is alpha amino acid, e.g., 4-amino-4-carboxy-tetrahydropyran, Achc Acpc, Acbc, Acvc, Aib, α-DiethylGly, α-MeLys, α-MeLys(Ac), α-Me-Leu, α-MeOrn, α-MeSer, α-MeVal.

**[00244]** In certain embodiments, X13 is Thr, Sarc, Glu, Phe, Arg, Leu, Lys, βhAla, Aib, Lys(Ac), Cit, Asp, Dab, Dap, Glu, hArg, Lys, Asn, Orn, or Gln. In certain embodiments, X13 is Thr, Sarc, Glu, Phe, Arg, Leu, Lys, βhAla or Aib.

**[00245]** In certain embodiments, X14 is Phe, Tyr, βhPhe, Asn, Arg, QGln, Lys(Ac), His; Dap(Ac), Dab(Ac), or Asp. In certain embodiments, X14 is Phe, Tyr or βhPhe.

**[00246]** In certain embodiments, X15 is Gly, Ser, Thr, Gln, Ala, Sarc, β-Ala, Glu, Arg or Asn. In certain embodiments, X15 is Gly, Ser, Thr, Gln, Ala or Sarc.

**[00247]** In certain embodiments, X13 is present.

**[00248]** In certain embodiments, X13 and X14 are present.

**[00249]** In certain embodiments, X13, X14 and X15 are present.

**[00250]** In certain embodiments, Iq comprises or consists of the sequence of Formula Iq':

X1-X2-X3-C-X5-X6-W-X8-C-X10-X11-X12-X13-X14-X15 (Iq'),

wherein X1-X14 have the definition provided for Iq, and

wherein the Cys at position X4 and and the Cys at position X9 are optionally linked.

**[00251]** In certain embodiments of Iq': X5 is Ala, Arg, Glu, Phe, Leu, Thr, Ser, Aib, Sarc, D-Ala, D-Arg, D-Glu, D-Phe, D-Leu, D-Thr, D-Ser, D-Aib, or D-Sarc; X10 is Tyr or Phe; X11 is Trp, 1-Nal, or 2-Nal; X12 is His, Phe, Arg, N-Me-His, Val, or D-His, Cav, Cpa, Leu, Cit, hLeu, 3-Pal, t-butyl-Ala, or t-butyl-Gly; X13 is Thr, Sarc, Glu, Phe, Arg, Leu, Lys, βhAla, Val, Aib or absent; X14 is Phe, Tyr, βhPhe or absent; X15 is Gly, Ser, Thr, Gln, Ala, Sarc or absent; X16 is Asp, Glu, Ala, AEA, AEP, βhAla, Gaba, Leu, or absent; and X17 is Leu, Lys, Arg, or absent.

**[00252]** In certain embodiments, X13 is Thr, Sarc, Glu, Phe, Arg, Leu, Lys, βhAla, Aib, Lys(Ac), Cit, Asp, Dab, Dap, Glu, hArg, Lys, Asn, Orn, or Gln. In certain embodiments, X13 is Thr, Sarc, Glu, Phe, Arg, Leu, Lys, βhAla or Aib.

**[00253]** In certain embodiments, X14 is Phe, Tyr, βhPhe, Asn, Arg, QGln, Lys(Ac), His; Dap(Ac), Dab(Ac) or Asp. In certain embodiments, X14 is Phe, Tyr or βhPhe.

**[00254]** In certain embodiments, X15 is Gly, Ser, Thr, Gln, Ala or Sarc, β-Ala, Glu, Arg or Asn. In certain embodiments, X14 is Phe, Tyr or βhPhe.

**[00255]** In certain embodiments, X13 is present.

**[00256]** In certain embodiments, X13 and X14 are present.

**[00257]** In certain embodiments, X13, X14 and X15 are present.

**[00258]** In certain embodiments of the peptide inhibitor of Formula I, X comprises or consists of the sequence of Formula Ir:

X1-X2-X3-X4-X5-X6-X7-X8-X9-X10-X11-X12-X13-X14-X15-X16-X17-X18-X19-X20 (Ir)

wherein

X1 is any amino acid or absent;

X2 is any amino acid or absent;

X3 is any amino acid or absent;

X4 is Cys, Pen, hCys, D-Pen, D-Cys, D-hCys, Met, Glu, Asp, Lys, Orn, Dap, Dab, D-Dap, D-Dab, D-Asp, D-Glu, D-Lys, Sec, 2-chloromethylbenzoic acid, mercapto-propanoic acid, mercapto-butyric acid, 2-chloro-acetic acid, 3-choro-propanoic acid, 4-chloro-butyric acid, 3-chloro-isobutyric acid, Abu, β-azido-Ala-OH, propargylglycine, 2-(3'-butenyl)glycine, 2-allylglycine, 2-(3'-butenyl)glycine, 2-(4'-pentenyl)glycine, 2-(5'-hexenyl)glycine, Abu or absent;

X5 is any amino acid;

X6 is any amino acid;

X7 is Trp, Glu, Gly, Ile, Asn, Pro, Arg, Thr or OctGly, or a corresponding α-methyl amino acid form of any of the foregoing;

**[00280]** In certain embodiments of the peptide inhibitor of Formula I, X comprises or consists of the sequence of Formula Is:

X1-X2-X3-C-X5-X6-W-X8-C-X10-X11-X12-X13-X14-G-X16-X17-X18-X19-X20 (Is) (SEQ ID NO: 1114)

wherein

X1 is any amino acid or absent;

X2 is any amino acid or absent;

X3 is any amino acid or absent;

X5 is any amino acid;

X6 is any amino acid;

X8 is any amino acid;

X10 is Tyr, 1-Nal 2-Nal, Phe(3,4-$F_2$), Phe(3,4-$Cl_2$), F(3-Me), Phe[4-(2-aminoethoxy)], Phe[4-(2-(acetyl-aminoethoxy)], Phe(4-Br), Phe(4-$CONH_2$), Phe(4-Cl), Phe(4-CN), Phe(4-guanidino), Phe(4-Me), Phe(4-$NH_2$), Phe(4-$N_3$), Phe(4-OMe), Phe(4-OBzl) or Tyr;

X11 is Trp 1-Nal, Phe(3,4-$OMe_2$) 5-Hydroxy-Trp, Phe(3,4-$Cl_2$) or Tyr(3-t-Bu);

X12 is Arg, Lys, His, hArg, Cit, Orn, 1-Nal, D-Ala, D-Leu, D-Phe, D-Asn, D-Asp, Agp, Leu, βhLeu, Aib, βhAla, βhVal, βhArg, hLeu, Dap, 4-amino-4-carboxy-tetrahydropyran, Achc Acpc, Acbc, Acvc, Agp, Aib, α-DiethylGly, α-MeLys, α-MeLys(Ac), α-Me-Leu, α-MeOrn, α-MeSer, α-MeVal, Cha, Cit, Cpa, (D)Asn, Glu, hArg, or Lys;

X13 is Cha, Ogl, Aib, Leu, Val, Dab, Glu, Lys, βhLeu, βhAla, βhVal βGlu, Lys(Ac), Cit, Asp, Dab, Dap, Glu, hArg, Lys, Asn, Orn, Lys(Ac), or Gln;

X14 is Phe, Tic, Asn Tyr, Asn, Arg, QGln, Lys(Ac), His; Dap(Ac), Dab(Ac) or Asp;

X16 is any amino acid;

In certain embodiments, neither of the two amino acid residues, e.g., Pens, participating in the intramolecular bond is located at the C-terminal position of the peptide inhibitor.

**[00351]** In some embodiments, wherein a peptide of the invention is conjugated to an acidic compound such as, e.g., isovaleric acid, isobutyric acid, valeric acid, and the like, the presence of such a conjugation is referenced in the acid form. So, for example, but not to be limited in any way, instead of indicating a conjugation of isovaleric acid to a peptide by referencing isovaleroyl (e.g., isovaleroyl-[Pen]-QTWQ[Pen]-[Phe(4-OMe)]-[2-Nal]-[a-MeLys]-[Lys(Ac)]-NG-$NH_2$ (SEQ ID NO: 262) in some embodiments, the present application references such a conjugation as isovaleric acid-[Pen]-QTWQ[Pen]-[Phe(4-OMe)]-[2-Nal]-[a-MeLys]-[Lys(Ac)]-NG-$NH_2$ (SEQ ID NO: 263).

**[00352]** The present invention further includes peptide inhibitors that selectively bind to an epitope or binding domain present within amino acid residues 230 – 349 of the human IL23R protein. In particular embodiments, the peptide inhibitor binds human IL23R and not mouse IL-23R. In certain embodiments, the peptide inhibitor also binds to rat IL-23R.

**[00353]** In certain embodiments of peptide inhibitors of Formula I, X4 is Abu; X9 is Cys, Pen, homocys, and the intramolecular bond is a thioether bond.

**[00354]** In certain embodiments of Formula I, X4 is Cys, Pen, hCys, D-Pen, D-Cys or D-hCys; X9 is Abu; and the intramolecular bond is a thioether bond.

Illustrative Peptide Inhibitors Comprising Pen-Pen Disulfide Bonds

**[00355]** In certain embodiments, the present invention includes a peptide inhibitor of an interleukin-23 receptor, wherein the peptide inhibitor has the structure of Formula II:

$$R^1\text{-}X\text{-}R^2 \text{ (II)}$$

**[00356]** or a pharmaceutically acceptable salt or solvate thereof,

wherein $R^1$ is a bond, hydrogen, a C1-C6 alkyl, a C6-C12 aryl, a C6-C12 aryl, a C1-C6 alkyl, a C1-C20 alkanoyl, an alkylsulphonate, an acid, γ-Glu or pGlu, appended to the N-terminus, and including PEGylated versions (e.g., 200 Da to 60,000 Da), alone or as a spacer of any of the foregoing;

not to be limited in any way, instead of indicating a conjugation of isovaleric acid to a peptide by referencing isovaleroyl (e.g., isovaleroyl-[Pen]-QTWQ[Pen]-[Phe(4-OMe)]-[2-Nal]-[α-MeLys]-[Lys(Ac)]-NG-$NH_2$ (SEQ ID NO: 262), in some embodiments, the present application references such a conjugation as isovaleric acid-[Pen]-QTWQ[Pen]-[Phe(4-OMe)]-[2-Nal]-[α-MeLys]-[Lys(Ac)]-NG-$NH_2$ (SEQ ID NO: 263). Reference to the conjugation in its acid form is intended to encompass the form present in the peptide inhibitor.

**[00460]** In certain embodiments, the peptide inhibitor comprises a C-terminus (e.g., $R^2$) selected from a bond, OH or $NH_2$. In certain embodiments, $R^2$ is a bond. In various embodiments of any of the peptide inhibitors having any of the various Formulas set forth herein, $R^2$ is OH or $NH_2$. It is understood that the $R^2$ may replace or be present in addition to the carboxyl group typically located at the carboxy terminus of a peptide. It is further understood that $R^2$ may be absent.

**[00461]** In particular embodiments of any of the peptide inhibitors having any of the various Formulae set forth herein, X comprises or consists of 7 to 35 amino acid residues, 8 to 35 amino acid residues, 9 to 35 amino acid residues, 10 to 35 amino acid residues, 7 to 25 amino acid residues, 8 to 25 amino acid residues, 9 to 25 amino acid residues, 10 to 25 amino acid residues, 7 to 20 amino acid residues, 8 to 20 amino acid residues, 9 to 20 amino acid residues, 7 to 18 amino acid residues, 8 to 18 amino acid residues, 9 to 18 amino acid residues, or 10 to 18 amino acid residues.

**[00462]** In certain embodiments of any of the Formulae set forth herein, X either or both does not comprise or does not consist of an amino acid sequence set forth in US Patent Application Publication No. US2013/0029907. In certain embodiments of any of the Formulae set forth herein, X either or both does not comprise or does not consist of an amino acid sequence set forth in US Patent Application Publication No. US2013/0172272.

**[00463]** In certain embodiments of any of the peptide inhibitors described herein, the peptide inhibitor, or each monomer subunit thereof, comprises or consists of at least 3, at least 4 at least 5, at least 6, or at least 7 amino acid residues carboxy terminal of the X9 amino acid residue. In particular embodiments of any of the peptide inhibitors described herein, the peptide inhibitor comprises 3 to 11, 3 to 10, 3 to 9, 3 to 8, 3 to 7, 3 to 6, 3 to 5, 3 to 4, 3, 4, 5, 6, 7, 8, 9, 10, or 11 amino acid residues carboxy terminal of the X9 amino acid residue.

**[00464]** In certain embodiments of any of the peptide inhibitors described herein, the peptide inhibitor, or each monomer subunit thereof, comprises or consists of 4 amino acid residues between X4 and X9. In one embodiment, both X4 and X9 are cysteines.

**[00465]** In certain embodiments of any of the peptide inhibitors described herein, the peptide inhibitor, or each monomer subunit thereof, comprises the amino acid sequence motif, W-X-X-Y-W, e.g., at positions X7-X11. In certain embodiments, the peptide inhibitor, or each monomer subunit thereof, comprises the amino acid sequence motif, C-X-X-W-X-C-Y-W (SEQ ID NO: 264), e.g., at positions X4-X11. In certain embodiments, the peptide inhibitor, or each monomer subunit thereof, comprises the amino acid sequence motif, Pen-X-X-W-X-Pen-Y-W, e.g., at positions X4-X11. In certain embodiments of any of the peptide inhibitors described herein, the peptide inhibitor, or both monomer subunit thereof, does not comprise the amino acid sequence motif, W-X-X-Y-W, e.g., at positions X7-X11, where X is any amino acid.

**[00466]** In certain embodiments of any of the Formula or peptide inhibitors described herein, the peptide inhibitor comprises one or more amino acid residues N-terminal to X4. In particular embodiments, X3 is present. In certain embodiments, X3 is Glu, (D)Glu, Arg, (D)Arg, Phe, (D)Phe, 2-Nal, Thr, Leu, or (D)Gln. In certain embodiments, X3 is (D)Arg or (D)Phe.

**[00467]** In particular embodiments of any of the Formula or peptide inhibitors described herein, the peptide inhibitor comprises an amino acid at X2. In particular embodiments, X2 is Glu, (D)Asp, Arg, (D)Arg, Phe, (D)Phe, 2-Nal, Thr, Leu, (D)Gln, or (D)Asn. In certain embodiments, X2 and X3 are present. In particular embodiments, X2 is Glu, (D)Asp, Arg, (D)Arg, Phe, (D)Phe, 2-Nal, Thr, Leu, (D)Gln, or (D)As, and X3 is (D)Arg.

**[00468]** In certain embodiments, a peptide inhibitor of the present invention, or one or both monomer subunits thereof, comprises, optionally at its C-terminus, one of the following amino acid sequences:

ENG;

ENN;

[4-amino-4-carboxy-tetrahydropyran]-ENN;

[Lys(Ac)]-NN;

[α-MeLys]-ENG (SEQ ID NO: 265);

[α-MeLys]- [Lys(Ac)]-NN (SEQ ID NO: 266);

[α-MeLeu]- [Lys(Ac)]-NN (SEQ ID NO: 267)

[α-MeLeu]-ENG (SEQ ID NO: 268);

[α-MeOrn]-[Lys(Ac)]-NG;

[α-MeLeu]-ENG (SEQ ID NO: 269);

Aib-[Lys(Ac)]-NG;

Aib-[Lys(Ac)]-NN;

NG-[AEA]-[(D)-Lys];

[Dapa]-NG-[AEA]-[(D)-Lys];

[Orn]-NG-[AEA]-[(D)-Lys];

[α-MeLys]-ENN (SEQ ID NO: 270);

[4-amino-4-carboxy-tetrahydropyran]- [Lys(Ac)]-NN;

[Achc]-[Lys(Ac)]-NN; or

[Acpc]-[Lys(Ac)]-NN.

**[00469]** In particular embodiments, one of these amino acid sequences constitutes the terminal C-terminal amino acids of the peptide. In particular embodiment, these amino acid sequences correspond to X13-X15 or X12-X15 or X14-X16 or X13-X17.

**[00470]** In certain embodiments, a peptide inhibitor of the present invention, or one or both monomer subunits thereof, comprises, optionally at its C-terminus, one of the following amino acid sequences:

WQCY-[2-Nal]-[α-MeLys] (SEQ ID NO: 271);

WQC-[Phe(4-OMe)]-[2-Nal]-[α-MeLys] (SEQ ID NO: 272);

WQC-[Phe(4-OMe)]-[2-Nal]-[Aib] (SEQ ID NO: 273);

WQ-[Pen]-[Phe(4-OMe)]-[2-Nal]-[α-MeLys] (SEQ ID NO: 274);

W-Xaa8-C-Phe[4-(2-aminoethoxy)] -[2-Nal];

W-Xaa8-C-Phe[4-(2-aminoethoxy)] -[1-Nal] ;

W-Xaa8-C-Phe[4-(2-aminoethoxy)]; or

**[00471]** W-Xaa8-C-[Phe(4-$OCH_3$)]. In particular embodiments, one of these amino acid sequences constitutes the terminal C-terminal amino acids of the peptide. In particular embodiment, these amino acid sequences correspond to X7 to X12 or X7 to X11 or X7 to X10.

**[00472]** In certain embodiments of any of the peptide inhibitors described herein, including both peptide monomer inhibitors and monomer subunits of peptide dimer inhibitors, the peptide monomer inhibitor or monomer subunit is cyclized via a peptide bond between its N-terminal amino acid residue and its C-terminal amino acid residue. In particular embodiments, the peptide inhibitor (or monomer subunit thereof) comprises both an intramolecular bond between X4 and X9 and a peptide bond between its N-terminal amino acid residue and its C-terminal amino acid residue. In certain embodiments, the intramolecular bond is any of those described herein, e.g., a disulfide bond or a thioether bond.

**[00473]** In certain embodiments, the present invention includes a peptide inhibitor that comprises a core consensus sequence selected from one of the following (shown in N-terminal to C-terminal direction):

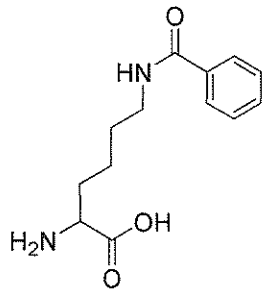
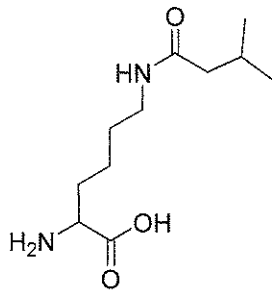
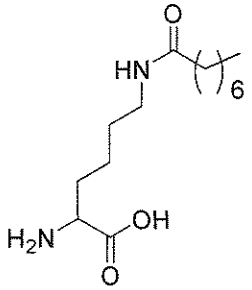
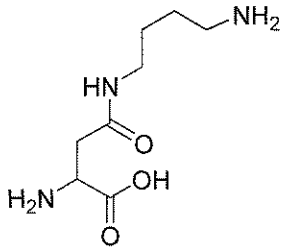
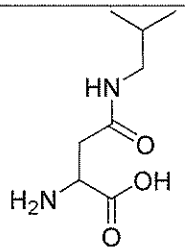
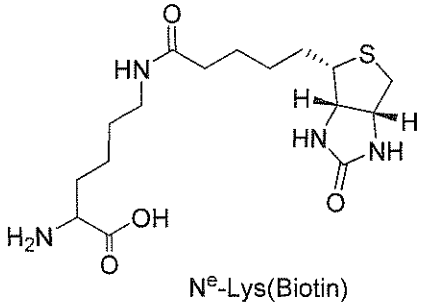
X1-X2-X3-Pen-X5-X6-W-X8-Pen-X10-X11-X12-X13-X14-X15;

Pen-X5-X6-W-Q-Pen;

Pen-X5-X6-W-X8-Pen;

Pen-X5-X6-W-X8-Pen-[Phe(4-CONH2)]; and

Pen-X5-X6-W-X8-Pen-[Phe[4-(2-aminoethoxy)]],

| | |
|---|---|
|  $N^e$-Lys(Benzoic acid) |  $N^e$-Lys(IVA) |
|  $N^e$-Lys(octanoic acid) |  Asp(1,4 diaminobutane) |
|  Asn(isobutyl) |  $N^e$-Lys(Biotin) |

**[00538]** In further embodiments of the present invention, alternatively or additionally, a side-chain of one or more amino acid residues in a peptide inhibitor of the invention is conjugated to a polymeric moiety, for example, in order to increase solubility and/or half-life *in vivo* (e.g. in plasma) and/or bioavailability. Such modifications are also known to reduce clearance (e.g. renal clearance) of therapeutic proteins and peptides.

**[00539]** As used herein, "Polyethylene glycol" or "PEG" is a polyether compound of general formula H-(O-CH2-CH2)n-OH. PEGs are also known as polyethylene oxides (PEOs) or polyoxyethylenes (POEs), depending on their molecular weight. PEO, PEE, or POG, as used herein, refers to an oligomer or polymer of ethylene oxide. The three names are chemically synonymous, but PEG has tended to refer to oligomers and polymers with a molecular mass

region corresponding to about amino acid residue 315 to about amino acid residue 340 of the mouse IL23R protein, e.g., amino acid region NWQPWSSPFVHQTSQETGKR (SEQ ID NO: 261) (see, e.g., Figure 1). In particular embodiments, the peptide inhibitors bind to a region of human IL-23R from about amino acid 230 to about amino acid residue 370.

**[00589]** The present invention provides a new method to identify an inhibitor (e.g., a peptide inhibitor) of IL-23R, based on identifying an agent (e.g., a peptide) that preferentially binds to human IL-23R or rat IL-23R as compared to mouse IL-23R. In certain embodiments, the method comprises: (a) determining an amount of binding of a candidate agent to a human IL-23R polypeptide or a rat IL-23R polypeptide; (b) determining an amount of binding of the candidate agent to the mouse IL-23R polypeptide; and (c) comparing the determined amount of binding to the human IL-23R polypeptide or the rat IL-23R polypeptide to the determined amount of binding to the mouse IL-23R polypeptide, wherein if the determined amount of binding to the human IL-23R polypeptide or the rat IL-23R polypeptide is greater than the amount of binding to the mouse IL-23R polypeptide, the candidate compound is an inhibitor of IL-23R. In particular embodiments, the candidate compound is identified as an inhibitor of IL-23R if the determined amount of binding to the human IL-23R polypeptide or the rat IL-23R polypeptide is at least 1.5-fold, at least 2-fold, at least 3-fold, at least 4-fold, at least 5-fold, at least 10-fold, at least 20-fold, at least 30-fold, at least 40-fold, at least 50-fold, at least 100-fold, at least 200-fold, at least 500-fold, or at least 100-fold the determined amount of binding to the mouse IL-23R polypeptide. In particular embodiments, the candidate compound is a peptide. In particular embodiments, the peptide is a peptide of one of the formulas described herein. In particular embodiments, the human IL-23 polypeptide or rat IL-23R polypeptide comprises or consists of the full length human IL-23R or rat IL-23R protein, respectively. In other embodiments, the human IL-23R polypeptide is a fragment of the full length human IL-23R protein, comprising 8 or more amino acid residues within the region of human IL-23R from about amino acid residue 230 to about amino acid residue 370. In other embodiments, the rat IL-23R polypeptide is a fragment of the full length rat IL-23R protein, comprising 8 or more amino acid residues within the region of rat IL-23R from about amino acid residue 245 to about amino acid residue 385.

| | | | | |
|---|---|---|---|---|
| 28 | Ac-CQTWQCYWHENGA-[(D)Lys]-$NH_2$ | 220 | | |
| 29 | Ac-CRTWQCYWRENGA-[(D)Lys]-$NH_2$ | 102 | 86 | 17 |
| 30 | Ac-CRTWQCYWREYGA-[(D)Lys]-$NH_2$ | 78 | 80 | 8 |
| 31 | Ac-C-[N-MeAla]-DWVCYWHTFG-[AEA]-[(D)Lys]-$NH_2$ | 183 | | |
| 32 | Ac-CADWVCYWRKFG-[βAla]-[(D)Lys]-$NH_2$ | 57 | 33(1) | 13 |
| 33 | Ac-CADWVCYW-[Cit]-KFG-[β-Ala]-[(D)Lys]-$NH_2$ | 52 | | 29 |
| 34 | Ac-CADWVCYW-[Cit]-[Tle]-FG-[β-Ala]-[(D)Lys]-$NH_2$ | 518 | | |
| 35 | Ac-CADWVCYW-[Cit]-[Tba]-FG-[β-Ala]-[(D)Lys]-$NH_2$ | 153 | | |
| 36 | Ac-CADWVCYW-[Cit]-[Cha]-FG-[β-Ala]-[(D)Lys]-$NH_2$ | 223 | | |
| 37 | Ac-CADWVCY-[1-Nal]-[Cit]-VFG-[β-Ala]-[(D)Lys]-$NH_2$ | 79 | | 22 |
| 38 | Ac-CADWVCYW-[Cit]-VFG-[β-Ala]-[(D)Lys]-$NH_2$ | 124 | | |
| 39 | Ac-CADWVCYW-[Cit]-[Chg]-FG-[β-Ala]-[(D)Lys]-$NH_2$ | >30000 | | |
| 40 | Ac-CADWVCYW-[Cit]-[βAla]-FG-[β-Ala]-[(D)Lys]-$NH_2$ | 2584 | | |
| 41 | Ac-CADWVCYW-[Tle]-[Tle]-FG-[β-Ala]-[(D)Lys]-$NH_2$ | ~30000 | | |
| 42 | Ac-CADWVCYW-[Tle]-KFG-[β-Ala]-[(D)Lys]-$NH_2$ | 199 | | |
| 43 | Ac-CQTWQCYW-[(D)Ala]-VFG-[AEA]-[(D)Lys]-$NH_2$ | 232 | | |
| 44 | Ac-CQTWQCYW-[βAla]-VFG-[AEA]-[(D)Lys]-$NH_2$ | 2207 | | |
| 45 | Ac-CQTWQCYW-[(D)Leu]-VFG-[AEA]-[(D)Lys]-$NH_2$ | 188 | | |
| 46 | Ac-CQTWQCYW-[(D)Phe]-VFG-[AEA]-[(D)Lys]-$NH_2$ | 848 | | |
| 47 | Ac-CQTWQCYW-[(D)Asn]-VFG-[AEA]-[(D)Lys]-$NH_2$ | 61 | | |
| 48 | Ac-CQTWQCYW-[(D)Thr]-VFG-[AEA]-[(D)Lys]-$NH_2$ | 3662 | | |
| 49 | Ac-CQTWQCYW-[(D)Asp]-VFG-[AEA]-[(D)Lys]-$NH_2$ | 129 | | |
| 50 | Ac-CQTWQCYW-[Cit]-[(D)Leu]-FG-[AEA]-[(D)Lys]-$NH_2$ | 709 | | |
| 51 | Ac-CQTWQCYW-[Cit]-[(D)Phe]-FG-[AEA]-[(D)Lys]-$NH_2$ | 1304 | | |
| 52 | Ac-CQTWQCYW-[Cit]-[(D)Asn]-FG-[AEA]-[(D)Lys]-$NH_2$ | 269 | | |
| 53 | Ac-CQTWQCYW-[Cit]-[(D)Thr]-FG-[AEA]-[(D)Lys]-$NH_2$ | 1214 | | |
| 54 | Ac-CQTWQCYW-[Agp]-VNG-[AEA]-[(D)Lys]-$NH_2$ | 241 | | |
| 55 | Ac-CQTWQCY-[α-MeTrp]-RVNG-[AEA]-[(D)Lys]-$NH_2$ | ~6000 | | |
| 56 | Ac-CQTWQCY-[α–MeTrp]-[Cit]-[hLeu]-NG-[AEA]-[(D)Lys]-$NH_2$ | ~6000 | | |
| 57 | Ac-CQTWQCYW-[Cit]-VNG-[AEA]-[(D)Lys]-$NH_2$ | 73 | | |
| 58 | Ac-CQTWQCYW-[Agp]-[Dap]-NG-[AEA]-[(D)Lys]-NH2 | 38 | | |
| 59 | Ac-CQTWQCYW-[Cit]-VF-[(D)Ala]-[AEA]-[(D)Lys]-$NH_2$ | 397 | | |
| 60 | Ac-CQTWQCYW-[Cit]-VF-[(D)Leu]-[AEA]-[(D)Lys]-$NH_2$ | 444 | | |
| 61 | Ac-CQTWQCYW-[Cit]-VF-[(D)Phe]-[AEA]-[(D)Lys]-$NH_2$ | 784 | | |
| 62 | Ac-CQTWQCYW-[Cit]-VF-[(D)Asn]-[AEA]-[(D)Lys]-$NH_2$ | 93 | | |
| 63 | Ac-CQTWQCYW-[Cit]-VF-[(D)Thr]-[AEA]-[(D)Lys]-$NH_2$ | 518 | | |
| 64 | Ac-CQTWQCYW-[Cit]-VF-[(D)Asp]-[AEA]-[(D)Lys]-$NH_2$ | 551 | | |
| 65 | Ac-C-[N-MeArg]-TWQCYWRVFG-[AEA]-[(D)Lys]-$NH_2$ | 149 | 192 | 107 |
| 66 | Ac-C-[N-MeGlnMeGln]-TWQCYWRVFG-[AEA]-[(D)Lys]-$NH_2$ | 69 | 85 | 101 |
| 67 | Ac-C-[Cit]-TWQCYWRVFG-[AEA]-[(D)Lys]-$NH_2$ | 50 | 76 | 107 |
| 68 | Ac-CADWVCYW-[Orn]-[Dap]-FG-[AEA]-[(D)Lys]-$NH_2$ | 382 | | |
| 69 | Ac-CADWVCY-[1-Nal]-[Orn]-[Dap]-FG-[AEA]-[(D)Lys]-$NH_2$ | 302 | | |
| 70 | Ac-CADWVCY-[(D)Trp]-[Orn]-[Dap]-FG-[AEA]-[(D)Lys]-$NH_2$ | >30000 | | |

| | | | | |
|---|---|---|---|---|
| | $NH_2$ | | | |
| 337 | Ac-CQTWQCYW-[βhArg]-VNG-[AEA]-[(D)Lys]-$NH_2$ | 922 | | |
| 338 | Ac-MRTWQ-[MeCys]-YWRKFG-[AEA]-[(D)Lys]-$NH_2$ | 4251 | | |
| 339 | Ac-ACDWVCYWRKFG-[AEA]-[(D)Lys]-$NH_2$ | 630 | | |
| 340 | Ac-SRTWQSYWRKFG-[AEA]-[(D)Lys]-$NH_2$ | 2816 | | |
| 341 | Ac-CDWVCYWRKFG-[AEA]-[(D)Lys]-$NH_2$ | 664 | | |
| 342 | Ac-ARTWQ-[MeCys]-YWRKFG-[AEA]-[(D)Lys]-$NH_2$ | 7571 | | |
| 343 | Ac-ARTWQAYWRKFG-[AEA]-[(D)Lys]-$NH_2$ | 3194 | | |
| 344 | Ac-CQTWQCYW-[hLeu]-EN-[AEA]-[(D)Lys]-$NH_2$ | 132 | | |
| 345 | Ac-CQTWQCYW-[hLeu]-ENG-[AEA]-[(D)Lys]-$NH_2$ | 222 | | |
| 346 | Ac-CSTWECYWRVYG-[AEA]-[(D)Lys]-$NH_2$ | 47 | | |
| 347 | Ac-C-[Orn]-TWQCYWRVFG-[AEA]-[(D)Lys]-$NH_2$ | 22 | 69 | 95 |
| 348 | Ac-CQTWQCYW-[Orn]-[Dap]-FG-[AEA]-[(D)Lys]-$NH_2$ | 96 | | |
| 349 | Ac-C-[N-MeAsn]-TWQCYWRVFG-[AEA]-[(D)Lys]-$NH_2$ | 148 | | |
| 350 | Ac-C-[N-MeLys]-TWQCYWRVFG-[AEA]-[(D)Lys]-$NH_2$ | 80 | | |
| 351 | Ac-C-[Dab]-TWQCYWRVFG-[AEA]-[(D)Lys]-$NH_2$ | 23 | 51 | 99 |
| 352 | Ac-CQTWQCYY-[Orn]-[Dap]-FG-[AEA]-[(D)Lys]-$NH_2$ | 710 | | |
| 353 | Ac-CSTWQCYW-[Orn]-[Dap]-YG-[AEA]-[(D)Lys]-$NH_2$ | 371 | | |
| 354 | Ac-CSTWECYW-[Cit]-[Dap]-YG-[AEA]-[(D)Lys]-$NH_2$ | 74 | | |
| 355 | Ac-CQTWQCFF-[Orn]-[Dap]-FG-[AEA]-[(D)Lys]-$NH_2$ | 4274 | | |
| 356 | Ac-CPTWQCYWRVFG-[AEA]-[(D)Lys]-$NH_2$ | 422 | | |
| ~~347~~357 | Ac-CSTWECYW-[Orn]-[Dab]-YG-[AEA]-[(D)Lys]-$NH_2$ | 338 | | |
| 358 | Ac-CSTWECYWRVFG-[AEA]-[(D)Lys]-$NH_2$ | 48 | | |
| 359 | Ac-CLTWQCYWRVFG-[AEA]-[(D)Lys]-$NH_2$ | 134 | | |
| 360 | Ac-CQTWQCYF-[Orn]-[Dap]-FG-[AEA]-[(D)Lys]-$NH_2$ | 1885 | | |
| ~~461~~361 | Ac-CNTWQCYWRVFG-[AEA]-[(D)Lys]-$NH_2$ | 21 | 79 | 96 |
| 362 | Ac-C-[Dap]-TWQCYWRVFG-[AEA]-[(D)Lys]-$NH_2$ | 31 | | 100 |
| 363 | Ac-C-[N-Me-Ala]-TWQCYWRVFG-[AEA]-[(D)Lys]-$NH_2$ | 139 | | |
| 364 | Ac-CKTWQCYWRVFG-[AEA]-[(D)Lys]-$NH_2$ | 40 | | |
| 365 | Ac-CQDWQCYWR-[Cha]-FG-[AEA]-[(D)Lys]-$NH_2$ | 113 | | |
| 366 | Ac-CQTWQCYWR-[Ogl]-FG-[AEA]-[(D)Lys]-$NH_2$ | 206 | | |
| 367 | Ac-CQTWQCYWK-[Dap]-FG-[AEA]-[(D)Lys]-$NH_2$ | 32 | | |
| 368 | Ac-CQTWQCYWH-[Dap]-FG-[AEA]-[(D)Lys]-$NH_2$ | 49 | | 59 |
| 369 | Ac-CQTWQCYWRLFG-[AEA]-[(D)Lys]-$NH_2$ | 51 | | 47 |
| 370 | Ac-CQTWQCYW-[hArg]-[Dap]-FG-[AEA]-[(D)Lys]-$NH_2$ | 56 | | |

Table 3H. IC50 of Illustrative Peptides Containing the CXXWXCXXXX Motif

| SEQ ID NO. | Sequence | Human IL23/ IL23R ELISA (nM) | Rat IL23/ IL23R ELISA (nM) | pStat3 HTRF (nM) |
|---|---|---|---|---|
| 371 | Ac-CSTWECYWRTFG-$NH_2$ | 252 | | |
| 372 | Ac-CDSWECYWRTYG-$NH_2$ | 366 | | |
| 373 | Ac-CSTWECYWHTYG-$NH_2$ | 181 | 286 | 97 |

| | | | | |
|---|---|---|---|---|
| 374 | Ac-CKTWTCYWHTYG-$NH_2$ | 381 | | |
| 375 | Ac-CRTWECYWHEYS-$NH_2$ | 416 | | |
| 376 | Ac-CRTWTCYWHEYG-$NH_2$ | 434 | | |
| 377 | Ac-CFTWQCYWHEYS-$NH_2$ | 515 | | |
| 378 | Ac-CQTWQCYW-[3-Pal]-ENG-$NH_2$ | 56 | 20 | 101 |
| 379 | Ac-CQTWQC-$NH_2$ | >30000 | | |
| 380 | Ac-CRTWQC-$NH_2$ | >30000 | | |
| 381 | Ac-CADWVCY-$NH_2$ | >30000 | | |
| 382 | Ac-CADWVCYW-$NH_2$ | >30000 | | |
| 383 | Ac-CADWVCYWH-$NH_2$ | ~30000 | | |
| 384 | Ac-CADWVCYWHT-$NH_2$ | 4795 | | |
| 385 | Ac-CADWVCYWHTF-$NH_2$ | 3277 | | |
| 386 | Ac-CMTWQCYWLYGR-$NH_2$ | 613 | | |
| 387 | Ac-CRTWQCYWHEFG-$NH_2$ | | | |
| 388 | Ac-CRTWECYWHTFG-$NH_2$ | | | |
| 389 | Ac-CQTWQCYWHEFG-$NH_2$ | | | |
| 390 | Ac-CRTWQCYWQQFGGE-$NH_2$ | 81 | | |
| 391 | Ac-CRSWQCYWLNFGPD-$NH_2$ | 101 | | |
| 392 | Ac-CRTWQCYWLKMGDS-$NH_2$ | 39 | | |
| 393 | Ac-CQTWQCYWIKRDQG-$NH_2$ | 67 | | |
| 394 | Ac-CSTWQCYWLKHGGE-$NH_2$ | 19 | 24 | 2 |
| 395 | Ac-CSTWECYWSQRADQ-$NH_2$ | 240 | | |
| 396 | Ac-CQTWECYWRTFGPS-$NH_2$ | 58 | | |
| 397 | Ac-CRTWQCYWQEKGTD-$NH_2$ | 118 | | |
| 398 | Ac-CQTWQCYWLDSLGD-$NH_2$ | 93 | | |
| 399 | Ac-CRTWQCYWTKFGSEP-$NH_2$ | 87 | | 57 |
| ~~340~~1051 | Ac-CRSWQCYWNKFGADD-$NH_2$ | 142 | | |
| ~~341~~1052 | Ac-CHTWQCYWLNFGDEE-$NH_2$ | 323 | | |
| ~~342~~1053 | Ac-CRTWQCYWLNFGNEQ-$NH_2$ | 127 | | |
| ~~343~~1054 | Ac-CRTWQCYWSEFGTGE-$NH_2$ | 180 | 778 | 103 |
| ~~344~~1055 | Ac-CRTWQCYWLRLGDEG-$NH_2$ | 352 | 483 | 181 |
| ~~345~~1056 | Ac-CHTWQCYWSTLGPEA-$NH_2$ | 222 | | |
| ~~346~~1057 | Ac-CSTWQCYWSKQSGGS-$NH_2$ | 133 | 204 | 89 |
| ~~347~~1058 | Ac-CHTWQCYWLNNGTSQ-$NH_2$ | 113 | | |
| ~~348~~1059 | Ac-CHTWQCYWRANDGRD-$NH_2$ | 210 | | |
| ~~349~~1060 | Ac-SGCRTWQCYWHEFG-$NH_2$ | 390 | | |
| ~~350~~1061 | Ac-NKCRTWQCYWHEYG-$NH_2$ | 112 | | |
| ~~351~~1062 | Ac-SGCRTWECYWHEYG-$NH_2$ | 257 | | |
| ~~352~~1063 | Ac-DACRTWECYWHKFG-$NH_2$ | 165 | | |
| ~~353~~1064 | Ac-PECRTWECYWHKFG-$NH_2$ | 197 | | |
| ~~354~~1065 | Ac-QVCQTWECYWREFG-$NH_2$ | 145 | | |
| ~~355~~1066 | Ac-DRCVTWECYWREFG-$NH_2$ | 217 | | |
| ~~356~~1067 | Ac-ADQCRTWQCYWHEFG-$NH_2$ | 228 | | |
| ~~357~~1068 | Ac-KENCRTWECYWREFG-$NH_2$ | 148 | | |
| ~~358~~1069 | Ac-VQECSTWQCYWRTFG-$NH_2$ | 138 | | |
| ~~359~~1070 | Ac-GEECSTWQCYWRKFG-$NH_2$ | 53 | | 24 |
| ~~360~~1071 | Ac-DGSCRTWQCYWHQFG-$NH_2$ | 240 | | |
| ~~361~~1072 | Ac-NADCHSWECYWREFG-$NH_2$ | 872 | | |
| ~~362~~1073 | Ac-ERNCSTWECYWRAFG-$NH_2$ | 855 | | |

| | | | | |
|---|---|---|---|---|
| 3631074 | Ac-RVGCSTWECYWREFG-$NH_2$ | 417 | | |
| 3641075 | Ac-KANCRTWQCYWRKFE-$NH_2$ | 412 | | |
| 3651076 | Ac-YEDCRTWQCYWENFG-$NH_2$ | 280 | | |
| 3661077 | Ac-CQTWQCYWRNFGDS-$NH_2$ | | | |
| 3671078 | Ac-CQTWQCYWRNFESG-$NH_2$ | | | |
| 3681079 | Ac-CQDWQCYWREFGPG-$NH_2$ | | | |
| 3691080 | Ac-CQDWQCYWRSFGPQ-$NH_2$ | | | |
| 3701081 | Ac-CQTWQCYWRTLGPS-$NH_2$ | | | |
| 3711082 | Ac-CRTWQCYWQNFG-$NH_2$ | 235 | | |
| 3721083 | Ac-CGTWQCYWRTFGPS-$NH_2$ | 76 | | |
| 3731084 | Ac-CSTWQCYWHKFGNE-$NH_2$ | 182 | | |
| 3741085 | Ac-CRTWECYWRTYGPS-$NH_2$ | 116 | | |
| 3751086 | Ac-CRTWQCYWWENSQM-$NH_2$ | 99 | | |
| 3761087 | Ac-CQTWQCYWREFGGG-$NH_2$ | 165 | | |
| 3771088 | Ac-CQTWQCYWRTHGDR-$NH_2$ | 83 | | |
| 3781089 | Ac-CRDWQCYWLSRP-$NH_2$ | 330 | | |
| 3791090 | Ac-CQTWQCYW-[K(Palm)]-ENG-$NH_2$ | 4880 | | |
| 3801091 | Ac-CQTWQCYW-[K(PEG8)]-ENG-$NH_2$ | 153 | | |
| 3811092 | Ac-CQTWQCYW-[hLeu]-EQG-$NH_2$ | 128 | | |
| 3821093 | Ac-CQTWQABUC-[(D)Tyr]-W-[hLeu]-ENG-$NH_2$ | >30000 | | |
| 3831094 | Ac-CQTWQC-[(N-MeTyr]-W-[hLeu]-ENG-$NH_2$ | >30000 | | |
| 3841095 | Ac-CQTWQC-[Tic-OH]-W-[hLeu]-ENG-$NH_2$ | >30000 | | |
| 3851096 | Ac-CQTWQCEW-[hLeu]-ENG-$NH_2$ | >30000 | | |
| 3861097 | Ac-CQTWQCTW-[hLeu]-ENG-$NH_2$ | >30000 | | |
| 3871098 | Ac-CQTWQC-[Cha]-W-[hLeu]-ENG-$NH_2$ | ~6000 | | |
| 3881099 | Ac-CQTWQCYW-[α-MeLeu]-ENG-$NH_2$ | 22 | 27 | 5 |
| 3891100 | Ac-CQTWQCYW-[(D)Leu]-ENG-$NH_2$ | 319 | | |
| 3901101 | Ac-CQTWQCYW-[hLeu]-ENG-[(D)Lys]-$NH_2$ | 121 | | |
| 3911102 | Ac-CQTWQCYW-[hLeu]-ENG-OH | 317 | | |
| 3921103 | Ac-CQTWQCYW-[hLeu]-ENE-$NH_2$ | 222 | 1002 | 310 |
| 3931104 | Ac-CQTWQCYW-[hLeu]-ENR-$NH_2$ | 93 | | |
| 3941105 | Ac-CQTWQCYW-[hLeu]-ENF-$NH_2$ | 82 | 182 | 69 |
| 3951106 | Ac-CQTWQCYW-[hLeu]-ENP-$NH_2$ | 253 | 114 | 31 |
| 3961107 | Ac-CQTWQCYW-[hLeu]-ENQ-$NH_2$ | 347 | | |
| 3971108 | Ac-CQTWQCYW-[hLeu]-ENL-$NH_2$ | 45 | | |
| 3981109 | Ac-CQTWQCYW-[hLeu]-EEG-$NH_2$ | 135 | 53 | 16 |
| 3991110 | Ac-CQTWQCYW-[hLeu]-ERG-$NH_2$ | 647 | | |
| 400 | Ac-CQTWQCYW-[hLeu]-EPG-$NH_2$ | 108 | 140 | 27 |
| 401 | Ac-CQTWQCYW-[hLeu]-ELG-$NH_2$ | 158 | | |
| 402 | Ac-CQTWQCYW-[hLeu]-ETG-$NH_2$ | 818 | | |
| 403 | Ac-CQTWQCYW-[hLeu]-FNG-$NH_2$ | 395 | | |
| 404 | Ac-CQTWQCYW-[hLeu]-PNG-$NH_2$ | 4828 | | |
| 405 | Ac-CQTWQCYW-[hLeu]-NNG-$NH_2$ | 89 | | 26 |
| 406 | Ac-CQTWQCYW-[hLeu]-LNG-$NH_2$ | 78 | | |
| 407 | Ac-CQTWQCYW-[hLeu]-TNG-$NH_2$ | 109 | | |
| 408 | Ac-CQTWQCYWFENG-$NH_2$ | 185 | | |
| 409 | Ac-CQTWQCYWPENG-$NH_2$ | >30000 | | |
| 410 | Ac-CQTWQCYWQENG-$NH_2$ | 173 | | |
| 411 | Ac-CQTWQCYWTENG-$NH_2$ | 114 | | |

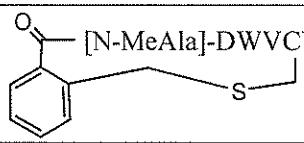
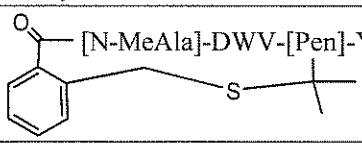
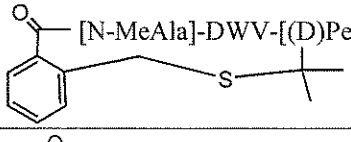
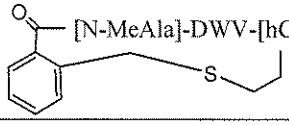
| | | | | |
|---|---|---|---|---|
| 480 | Ac-FCQTWQCYW-[hLeu]-ENG-$NH_2$ | 56 | 25 | 16 |
| 481 | Ac-ECQTWQCYW-[hLeu]-ENG-$NH_2$ | | | |
| 482 | Ac-NCQTWQCYW-[hLeu]-ENG-$NH_2$ | | | |
| 483 | Ac-RCQTWQCYW-[hLeu]-ENG-$NH_2$ | | | |
| 484 | Ac-CQTWQCY-[2-Nal]-[hLeu]-ENG-$NH_2$ | | | |
| 485 | Ac-CQTWQCY-[1-Nal]-[hLeu]-ENG-$NH_2$ | 18 | 37 | 6 |
| 486 | Ac-CQTWQC-[2-Nal]-W-[hLeu]-ENG-NH2 | 48 | 73 | 11 |
| 487 | Ac-CQTWQC-[1-Nal]-[2-Nal]-[hLeu]-ENG-$NH_2$ | 78 | 125 | 17 |
| 488 | Ac-CQTWQC-[2-Nal]-[1-Nal]-[hLeu]-ENG-$NH_2$ | 117 | | |
| 489 | Ac-CQTWQC-[Aic]-W-[hLeu]-ENG-$NH_2$ | 126 | | |
| 490 | Ac-CQTWQCHW-[hLeu]-ENG-$NH_2$ | ~6000 | | |
| 491 | Ac-CQTWQCYH-[hLeu]-ENG-$NH_2$ | 398 | | |
| 492 | Ac-CQTWQC-[Tyr(OMe)]-W-[hLeu]-ENG-$NH_2$ | ~30000 | | |
| 493 | Ac-CQTWQCY-[Bip]-[hLeu]-ENG-$NH_2$ | 42 | 51 | 11 |
| 494 | Ac-CQTWQCY-[Tyr(OMe)]-[hLeu]-ENG-$NH_2$ | 998 | | |
| 495 | Ac-CQTWQCHH-[hLeu]-ENG-$NH_2$ | 148 | | |
| 496 | Ac-CQTWQCY-[α–MeTrp]-[hLeu]-EQG-$NH_2$ | >30000 | | |
| 497 | Ac-CQTW-[(K(PEG8)]-CYWLENG-$NH_2$ | 212 | | |
| 498 | Ac-CQTWQCYWZX-LNG-$NH_2$ | 800 | | |
| 499 | Ac-CQTW-[K(PEG8)]CYW-[K(PEG8)]-ENG-$NH_2$ | 753 | | |
| 500 | Ac-CQTW-[K(Palm)]-CYWLENG-$NH_2$ | ~30000 | | |
| 501 | Ac-CQTWQCYW-[Orn]-[K(Palm)]-NG-$NH_2$ | >6000 | | |
| 502 | Ac-Gly-[(D)Asn]-(D)Glu-(D)Leu-(D)Trp-(D)Tyr-(D)Cys-(D)Gln-(D)Trp-(D)Thr-(D)Gln-(D)Cys-$NH_2$ | >30000 | | |
| 503 | Ac-CQTWQCYW-[(Orn)]-[K(Peg8)]-NG-$NH_2$ | 169 | | |
| 504 | Ac-CRTWQCYWHEFG-$NH_2$ | 166 | | |
| 505 | Ac-CRTWECYWHTFG-$NH_2$ | 333 | | |
| 506 | Ac-CQTWQCYWHEFG-$NH_2$ | 169 | | |
| 507 | Ac-CQTWQCYWRNFGDS-$NH_2$ | 96 | | |
| 508 | Ac-CQTWQCYWRNFESG-$NH_2$ | 315 | | |
| 509 | Ac-CQDWQCYWREFGPG-$NH_2$ | 82 | | |
| 510 | Ac-CQDWQCYWRSFGPQ-$NH_2$ | 117 | | |
| 511 | Ac-CQTWQCYWRTLGPSNH2 | 66 | | |
| 512 | Ac-CQTWQCYW-[(D)Pro]-ENG-$NH_2$ | >30000 | | |
| 513 | Ac-CQTWQCYWELNG-$NH_2$ | 79 | | |
| 514 | Ac-CQTWECYWELNG-$NH_2$ | 154 | | |
| 515 | Ac-CQTWQCY[(1-Nal]-[α-MeLeu]-ENG-$NH_2$ | 22 | 67 | 13 |
| 516 | Ac-CQTWQCY-[1-Nal]-[(D)Asn]-ENG-$NH_2$ | 145 | | 98 |
| 517 | Ac-CQTWQCYWLE-[K(Palm)]-G-$NH_2$ | >6000 | | |
| 518 | Ac-CQTWQCYWLEN-[K(Palm)]-$NH_2$ | 2800 | | |
| 519 | Ac-CSTWECYWRTFG-$NH_2$ | 252 | | |
| 520 | Ac-CDSWECYWRTYG-$NH_2$ | 366 | | |
| 521 | Ac-CSTWECYWHTYG-$NH_2$ | 181 | 286 | 97 |

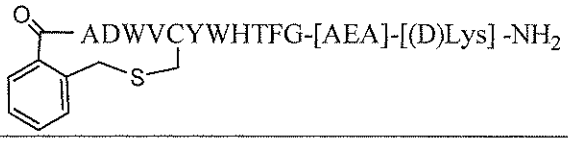
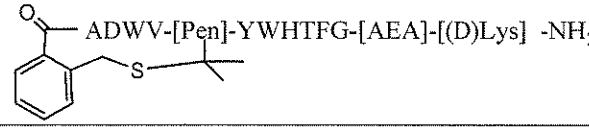
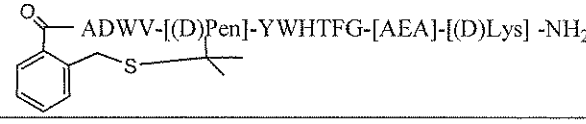
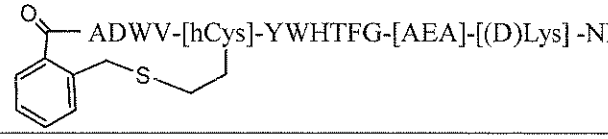
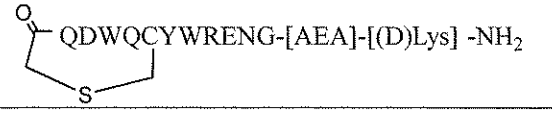
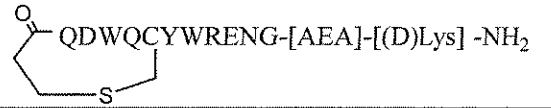
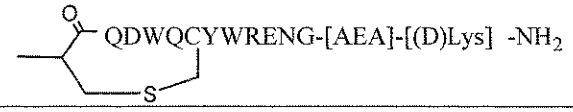
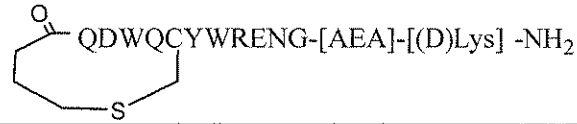
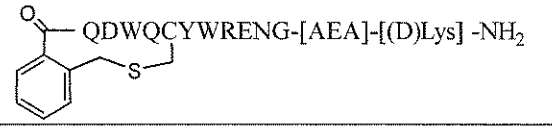
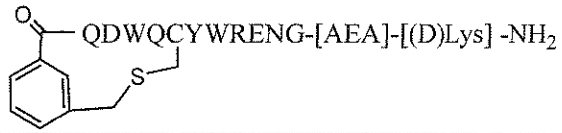
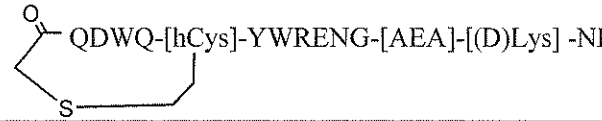
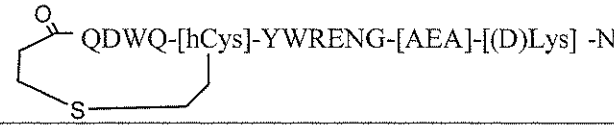
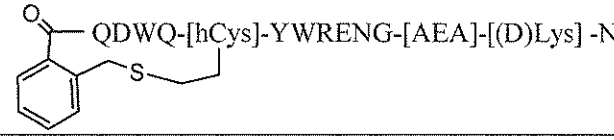
Table 4A. IC50 of Illustrative examples of dimers of Peptides Containing the Ac-[Pen]-XXWX-[Pen]-XXXX Motif and analogues

| | | | | |
|---|---|---|---|---|
| 680 | Ac-[(D)Phe]-[Pen]-NTWQ-[Pen]-[Phe(4-OMe)]-[2-Nal]-[Achc]-[Cit]-NN-$NH_2$ | | | |
| 681 | Ac-[(D)Phe]-[Pen]-NTWQ-[Pen]-[Phe(4-OMe)]-[2-Nal]-[Achc]-ENN-$NH_2$ | | | |
| 682 | Ac-[Pen]-NTWQ[Pen]-[Phe(4-$CONH_2$)]-[2-Nal]-[Aib]-[Lys(Ac)]-NN-$NH_2$ | | | |
| 683 | Ac-[Pen]-NTWQ[Pen]-[Phe(4-$CONH_2$)]-[2-Nal]-[4-amino-4-carboxy-tetrahydropyran]-Lys(Ac)]-NN-$NH_2$ | | | |
| 684 | Ac-[Pen]-NTWQ[Pen]-[Phe(4-$CONH_2$)]-[2-Nal]-[Achc]-[Lys(Ac)]-NN-NH2 | | | |
| 685 | Ac-[Pen]-NTWQ[Pen]-[Phe(4-$CONH_2$)]-[2-Nal]-[Acpc]-[Lys(Ac)]-NN-$NH_2$ | | | |
| 686 | Ac-[Pen]-NTWQ[Pen]-[Phe(4-$CONH_2$)]-[2-Nal]-[α-MeLeu]-[Lys(Ac)]-NN-$NH_2$ | | | |
| 687 | Ac-[Pen]-NTWQ[Pen]-[Phe(4-OMe)]-[2-Nal]-[Aib]-[Lys(Ac)]-NN-$NH_2$ | | | |
| 688 | Ac-[Pen]-NTWQ[Pen]-[Phe(4-OMe)]-[2-Nal]-[4-amino-4-carboxy-tetrahydropyran]-[Lys(Ac)]-NN-$NH_2$ | | | |
| 689 | Ac-[Pen]-NTWQ[Pen]-[Phe(4-OMe)]-[2-Nal]-[Achc]-[Lys(Ac)]-NN-$NH_2$ | | | |
| ~~670~~730 | Ac-[Pen]-NTWQ[Pen]-[Phe(4-OMe)]-[2-Nal]-[Acpc]-[Lys(Ac)]-NN-$NH_2$ | | | |
| ~~671~~731 | Ac-[Pen]-NTWQ[Pen]-[Phe(4-OMe)]-[2-Nal]-[α-MeLeu]-[Lys(Ac)]-NN-$NH_2$ | | | |

*=<10nM; **=10-25 nM *** = 25-100 nM, **** = 100-1000 nM, *****=1000-10,000 nM.

Table 5A. IC50 of Illustrative Peptide Inhibitors (Thioethers)

| SEQ ID NO. | Sequence/Structure | Human ELISA (nM) |
|---|---|---|
| ~~672~~732 |  [N-MeAla]-DWVCYWHTFG-[AEA]-[(D)Lys] -$NH_2$ | ~6000 |
| ~~673~~733 |  [N-MeAla]-DWV-[Pen]-YWHTFG-[AEA]-[(D)Lys] -$NH_2$ | >30000 |
| ~~674~~734 |  [N-MeAla]-DWV-[(D)Pen]-YWHTFG-[AEA]-[(D)Lys] -$NH_2$ | >30000 |
| ~~675~~735 |  [N-MeAla]-DWV-[hCys]-YWHTFG-[AEA]-[(D)Lys] -$NH_2$ | ~6000 |

| | | |
|---|---|---|
| ~~67673~~ 6 |  ADWVCYWHTFG-[AEA]-[(D)Lys] -$NH_2$ | ~3000 |
| ~~67773~~ 7 |  ADWV-[Pen]-YWHTFG-[AEA]-[(D)Lys] -$NH_2$ | >30000 |
| ~~67873~~ 8 |  ADWV-[(D)Pen]-YWHTFG-[AEA]-[(D)Lys] -$NH_2$ | >30000 |
| ~~67973~~ 9 |  ADWV-[hCys]-YWHTFG-[AEA]-[(D)Lys] -$NH_2$ | ~6000 |
| ~~68074~~ 0 |  QDWQCYWREN G-[AEA]-[(D)Lys] -$NH_2$ | >6000 |
| ~~68174~~ 1 |  QDWQCYWREN G-[AEA]-[(D)Lys] -$NH_2$ | ~30000 |
| ~~68274~~ 2 |  QDWQCYWREN G-[AEA]-[(D)Lys] -$NH_2$ | ~6000 |
| ~~68374~~ 3 |  QDWQCYWREN G-[AEA]-[(D)Lys] -$NH_2$ | ~6000 |
| ~~68474~~ 4 |  QDWQCYWREN G-[AEA]-[(D)Lys] -$NH_2$ | ~30000 |
| ~~68574~~ 5 |  QDWQCYWREN G-[AEA]-[(D)Lys] -$NH_2$ | >6000 |
| ~~68674~~ 6 |  QDWQ-[hCys]-YWRENG-[AEA]-[(D)Lys] -$NH_2$ | >6000 |
| ~~68774~~ 7 |  QDWQ-[hCys]-YWRENG-[AEA]-[(D)Lys] -$NH_2$ | >6000 |
| ~~68874~~ 8 |  QDWQ-[hCys]-YWRENG-[AEA]-[(D)Lys] -$NH_2$ | >6000 |

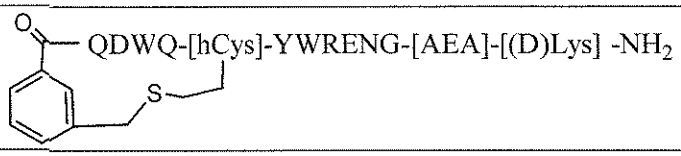
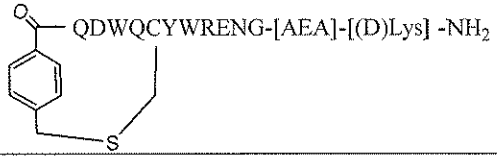
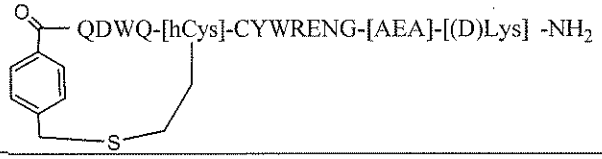
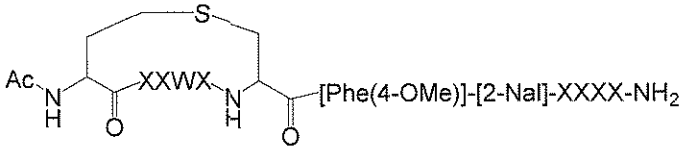
| | | |
|---|---|---|
| 68974<br>9 |  | ~30000 |
| 690 |  | >30000 |
| 691 |  | >30000 |

Table 5B. IC50 of Illustrative Peptide Inhibitors (Thioethers)




Ac-Cyclo-[[Abu]-XXWXC]-[Phe(4-OMe)]-[2-Nal]-XXX-NH $_2$

| SEQ ID NO. | Sequence | Human ELISA (nM) | Rat ELISA (nM) | pStat3 HTRF (nM |
|---|---|---|---|---|
| 692 | Ac-Cyclo-[[Abu]RTWQC]-YWRKFG-[AEA]-[(D)Lys]-$NH_2$ | *** | **** | *** |
| 693 | Ac-Cyclo-[CRTWQ-[Abu]]-YWRKFG-[AEA]-[(D)Lys]- $NH_2$ | **** | **** | *** |
| 694 | Ac-Cyclo-[[Abu]-QTWQC]-YWRENG-[AEA]-[(D)Lys]- $NH_2$ | **** | **** | *** |
| 695 | Ac-Cyclo-[[Abu]-RTWQ-[Pen]]-YWRKFG-[AEA]-[(D)Lys]- $NH_2$ | ***** | | |
| 696 | Ac- Cyclo-[[Pen]-RTWQ-[Abu]]-YWRKFG-[AEA]-[(D) Lys]-NH2 | **** | | |
| 697 | Ac-Cyclo-[[(D)Cys]-RTWQ-[Abu]]-YWRKFG-[AEA]-[(D)-Lys]- $NH_2$ | **** | | |
| 698 | Ac-Cyclo-[[Abu]-QTWQC]-YW-[Orn]-[Dap]-NG-[AEA]-[(D) Lys]- $NH_2$ | **** | | |
| 699 | Ac-Cyclo-[[Abu]-QTWQC]-YW-[hLeu]-ENG- $NH_2$ | *** | | ** |

| | | | | |
|---|---|---|---|---|
| 844 | Ac-Cyclo-[[Abu]-QT-[6-chloroTrp]-QC]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[α-MeLys]-ENG-$NH_2$ | ** | ** | * |
| 845 | Ac-Cyclo-[[Abu]-QT-[N-MeTrp]-QC]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[α-MeLys]-ENG-$NH_2$ | >3000 | | |
| 846 | Ac-Cyclo-[[Abu]-QT-[1,2,3,4-tetrahydro-norharman]-QC]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[α-MeLys]-ENG-$NH_2$ | **** | | |
| 847 | Ac-Cyclo-[[Abu]-QT-[Phe(4-CO2H)]-QC]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[α-MeLys]-ENG-$NH_2$ | >3000 | | |
| 848 | Ac-Cyclo-[[Abu]-QT-[Phe(4-CONH2)]-QC]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[α-MeLys]-ENG-$NH_2$ | >3000 | | |
| 849 | Ac-Cyclo-[[Abu]-QT-[Phe(4-CONH2)]-QC]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[α-MeLys]-ENG-$NH_2$ | >3000 | | |
| 850 | Ac-Cyclo-[[Abu]-QT-[Phe(3,4-OMe)]-QC]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[α-MeLys]-ENG-$NH_2$ | ~3000 | | |
| 851 | Ac-Cyclo-[[Abu]-QT-[α-MePhe]-QC]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[α-MeLys]-ENG-$NH_2$ | **** | | |
| 852 | Ac-Cyclo-[[Abu]-QT-[Phe(4-CF3)]-QC]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[α-MeLys]-ENG-$NH_2$ | ~3000 | | |
| 853 | Ac-Cyclo-[[Abu]-QT-[Phe(4-tBu)]-QC]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[α-MeLys]-ENG-$NH_2$ | >3000 | | |
| 854 | Ac-Cyclo-[[Abu]-QT-[Phe(2,4-Me2)]-QC]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[α-MeLys]-ENG-$NH_2$ | **** | | |
| 855 | Ac-Cyclo-[[Abu]-QTWQC]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[α-MeLys]-DNG-$NH_2$ | * | ** | * |
| 856 | Ac-Cyclo-[[Abu]-QTWQC]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[α-MeLys]-QNG-$NH_2$ | * | | * |
| 857 | Ac-Cyclo-[[Abu]-QTWQC]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[α-MeLys]-[Lys(Benzoic acid)]-NG-$NH_2$ | * | | * |

[00634] SAR analysis of the activities of the peptide inhibitors tested indicated that the CXXXXC disulphide is associated with high activity. The two Trp residues and the Phe residue are also associated with high activity, but it is recognized that these amino acids can be readily exchanged with similar homologs (e.g., 1-Nal substitued for Trp and/or Phe substituted for Tyr). In addition, the data suggested that the presence of one or more basic residues at the C-terminus is associated with high activity. Also, His-9 can be replaced by Arg or another homolog and maintain or improve activity. The schematic below provides one illustrative consensus sequence (SEQ ID NO: 275) showing certain residues associated with high activity.

1 2 3 4 5 6 7 8 9 10 11 12 13 14

Cys-Xxx-Xxx-Trp-Xxx-Cys-Tyr-Trp-His-Xxx-Phe-Xxx-Xxx-(D)Lys-OH

EXAMPLE 3

STABILITY OF PEPTIDE INHIBITORS IN SIMULATED INTESTINAL FLUID (SIF), SIMULATED GASTRIC FLUID (SGF) AND REDOX CONDITIONS

[00635] Studies were carried out in simulated intestinal fluid (SIF) and simulated gastric fluid (SGF) to evaluate gastric stability of the peptide inhibitors of the present invention. In addition, studies were carried out to assess redox stability of the peptide inhibiotrs of the present invention.

[00636] SIF was prepared by adding 6.8 g of monobasic potassium phosphate and 10.0 g of pancreatin to 1.0 L of water. After dissolution, the pH was adjusted to 6.8 using NaOH. DMSO stocks (2 mM) were first prepared for the test compounds. Aliquots of the DMSO solutions were dosed into 6 individual tubes, each containing 0.5 mL of SIF, which is pre-warmed to 37°C. The final test compound concentration was 20 μM. The vials were kept in a benchtop Thermomixer® for the duration of the experiment. At each timepoint (0, 5, 10, 20, 40, 60, or 360 minutes or 24 hours), 1.0 mL of acetonitrile containing 1% formic acid was added to one vial to terminate the reaction. Samples were stored at 4°C until the end of the experiment. After the final timepoint is sampled, the tubes were mixed and then centrifuged at 3,000 rpm for 10 minutes. Aliquots of the supernatant were removed, diluted 1:1 into distilled water containing internal standard, and analyzed by LCMS/MS. Percent remaining at each timepoint was calculated based on the peak area response ratio of test to compound to internal standard. Time 0 was set to 100%, and all

later timepoints were calculated relative to time 0. Half-lives were calculated by fitting to a first-order exponential decay equation using Graphpad. Stablity in SIF assays is shown in Tables 9 and 10.

**[00637]** SGF was prepared by adding 20 mg NaCl, 32 mg porcine pepsin (MP Biochemicals, catalog 02102599), and 70µl HCl to 10ml water (final pH=2). Aliquots of SGF (0.5ml each) were pre-warmed at 37°C. To start the reaction, 1µl of peptide stock solution (10mM in DMSO) was added to 0.5ml SGF and thoroughly mixed such that the final peptide concentration was 20µM. The reactions were incubated at 37°C with gentle shaking. At each time point (0, 15, 30, 60 min) 50µl aliquots were removed and added to 200 ul acetonitrile containing 0.1% formic acid to quench the reaction. Samples are stored at 4°C until the end of the experiment and centrifuged at 10,000 rpm for 5 minutes. Aliquots of the supernatant were removed, diluted 1:1 into distilled water containing internal standard, and analyzed by LCMS/MS. Percent remaining at each timepoint was calculated based on the peak area response ratio of test to compound to internal standard. Time 0 was set to 100%, and all later timepoints were calculated relative to time 0. Half-lives were calculated by fitting to a first-order exponential decay equation using GraphPad. Stability in SGF assays in shown in Tables 9 and 10.

Table 9. Stability of Illustrative Peptides containing the Ac-[Pen]-XXWX-[Pen]-XXXX Motif and Analogues in Simulated Intestinal Fluid (SIF) and Simulated Gastric Fluid (SGF)

| SEQ ID NO: | Sequence | SGF t1/2 (min) | SIF t1/2 (min) |
|---|---|---|---|
| 549 | Ac-[[Pen]-QTWQ-[Pen]-YW-[hLeu]-ENG-$NH_2$ | | *****§ |
| 1030 | Ac-[Pen]-QTWQ-[Pen]-YWN-Me-RENG-$NH_2$ | | ****§ |
| 551 | Ac-[Pen]-QTWQ-[Pen]-YW-[hLeu]-ENG-$NH_2$ | | *****§ |
| 552 | Ac-[Pen]-QTWQ-[Pen]-YW-[N-MeArg]-ENG-$NH_2$ | | *** |
| 554 | Ac-[Pen]-QTWQ-[Pen]-YW-[α-MeLeu]-ENG-$NH_2$ | | ** |
| 1028 | Ac-CQTWQ-[Pen]-YW-[α-MeLeu]-ENG-$NH_2$ | | ***** |
| 555 | Ac-[Pen]-QTWQ-[Pen]-YW-[(D)Asn]-ENG-$NH_2$ | | ** |
| 1029 | Ac-CQTWQ-[Pen]-YW-[(D)Asn]-ENG-$NH_2$ | | ***** |

| | | | |
|---|---|---|---|
| 556 | Ac-[Pen]-QTWQ-[Pen]-Y-[2-Nal]-[α-MeLys]-ENG-$NH_2$ | | ** |
| 557 | Ac-[Pen]-QTWQ-[Pen]-[Phe(4-OMe)]-[2-Nal]-[α-MeLys]-ENG-$NH_2$ | *** | ** |
| 558 | Ac-[Pen]-QTWQ-[Pen]-[2-Nal]-[2-Nal]-[α-MeLys]-ENG-$NH_2$ | | ** |
| 559 | Ac-[Pen]-QTWQ-[Pen]-Y-[2-Nal]-[α-MeOrn]-ENG-$NH_2$ | | ** |
| 560 | Ac-[Pen]-QTWQ-[Pen]-YW-[α-MeOrn]-ENG-$NH_2$ | | ** |
| 561 | Ac-[Pen]-QTWQ-[Pen]-Y-[1-Nal]-[α-MeOrn]-ENG-$NH_2$ | | ** |
| 1031 | Ac-[Pen]-QTWQ-[Pen]-[[Phe(4-OMe)](OMe)]-[2-Nal]-[α-MeOrn]-[Lys(Ac)]-NG-$NH_2$ | | * |
| 563 | Ac-[Pen]-QTWQ-[Pen]-YW-[α-MeLys]-[Lys(Ac)]-NG-$NH_2$ | * | * |
| 1032 | Ac-[Pen]-QTWQ-[Pen]- [Phe(4-OMe)]-W-[α-MeLys]-[Lys(Ac)]-NG-$NH_2$ | | * |
| 565 | Ac-[Pen]-QTWQ-[Pen]-[Phe(4-OMe)]-[2-Nal]-[α-MeLys]-[Lys(Ac)]-NG-$NH_2$ | * | * |
| 566 | Ac-[Pen]-QTWQ-[Pen]-[Phe(4-OMe)]-[1-Nal]-[α-MeLys]-[Lys(Ac)]-NG-$NH_2$ | | * |
| 1033 | succinic anhydride-[Pen]-QTWQ[Pen]-[Phe(4-OMe)]-[2-Nal]-[α-MeLys]-[Lys(Ac)]-NG-$NH_2$ | ** | * |
| 585 | pyroglutamic acid-[Pen]-QTWQ[Pen]-[Phe(4-OMe)]-[2-Nal]-[α-MeLys]-[Lys(Ac)]-NG-$NH_2$ | ** | * |
| 1034 | Ac-[Pen]-QTWQ-[Pen]-[Phe[4-(2-aminoethoxy)]-[2-Nal]-[α-MeLys]-[Lys(Ac)]-NN-$NH_2$ | * | * |
| 601 | Ac-[Pen]-QTWQ-[Pen]-[Phe[4-(2-aminoethoxy)]-[2-Nal]-[α-MeLys]-ENA-$NH_2$ | * | * |
| 602 | Ac-[Pen]-QTWQ-[Pen]-[Phe[4-(2-aminoethoxy)]-[2-Nal]-[α-MeLeu]-[Lys(Ac)]-NN-$NH_2$ | ** | *** |
| 603 | Ac-[Pen]-QTWQ-[Pen]-[Phe[4-(2-aminoethoxy)]-[2-Nal]-[α-MeLeu]-QNN-$NH_2$ | * | * |
| 604 | Ac-[Pen]-QTWQ-[Pen]-[Phe[4-(2-aminoethoxy)]-[2-Nal]-[Aib]-ENN-$NH_2$ | * | * |
| 605 | Ac-[Pen]-QTWQ-[Pen]-[Phe[4-(2-aminoethoxy)]-[2-Nal]-Aib-[Lys(Ac)]-NN-$NH_2$ | ** | *** |
| 606 | Ac-[Pen]-QTWQ-[Pen]-[Phe[4-(2-aminoethoxy)]-[2-Nal]-[Aib]- | * | * |

| | | | |
|---|---|---|---|
| | [Lys(Ac)]-NQ-$NH_2$ | | |
| 607 | Ac-[Pen]-Dap(Ac)TWQ-[Pen]-[Phe[4-(2-acetylaminoethoxy)]-[2-Nal]-[α-MeLys(Ac)]-ENG-$NH_2$ | * | * |
| 608 | Ac-[Pen]-[α-MeOrn(Ac)]-TWQ-[Pen]-[Phe[4-(2-acetylaminoethoxy)]-[2-Nal]-[α-MeLys(Ac)]-ENG-$NH_2$ | ** | **** |
| 609 | Ac-[Pen]-QTWQ-[Pen]-[Phe[4-(2-acetylaminoethoxy)]-[2-Nal]-[α-MeLys(Ac)]-[Lys(Ac)]-NG-$NH_2$ | * | * |
| 610 | Ac-[Pen]-QTWQ-[Pen]-[Phe[4-(2-acetylaminoethoxy)]-[2-Nal]-[α-MeLys(Ac)]-[Lys(Ac)]-NN-$NH_2$ | * | * |
| 611 | Ac-[Pen]-QTWQ-[Pen]-[Phe[4-(2-acetylaminoethoxy)]-[2-Nal]-[α-MeLys(Ac)]-ENG-$NH_2$ | * | ** |
| 612 | Ac-[Pen]-QTWQ-[Pen]-[Phe[4-(2-acetylaminoethoxy)]-[2-Nal]-[α-MeLys(Ac)]-ENA-$NH_2$ | * | * |
| 613 | Ac-[Pen]-QTWQ-[Pen]-[Phe[4-(2-acetylaminoethoxy)]-[2-Nal]-[α-MeLeu]-[Lys(Ac)]-NN-$NH_2$ | * | * |
| 614 | Ac-[Pen]-QTWQ-[Pen]-[Phe[4-(2-acetylaminoethoxy)]-[2-Nal]-[α-MeLeu]-QNN-$NH_2$ | * | * |
| 615 | Ac-[Pen]-QTWQ-[Pen]-[Phe[4-(2-acetylaminoethoxy)]-[2-Nal]-[Aib]-ENN-$NH_2$ | * | * |
| 616 | Ac-[Pen]-QTWQ-[Pen]-[Phe[4-(2-acetylaminoethoxy)]-[2-Nal]-[Aib]-[Lys(Ac)]-NN-$NH_2$ | * | * |
| 617 | Ac-[Pen]-QTWQ-[Pen]-[Phe[4-(2-acetylaminoethoxy)]-[2-Nal]-[Aib]-[Lys(Ac)]-NQ-$NH_2$ | * | * |
| 522 | [Ac-[Pen]-QTWQ-[Pen]-[Phe(4-OMe)]-[2-Nal]-[α-MeLys]-ENG-$NH_2$]$_2$ DIG | **** | * |
| 618 | Ac-[Pen]-QTWQ-[Pen]-[Phe(4-OMe)]-[2-Nal]-[Aib]-ENN-$NH_2$ | * | *** |
| 619 | Ac-[Pen]-QTWQ-[Pen]-[Phe[4-(2-aminoethoxy)]-[2-Nal]-[hLeu]-ENA-$NH_2$ | ***** | ***** |
| 620 | Ac-[Pen]-TTWQ-[Pen]-[Phe[4-(2-aminoethoxy)]-[2-Nal]-[Aib]-[Lys(Ac)]-NN-$NH_2$ | * | * |
| 625 | Ac-[Pen]-QTWQ-[Pen]-[Phe(4-OMe)]-[2-Nal]-[Aib]-[Lys(Ac)]-NN-$NH_2$ | * | ** |
| 628 | Ac-[Pen]-QTWQ-[Pen]-[Phe[4-(2-aminoethoxy)]-[2-Nal]-[Aib]-[Lys(Ac)]-N-[βAla]-$NH_2$ | * | * |

| | | | |
|---|---|---|---|
| 630 | Ac-[Pen]-NTWQ-[Pen]-[Phe(4-OMe)]-[2-Nal]-[Aib]-ENN-$NH_2$ | * | *** |
| 631 | Ac-[Pen]-NTWQ-[Pen]-[Phe[4-(2-aminoethoxy)]-[2-Nal]-[hLeu]-ENA-$NH_2$ | ***** | **** |
| 632 | Ac-[Pen]-NTWQ-[Pen]-[Phe[4-(2-aminoethoxy)]-[2-Nal]-[Aib]-[Lys(Ac)]-NN-$NH_2$ | * | * |
| 633 | Ac-[Pen]-NTWQ-[Pen]-[Phe(4-OMe)]-[2-Nal]-[Aib]-[Lys(Ac)]-N-[βAla]-$NH_2$ | * | ** |
| 634 | Ac-[Pen]-NTWQ-[Pen]-[Phe[4-(2-aminoethoxy)]-[2-Nal]-[Aib]-[Lys(Ac)]-NQ-$NH_2$ | * | * |
| 636 | Ac-[Pen]-NTWQ-[Pen]-[Phe[4-(2-aminoethoxy)]-[2-Nal]-[Aib]-[Lys(Ac)]-NA-$NH_2$ | * | * |
| 637 | Ac-[Pen]-NTWQ-[Pen]-[Phe(4-OMe)]-[2-Nal]-[Aib]-[Lys(Ac)]-NN-$NH_2$ | * | * |
| 638 | Ac-[Pen]-NTWQ-[Pen]-[Phe(4-OMe)]-[2-Nal]-[Aib]-[Lys(Ac)]-NQ-$NH_2$ | * | * |
| 639 | Ac-[Pen]-NTWQ-[Pen]-[Phe[4-(2-aminoethoxy)]-[2-Nal]-[Aib]-[Lys(Ac)]-N-[βAla]-$NH_2$ | * | * |
| 640 | Ac-[Pen]-NTWQ-[Pen]-[Phe(4-OMe)]-[2-Nal]-[hLeu]-[Lys(Ac)]-N-[βAla]-$NH_2$ | ***** | ***** |
| 641 | Ac-[Pen]-NTWQ-[Pen]-[Phe[4-(2-aminoethoxy)]-[2-Nal]-[hLeu]-[Lys(Ac)]-N-[βAla]-NH2 | ***** | ***** |
| 669 | Ac-[Pen]-QTWQ-[Pen]-[Phe(4-$CONH_2$)]-[2-Nal]-[α-MeVal]-[Lys(Ac)]-NN-$NH_2$ | ** | * |
| 534 | [Ac-[Pen]-QTWQ-[Pen]-[Phe(4-$CONH_2$)]-[2-Nal]-[α-MeLys]-[Lys(Ac)]-NN-$NH_2$]$_2$ DIG | ** | * |
| 1035 | Ac-[(D)Phe]-[Pen]-NTWQ-[Pen]-[Phe[4-(2-aminoethoxy)]-[2-Nal]-[Aib]-[Lys(Ac)]-NN-$NH_2$ | * | * |
| 676 | Ac-[(D)Phe]-[Pen]-NTWQ-[Pen]-[Phe[4-(2-aminoethoxy)]-[2-Nal]-[Aib]-[Lys(Ac)]-N-[βAla]-$NH_2$ | ** | * |
| 682 | Ac-[Pen]-NTWQ[Pen]-[Phe(4-$CONH_2$)]-[2-Nal]-[Aib]-[Lys(Ac)]-NN-$NH_2$ | ** | **** |
| 683 | Ac-[Pen]-NTWQ[Pen]-[Phe(4-$CONH_2$)]-[2-Nal]-[4-amino-4-carboxy-tetrahydropyran]-Lys(Ac)]-NN-$NH_2$ | ** | * |
| 684 | Ac-[Pen]-NTWQ[Pen]-[Phe(4-$CONH_2$)]-[2-Nal]-[Achc]- [Lys(Ac)]-NN-NH2 | * | * |

| | | | |
|---|---|---|---|
| 1036 | Ac-[Pen]-NTWQ[Pen]-[Phe(4-$CONH_2$)]-[2-Nal]-[Acvc]- [Lys(Ac)]-NN-$NH_2$ | * | * |
| 686 | Ac-[Pen]-NTWQ[Pen]-[Phe(4-$CONH_2$)]-[2-Nal]-[α-MeLeu]-[Lys(Ac)]-NN-$NH_2$ | * | * |
| 688 | Ac-[Pen]-NTWQ[Pen]-[Phe(4-OMe)]-[2-Nal]-[4-amino-4-carboxy-tetrahydropyran]-[Lys(Ac)]-NN-$NH_2$ | * | * |
| 689 | Ac-[Pen]-NTWQ[Pen]-[Phe(4-OMe)]-[2-Nal]-[Achc]-[Lys(Ac)]-NN-$NH_2$ | * | ** |
| 1037 | Ac-[Pen]-NTWQ[Pen]-[Phe(4-OMe)]-[2-Nal]-[Acvc]-[Lys(Ac)]-NN-$NH_2$ | ** | * |
| ~~671~~731 | Ac-[Pen]-NTWQ[Pen]-[Phe(4-OMe)]-[2-Nal]-[α-MeLeu]-[Lys(Ac)]-NN-$NH_2$ | * | * |
| 535 | [Ac-[Pen]-NTWQ-[Pen]-[Phe(4-$CONH_2$)]-[2-Nal]-[Aib]-KNN-$NH_2$]$_2$ DIG | ** | ** |
| 536 | [Ac-[Pen]-NTWQ-[Pen]-[Phe(4-$CONH_2$)]-[2-Nal]-[4-amino-4-carboxy-tetrahydropyran]-KNN-$NH_2$]$_2$ DIG | * | * |
| 537 | [Ac-[Pen]-NTWQ-[Pen]-[Phe(4-$CONH_2$)]-[2-Nal]-[Achc]-KNN-$NH_2$]$_2$ DIG | ** | *** |
| 539 | [Ac-[Pen]-NTWQ-[Pen]-[Phe(4-$CONH_2$)]-[2-Nal]-[α-MeLeu]-KNN-$NH_2$]$_2$ DIG | ** | ** |

§ the matrix used is 100 fold dilution of standard SIF concentration
*=>360min; **=180-360minn; ***=120-180min; ****=<60-120min; *****=<60min

Table 10. Stability of Illustrative Peptides Containing Thioethers Motif and Analogues Within Simulated Intestinal Fluid (SIF) and Simulated Gastric Fluid (SGF)

| SEQ ID NO: | Sequence | SIF t1/2 (min) | SGF t1/2 (min) |
|---|---|---|---|
| 692 | Ac-Cyclo-[[Abu]RTWQC]-YWRKFG-[AEA]-[(D)Lys]-$NH_2$ | ***** | |
| 694 | Ac-Cyclo-[[Abu]-QTWQC]-YWRENG-[AEA]-[(D)Lys]- $NH_2$ | ***** | |
| 699 | Ac-Cyclo-[[Abu]-QTWQC]-YW-[hLeu]-ENG- $NH_2$ | ***** | ND |
| 700 | Ac-Cyclo-[Abu]-QTWQ-(D)Cys]]-YW-[hLeu]-ENG-$NH_2$ | **** § | |
| 701 | Ac-Cyclo-[[Abu]-QTWQ-[Pen]]-YW-[hLeu]-ENG-$NH_2$ | ***** | |

| | | | |
|---|---|---|---|
| 703 | Ac-Cyclo-[[Abu]-QTWQC]-YW-[α-MeLeu]-ENG-$NH_2$ | ***** | |
| 704 | Ac-Cyclo-[[Abu]-QTWQC]-Y-[2-Nal]-[α-MeLys]-ENG-$NH_2$ | ***** | |
| 702 | Ac-Cyclo-[[Abu]-QTWQC]-[Phe(4-OMe)]-[2-Nal]-[α-MeLys]-ENG-$NH_2$ | *** | ***** |
| 706 | Ac-Cyclo-[[Abu]-QTWQC]-[Phe(4-OMe)]-[2-Nal]-[α-MeOrn]-ENG-$NH_2$ | *** | ***** |
| 707 | Ac-Cyclo-[[Abu]-QTWQC]-[Phe(4-OMe)]-W-[α-MeOrn]-ENG-$NH_2$ | ** | ***** |
| 702 | Ac-Cyclo-[[Abu]-QTWQC]-[Phe(4-OMe)]-[2-Nal]-[α-MeLys]-ENG-$NH_2$ | ** | ***** |
| 709 | Ac-Cyclo-[[Abu]-QTWQC]-[Phe(4-OMe)]-W-[α-MeLys]-[Lys(Ac)]-NG-$NH_2$ | * | ***** |
| 710 | Ac-Cyclo-[[Abu]-QTWQC]-[Phe(4-OMe)]-W-[α-MeLys]-ENG-$NH_2$ | * | ***** |
| 711 | Ac-Cyclo-[[Abu]-QTWQC]-[Phe(4-OMe)]-[1-Nal]-[α-MeLys]-[Lys(Ac)]-NG-$NH_2$ | * | ***** |
| 712 | Ac-Cyclo-[[Abu]-QTWQC]-[Phe(4-OMe)]-[2-Nal]-[α-MeLys]-[Lys(Ac)]-NG-$NH_2$ | ** | ***** |
| 713 | Ac-Cyclo-[[Abu]-QTWQC]-YW-[α-MeOrn]-[Lys(Ac)]-NG-$NH_2$ | ** | |
| 714 | Ac-Cyclo-[[Abu]-QTWQC]-[Phe(4-OMe)]-[2-Nal]-[(D)Asn]-[Lys(Ac)]-NG-$NH_2$ | * | |
| 715 | Ac-Cyclo-[[Abu]-QTWQC]-[Phe(4-Phenoxy)]-[2-Nal]-[α-MeLys]-[Lys(Ac)]-NG-$NH_2$ | * | |
| 716 | Ac-Cyclo-[[Abu]-QTWQC]-[hPhe(3,4-dimethoxy)]-[2-Nal]-[α-MeLys]-[Lys(Ac)]-NG-$NH_2$ | ** | |
| 717 | Ac-Cyclo-[[Abu]-QTWQC]-[DMT]-[2-Nal]-[α-MeLys]-[Lys(Ac)]-NG-$NH_2$ | * | |
| 718 | Ac-Cyclo-[[Abu]-QTWQC]-[Phe(4-$CONH_2$)]-[2-Nal]-[α-MeLys]-[Lys(Ac)]NG-$NH_2$ | *** | ***** |
| 719 | Ac-Cyclo-[[Abu]-QTWQC]-Phe(3,4-$Cl_2$)[2-Nal]-[α-MeLys]-[Lys(Ac)]NG-$NH_2$ | *** | |
| 720 | Ac-Cyclo-[[Abu]-QTWQ-[Pen]]-[Phe(4-OMe)]-[2-Nal]-[α-MeLys]-ENG-$NH_2$ | ** | *** |
| 721 | Ac-Cyclo-[[Abu]-QTWQ-[Pen]]-[Phe(4-OMe)]-[2-Nal]-[α-MeLys]-[Lys(Ac)]NG-$NH_2$ | ** | *** |
| 782 | Ac-Cyclo-[[Abu]-QTWQC]-[Phe[4-(2-aminoethoxy)]-W-[α-MeLys]-ENG-$NH_2$ | * | *** |
| 790 | Ac-Cyclo-[[Abu]-QTWQC]-[Phe(4-OMe)]-[2-Nal]-[α-MeOrn]-[Lys(Ac)]-NG-$NH_2$ | *** | ***** |
| 791 | Ac-Cyclo-[[Abu]-QTWQC]-[2-Nal]-[2-Nal]-[α-MeOrn]-[Lys(Ac)]-NG-$NH_2$ | *** | ND |

| | | | |
|---|---|---|---|
| 794 | Ac-Cyclo-[[Abu]-QTWQC]-[2-Nal]-[2-Nal]-[α-MeLys]-[Lys(Ac)]-NG-$NH_2$ | ** | ND |
| 797 | Ac-Cyclo-[[Abu]-QTWQC]-[Phe(4-$CONH_2$)]-[2-Nal]-[α-MeLys]-[Lys(Ac)]-NG-$NH_2$ | **** | ***** |
| 798 | Ac-Cyclo-[[Abu]-QTWQC]-[2-Nal]-[2-Nal]-[α-MeLys]-ENG-$NH_2$ | ** | ND |
| 810 | Ac-Cyclo-[[Abu]-QTWQC]-[Phe(4-OMe)]-[2-Nal]-[Aib]-[Lys(Ac)]-NG-$NH_2$ | * | |
| 815 | Ac-Cyclo-[[Abu]-QTWQC]-[Phe(4-OMe)]-[2-Nal]-[Orn]-[Lys(Ac)]-NG- $NH_2$ | * | |
| 820 | Ac-Cyclo-[[Abu]-QTWQC]-[Phe(4-OMe)]-[2-Nal]-[Chg]-[Lys(Ac)]-NG-$NH_2$ | *** | |
| 822 | Ac-Cyclo-[[Abu]-QTWQC]-[Octgly]-[2-Nal]-[α-MeLys]-[Lys(Ac)]-NG-$NH_2$ | ***** | |
| 823 | Ac-Cyclo-[[Abu]-QTWQC]-[Phe(4-OMe)]-[Octgly]-[α-MeLys]-[Lys(Ac)]-NG-$NH_2$ | **** | |
| 823 | Ac-Cyclo-[[Abu]-QTWQC]-[Phe(4-OMe)]-[Octgly]-[α-MeLys]-[Lys(Ac)]-NG-$NH_2$ | ***** | |
| 829 | Ac-Cyclo-[[Abu]-QTWQC]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[α-MeLys]-ENG-$NH_2$ | * | * |
| 857 | Ac-Cyclo-[[Abu]-QTWQC]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[α-MeLys]-[Lys(Benzoic acid)]-NG-$NH_2$ | ** | * |
| 861 | Ac-Cyclo-[[Abu]-QTWQC]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[α-MeLys]-[Lys(isovaleric acid)]-NG-$NH_2$ | * | * |
| 876 | Ac-Cyclo-[[Abu]-QTWQC]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[Aib]-[Lys(Ac)]-QG-$NH_2$ | *** | ***** |
| 877 | Ac-Cyclo-[[Abu]-QTWQC]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[Aib]-QNG-$NH_2$ | *** | ** |
| 878 | Ac-Cyclo-[[Abu]-QTWQC]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[Aib]-ENG-$NH_2$ | ***** | *** |
| 879 | Ac-Cyclo-[[Abu]-QTWQC]-[Phe[4-(2-aminoethoxy)]]-1-Nal[Aib]-[Lys(Ac)]-NG-$NH_2$ | * | * |
| 880 | Ac-Cyclo-[[Abu]-QTWQC]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[Aib]-[Lys(Ac)]-NA-$NH_2$ | **** | ***** |
| 891 | Ac-Cyclo-[[Abu]-QTWQC]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[α-Me-Orn]-[Lys(Ac)]-NG-$NH_2$ | ** | ** |
| 892 | Ac-Cyclo-[[Abu]-QTWQC]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[α-MeLys]-[Lys(Ac)]-NG-$NH_2$ | * | * |
| 893 | Ac-Cyclo-[[Abu]-QTWQC]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[Orn]-[Lys(Ac)]-NG-$NH_2$ | ***** | |
| 894 | Ac-Cyclo-[[Abu]-QTWQC]-[Phe[4-(2-aminoethoxy)]]-W-[Orn]-ENG-$NH_2$ | ***** | |
| 895 | Ac-Cyclo-[[Abu]-QTWQC]-[Phe[4-(2-aminoethoxy)]]-W-[Orn]-[Dap]-NG-$NH_2$ | ***** | |

| | | | |
|---|---|---|---|
| 896 | Ac-Cyclo-[[Abu]-QTWQC]-[Phe[4-(2-aminoethoxy)]]-W-[Orn]-[Dap(Ac)]-NG-$NH_2$ | ***** | |
| 897 | Ac-Cyclo-[[Abu]-QTWQC]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[Orn]-[Dap]-NG-$NH_2$ | ***** | |
| 898 | Ac-Cyclo-[[Abu]-QTWQC]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[Orn]-[Dap(Ac)]-NG-$NH_2$ | ***** | |
| 899 | Ac-Cyclo-[[Abu]-QTWQC]-[Phe[4-(2-aminoethoxy)]]-W-[hLeu]-ENG-$NH_2$ | ***** | ***** |
| 900 | Ac-Cyclo-[[Abu]-QTWQC]-[Phe[4-(2-(acetyl-aminoethoxy)]]-[2-Nal]-[α-MeLys(Ac)]-[Lys(Ac)]-NG-$NH_2$ | ** | ***** |
| 901 | Ac-Cyclo-[[Abu]-QTWQC]-[Phe[4-(2-aminoethoxy)]]-W-[α-Me-Leu]-ENG-NH2 | * | ** |
| 902 | Succicinyl-Cyclo-[[Abu]-QTWQC]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[α-MeLys]-[Lys(Ac)]-NG-NH2 | * | ** |
| 906 | Ac-Cyclo-[[Abu]-QTWQC]-[Phe[4-(2-(acetyl-aminoethoxy)]]-[2-Nal]-[α-MeLys(Ac)]-ENG-$NH_2$ | **** | ***** |
| 820 | Ac-Cyclo-[[Abu]-QTWQC]-[Phe(4-OMe)]-[2-Nal]-[Chg]-[Lys(Ac)]-NG-$NH_2$ | * | ** |
| 911 | Ac-Cyclo-[[Abu]-QTWQC]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[α-MeLys]-ENQ-$NH_2$ | ** | ** |
| 912 | Ac-Cyclo-[[Abu]-QTWQC]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[α-MeLys]-ENN-$NH_2$ | ** | ** |
| 913 | Ac-Cyclo-[[Abu]-TTWQC]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[α-MeLys]-ENG-$NH_2$ | ** | ** |
| 914 | Ac-Cyclo-[[Abu]-QTWQC]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[α-Me-Gly(Ethyl)] Lys(Ac)]-NG-$NH_2$ | **** | ***** |
| 915 | Ac-Cyclo-[[Abu]-QTWQC]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[α-MeVal]-[Lys(Ac)]-NG-$NH_2$ | *** | **** |
| 916 | Ac-Cyclo-[[Abu]-QTWQC]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[α-MeSer]-[Lys(Ac)]-NG-$NH_2$ | ***** | *** |
| 925 | Ac-(D)Lys-[Cyclo-[[Abu]-QTWQC]]-[Phe(4-OMe)]-[2-Nal]-[α-MeLeu]-ENG-$NH_2$ | **** | ***** |
| 1039 | [Ac-[(D)Lys]-Cyclo-[[Abu]-QTWQC]-[Phe(4-OMe)]-[2-Nal]-[α-MeLeu]-ENG-$NH_2$]$_2$ DIG : dimerization through (D)Lys | **** | ***** |
| 930 | Ac-Cyclo-[[Abu]-QTWQC]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[hLeu]-[Lys(Ac)]-N-[βAla]-$NH_2$ | ***** | ND |
| 933 | Ac-Cyclo-[[Abu]-QTWQC]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[α-MeLys]-NNG-$NH_2$ | ** | ** |
| 946 | Ac-Cyclo-[[Abu]-QTWQC]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[Aib]-[Lys(Ac)]-NG-$NH_2$ | **** | **** |
| 955 | Ac-Cyclo-[[Abu]-QTWQC]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[α-MeLeu]-[Lys(Ac)]-NN-$NH_2$ | *** | ***** |
| 1040 | [Ac-Cyclo-[[Abu]-QTWQC]-Y(Bzl)-W-[α-MeLys]-ENG-$NH_2$]$_2$; PEG25 through [α-MeLys] | ** | ***** |

| | | | |
|---|---|---|---|
| 965 | Ac-E-Cyclo-[[Abu]-QTWQC]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[α-MeLys]-ENN-$NH_2$ | * | *** |
| 966 | Ac-(D)Glu-[Cyclo-[[Abu]-QTWQC]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[α-MeLys]-ENN-$NH_2$ | * | **** |
| 967 | Ac-Arg-Cyclo-[[Abu]-QTWQC]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[α-MeLys]-ENN-$NH_2$ | ***** | *** |
| 1041 | Ac-[(D)Arg-Cyclo-[[Abu]-QTWQC]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[α-MeLys]-ENN-$NH_2$ | * | ** |
| 969 | Ac-F-Cyclo-[[Abu]-QTWQC]]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[α-MeLys]-ENN-$NH_2$ | **** | *** |
| 970 | Ac-[(D)Phe]-Cyclo-[[Abu]-QTWQC]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[α-MeLys]-ENN-$NH_2$ | ** | *** |
| 972 | Ac-T-Cyclo-[[Abu]-QTWQC]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[α-MeLys]-ENN-$NH_2$ | * | *** |
| 973 | Ac-Leu-Cyclo-[[Abu]-QTWQC]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[α-MeLys]-ENN-$NH_2$ | * | *** |
| 1042 | Ac-[(D)~~Qln~~Gln]-Cyclo-[[Abu]-QTWQC]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[α-MeLys]-ENN-$NH_2$ | * | *** |
| 975 | Ac-Cyclo-[[Abu]-QTWQC]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[Acpc]-ENN-$NH_2$ | ***** | * |
| 976 | Ac-Cyclo-[[Abu]-QTWQC]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[Acbc]-ENN-$NH_2$ | ***** | **** |
| 1043 | Ac-Cyclo-[[Abu]-QTWQC]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[Acpc]- ENN-$NH_2$ | ** | * |
| 978 | Ac-Cyclo-[[Abu]-QTWQC]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[Acvc]-ENN-$NH_2$ | *** | * |
| 979 | Ac-Cyclo-[[Abu]-QTWQC]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[4-amino-4-carboxy-piperidine]-ENN-$NH_2$ | * | * |
| 972 | Ac-T-Cyclo-[[Abu]-QTWQC]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[α-MeLys]-ENN-$NH_2$ | * | * |

§ the matrix used is 100 fold dilution of standard SIF concentration
*=>360min; **=180-360minn; ***=120-180min; ****=<60-120min; *****=<60min

**[00638]** For each peptide tested, the DTT stability assay was conducted by adding 5µl of a 10mM peptide stock solution in DMSO to 1ml of 100mM Tris-Cl, pH 7.5 (final peptide concentration is 50µM). At time 0 min, 5ul of a freshly thawed 100mM DTT solution was added to the incubation tube containing the peptide, such that the final DTT concentration was 0.5mM. The reactions were incubated at room temperature. At different time points up to 120 minutes (20 min, 40 min, 80 min, 120 min), 50µl aliquots were removed, and the reaction was quenched by adding 10µl of 5M acetic acid. To measure disappearance of the parent peptide, the quenched samples (30µl) were analyzed by reverse phase HPLC and UV absorbance at 220nm. The

fraction oxidized remaining was graphed versus time, and half-lives were calculated by fitting to a first-order exponential decay equation using Excel. The results of these studies are shown in Table 11. The peptides having half-life >120 min are all considered stable.

Table 11. Stability of Illustrative Peptides in DTT Assay

| SEQ ID NO: | Sequence | DTT Stability (min) |
|---|---|---|
| 217 | Ac-CRTWECYWHEFG-$NH_2$ | <10 |
| 1044 | Ac-CQTWQCYW-[hLeu]-ENG-$NH_2$ | * |
| 1045 | Ac-CADWVWCYWHTFGA-[Azt]-[(D)Lys]-$NH_2$ | * |
| 1046 | Ac-Cyclo-[[Abu]-RTWQC]-YWRKFG-[AEA]-[(D)Lys]-$NH_2$ | >120 |
| 549 | Ac-[[Pen]-QTWQ-[Pen]-YW-[hLeu]-ENG-$NH_2$ | >120 |
| 554 | Ac-[Pen]-QTWQ-[Pen]-YW-[α-MeLeu]-ENG-$NH_2$ | >120 |
| 702 | Ac-Cyclo-[[Abu]-QTWQC]-[Phe(4-OMe)]-[2-Nal]-[α-MeLys]-ENG-$NH_2$ | >120 |
| 557 | Ac-[Pen]-QTWQ-[Pen]-[Phe(4-Ome)]-[2-Nal]-[α-MeLys]-ENG-$NH_2$ | >120 |
| 782 | Ac-Cyclo-[[Abu]-QTWQC]-[Phe[4-(2-aminoethoxy)]-W-[α-MeLys]-ENG-$NH_2$ | >120 |
| 980 | Ac-Cyclo-[[Abu]-QTWQC]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[4-amino-4-carboxy-tetrahydropyran]-ENN-$NH_2$ | >120 |
| 534 | [Ac-[Pen]-QTWQ-[Pen]-[Phe(4-$CONH_2$)]-[2-Nal]-[α-MeLys]-[Lys(Ac)]-NN-$NH_2$]$_2$ DIG | >120 |

*=10-120 min

## EXAMPLE 4

### CROSS-REACTIVITY OF PEPTIDE INHIBITORS

**[00639]** The amino acids of the extracellular domain of the human IL-23R are 95%, 77% and 70% identical to the cyno IL-23R, rat IL-23R and mouse IL-23R, respectively. Interestingly, the mouse receptor contains an insertion of 21 residues that are absent in human, mouse, chimp, dog and cow receptor. These additional amino acids are located in a region where human IL-23R is thought to bind to IL-23.

**[00640]** To identify peptide inhibitors that cross-reacted with species other than human IL-23R, the ability of certain peptide inhibitors to inhibit human IL-23R, cyno IL-23R, rat IL-23R and mouse IL-23R by ELISA assay. In line with the observation regarding the sequence differences between human IL-23R and mouse IL-23R, the peptide antagonists tested showed a lack of or

**[00646]** Natural killer (NK) cells, purified from human peripheral blood of healthy donors by negative selection (Miltenyi Biotech, Cat # 130-092-657), were cultured in complete media (RPMI 1640 containing 10% FBS, L-glutamine and penicillin-streptomycin) in the presence of IL-2 (RnD, Cat # 202-IL-010/CF) at 25 ng/mL. After 7 days, cells were centrifuged, and resuspended in complete media at 1E6 cells/mL. Recombinant IL-23 at predetermined EC50 to EC75 and IL-18 (RnD, Cat # B003-5) at 10 ng/mL were mixed with varying concentrations of peptides, and added to NK cells seeded at 1E5 cells per well. After 20 to 24 hours, IFNγ in the supernatant was quantified using Quantikine ELISA (RnD, Cat # DIF50).

Table 13. IC50 of Illustrative Peptide Inhibitors in Primary Cell Line (NK Cell Assay)

| SEQ ID NO: | Sequence | NK cell assay (nM) |
|---|---|---|
| 704 | Ac-Cyclo-[[Abu]-QTWQC]-Y-[2-Nal]-[α-MeLys]-ENG-$NH_2$ | * |
| 702 | Ac-Cyclo-[[Abu]-QTWQC]-[Phe(4-OMe)]-[2-Nal]-[α-MeLys]-ENG-$NH_2$ | * |
| 782 | Ac-Cyclo-[[Abu]-QTWQC]-[Phe[4-(2-aminoethoxy)]-W-[α-MeLys]-ENG-$NH_2$ | * |
| 861 | Ac-Cyclo-[[Abu]-QTWQC]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[α-MeLys]-[Lys(isovaleric acid)]-NG-$NH_2$ | * |
| 877 | Ac-Cyclo-[[Abu]-QTWQC]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[Aib]-QNG-$NH_2$ | * |
| 880 | Ac-Cyclo-[[Abu]-QTWQC]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[Aib]-[Lys(Ac)]-NA-$NH_2$ | * |
| 900 | Ac-Cyclo-[[Abu]-QTWQC]-[Phe[4-(2-(acetyl-aminoethoxy)]]-[2-Nal]-[α-MeLys(Ac)]-[Lys(Ac)]-NG-$NH_2$ | * |
| 908 | Ac-Cyclo-[[Abu]-QTWQC]-[Phe[4-(2-aminoethoxy)]]-[Phe(3,4-$OMe_2$]-[α-MeLys]-[Lys(Ac)]-NG-$NH_2$ | * |
| 911 | Ac-Cyclo-[[Abu]-QTWQC]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[α-MeLys]-ENQ-$NH_2$ | * |
| 912 | Ac-Cyclo-[[Abu]-QTWQC]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[α-MeLys]-ENN-$NH_2$ | * |
| 915 | Ac-Cyclo-[[Abu]-QTWQC]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[α-MeVal]-[Lys(Ac)]-NG-$NH_2$ | * |

| | | |
|---|---|---|
| 1038 | [Ac-Cyclo-[[Abu]-QTWQC]-[Phe(4-OMe)]-[2-Nal]-[α-MeLys]-ENG-NH2]$_2$; DIG through α-MeLys | * |
| 954 | Ac-Cyclo-[[Abu]-QTWQC]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[α-MeLeu)-[Cit]-NN-$NH_2$ | * |
| 970 | Ac-[(D)Phe]-Cyclo-[[Abu]-QTWQC]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[α-MeLys]-ENN-$NH_2$ | * |
| 972 | Ac-T-Cyclo-[[Abu]-QTWQC]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[α-MeLys]-ENN-$NH_2$ | * |
| 976 | Ac-Cyclo-[[Abu]-QTWQC]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[Acbc]-ENN-$NH_2$ | * |
| 1043 | Ac-Cyclo-[[Abu]-QTWQC]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[Acpc]- ENN-$NH_2$ | * |
| 1047 | Ac-Cyclo-[[Abu]-QTWQC]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[Achc]-ENN-$NH_2$ | * |
| 980 | Ac-Cyclo-[[Abu]-QTWQC]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[4-amino-4-carboxy-tetrahydropyran]-ENN-$NH_2$ | * |
| 984 | Ac-Cyclo-[[Abu]-QTWQC]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[α-MeLeu]-QN-[βAla]-$NH_2$ | * |
| 992 | Ac-(D)Phe-Cyclo-[[Abu]-QTWQC]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[4-amino-4-carboxy-tetrahydropyran]-ENN-$NH_2$ | * |
| 993 | Ac-[(D)Arg]-Cyclo-[[Abu]-QTWQC]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[4-amino-4-carboxy-tetrahydropyran]-ENN-$NH_2$ | * |

*=<25nM

Table 14. IC50 of Illustrative Peptides Containing the Ac-[Pen]-XXWX-[Pen]-XXXX Motif and analogues (NK cell assay)

| SEQ ID NO: | Sequence | NK Cell assay (nM) |
|---|---|---|
| 602 | Ac-[Pen]-QTWQ-[Pen]-[Phe[4-(2-aminoethoxy)]-[2-Nal]-[α-MeLeu]-[Lys(Ac)]-NN-$NH_2$ | * |
| 632 | Ac-[Pen]-NTWQ-[Pen]-[Phe[4-(2-aminoethoxy)]-[2-Nal]-[Aib]-[Lys(Ac)]-NN-$NH_2$ | * |
| 639 | Ac-[Pen]-NTWQ-[Pen]-[Phe[4-(2-aminoethoxy)]-[2-Nal]-[Aib]-[Lys(Ac)]-N-[βAla]-$NH_2$ | * |
| 666 | Ac-[Pen]-QTWQ-[Pen]-[Phe(4-OMe)]-[2-Nal]-[α-MeLys]-[Lys(Ac)]-NN-$NH_2$ | * |

| | | |
|---|---|---|
| 668 | Ac-[Pen]-QTWQ-[Pen]-[Phe(4-CONH2)]-[2-Nal]-[α-MeLys]-[Lys(Ac)]-NN-$NH_2$ | * |
| 669 | Ac-[Pen]-QTWQ-[Pen]-[Phe(4-CONH2)]-[2-Nal]-[α-MeVal]-[Lys(Ac)]-NN-$NH_2$ | ** |
| 530 | [Ac-[Pen]-QTWQ[Pen]-[Phe[4-(2-acetylaminoethoxy)]-[2-Nal]-[α-MeVal]-KNN-$NH_2$]$_2$ DIG | * |
| 531 | [Ac-[Pen]-QTWQ[Pen]-[Phe[4-(2-acetylaminoethoxy)]-[2-Nal]-K-[Lys(Ac)]-NN-$NH_2$]$_2$ DIG | * |
| 532 | [Ac-[Pen]-QTWQ-[Pen]-[Phe(4-OMe)]-[2-Nal]-[α-MeLys]-[Lys(Ac)]-NN-$NH_2$]$_2$ DIG | * |
| 534 | [Ac-[Pen]-QTWQ-[Pen]-[Phe(4-$CONH_2$)]-[2-Nal]-[α-MeLys]-[Lys(Ac)]-NN-$NH_2$]$_2$ DIG | * |
| 1048 | Ac-[(D)Phe]-[Pen]-NTWQ[Pen]-[Phe(4-OMe)]-[2-Nal]-[4-amino-4-carboxy-tetrahydropyran]-[Cit]-NN-$NH_2$ | * |
| 1049 | Ac-[(D)Phe]-[Pen]-NTWQ[Pen]-[Phe(4-OMe)]-[2-Nal]-[Achc]-ENN-$NH_2$ | * |
| 1050 | Ac-[Pen]-NTWQ[Pen]-[Phe($CONH_2$)]-[2-Nal]-[Aib]-[Lys(Ac)]-NN-$NH_2$ | * |
| 535 | [Ac-[Pen]-NTWQ-[Pen]-[Phe(4-$CONH_2$)]-[2-Nal]-[Aib]-KNN-$NH_2$]$_2$ DIG | * |

*=<10nM; **=10-25nM

## EXAMPLE 6

### BIOASSAY CHARACTERIZATION OF PEPTIDE INHIBITORS

**[00647]** The potency, cross reactivity, and selectivity of certain peptide inhibitors was determined using various bioassays developed for this purpose and described below.

Rat Splenocyte Assay

**[00648]** A new assay developed was the rat splenocyte assay. This assay examined the levels of IL-17A in activated rat splenocytes following stimulation with IL-23 in the presence of test compound.

**[00649]** Briefly, splenocytes freshly isolated from rat were seeded in 96-well tissue culture plates in complete medium containing concanavalin A. Serial dilutions of test compounds were distributed to each well along with rat IL-23 at a final concentration of 4 ng/mL; plates then were incubated for 3 days at 37 °C in a 5% $CO_2$ humidified incubator. Changes in IL-17A levels in the supernatants were detected using an ELISA. Figure 1 shows an example of IL-17A levels produced by rat splenocytes in response to rat IL-23 stimulation.

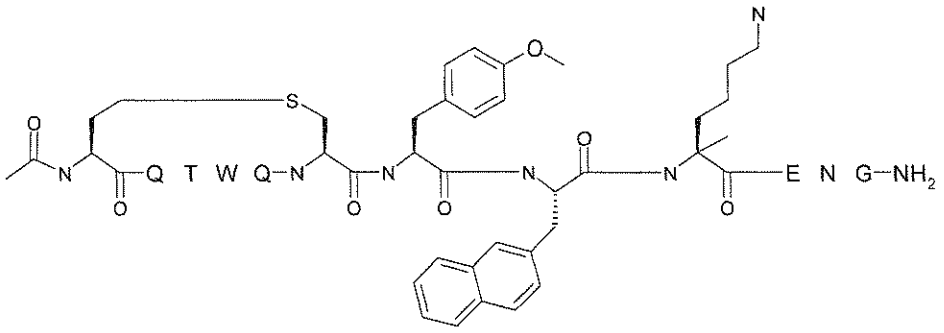
**[00653]** Assays for selectivity of peptide inhibitors included a human IL-12Rb1 ELISA and measurement of the production of IL-12 in PHA activated human PBMC, which are described briefly below.

Human IL-12Rβ1 ELISA

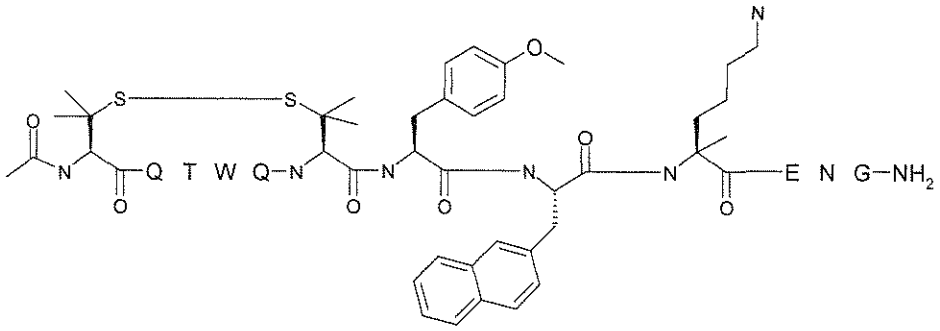
**[00654]** An assay plate was coated with 100 ng/well of human IL-12Rb1_huFC and incubated overnight at 4°C. The wells were washed, blocked, and washed again. Serial dilutions of test peptides and IL-23 at a final concentration of 2.5 nM were added to each well, and incubated for 2 hours at room temperature. After the wells were washed, bound IL-23 was detected with goat anti-p40 polyclonal antibodies, followed by an HRP conjugated donkey anti-goat IgG. Signals were visualized with TMB One Component HRP Membrane Substrate and quenched with 2 M sulfuric acid. Data from these assays is provided herein.

Production of IFNγ by IL-12 in PHA Activated Human PBMC

**[00655]** This assay examined the ability of IL-23R antagonists to neutralize production of IFNγ proteins in IL-12-stimulated human PBMCs. IL-23R peptide inhibitors specific to the IL-23/IL-23R pathway are not expected to alter the levels of IFNγ produced. Compound A and Compound B were tested in this assay, and a graph showing that they do not alter the levels of IFNγ produced at most concentrations tested is provided in Figure 2.




Compound A (SEQ ID NO: 276)




Compound B (SEQ ID NO: 279)

In Vivo Activity

**[00656]** Acute colitis was induced by feeding female Sprague Dawley rats with 3% (wt/vol) DSS dissolved in drinking water. For nine days starting at the same day as DSS, Compounds A or B was administered orally three times per day at 20 mg/kg or 30 mg/kg. Compounds A was also administered intraperitoneally three times per day at 30 mg/kg. A neutralizing anti-IL-23p19 antibody was used as a comparator, and was administered intraperitoneally at 4 mg/kg on the same day and fifth day after starting DSS. To quantify colitis with clinical activity, disease activity index (DAI) was determined daily for each animal as an average of three parameters: body weight change (scale 0-3), stool consistency (scale 0-3) and hemoccult blood (scale 0-3), as shown in Table 15. At necropsy, the entire colon was removed from the cecum to the rectum. The colon was measured for length, flushed with PBS to remove feces, weighed, and opened longitudinally to determine macroscopic score. The visible damage of the colon was scored on a scale from 0-3, as shown in Table 16.

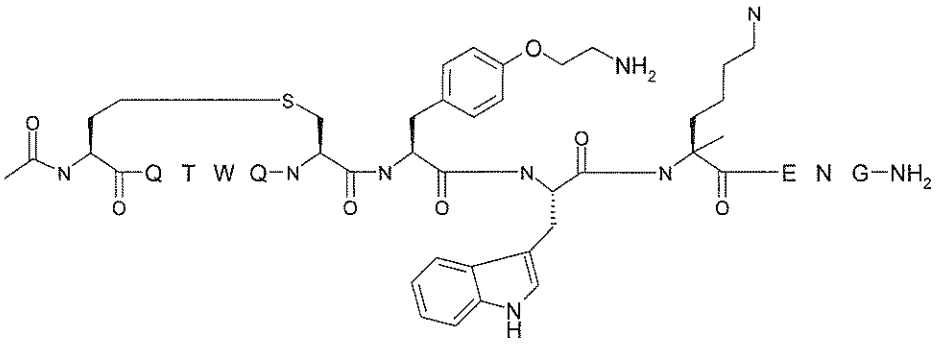
**[00657]** Table 17 shows that at Day 7, treatment with Compound A and B significantly improved DAI scores compared to vehicle treated group. Figure 3 shows results for DAI values from Day 7. In addition, a significant reduction was also observed in the colon weight to colon length ratios, and colon macroscopic scores. The reduction in inflammation observed with orally delivered peptides was similar to the effects observed from neutralizing anti-IL23p19 monoclonal antibody. Statistical analysis for significance was compared to the vehicle treated group and was determined using Student's T-test (GraphPad Prism). Differences were noted as signficant *$p<0.05$, **$p<0.01$, ***$p<0.001$, ****$p<0.0001$.

| | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| B, PO | | | | | | | | | | | | |
| Compound A, IP | -0.50 | 1.88*** | 1.17 | 0.69 | 0.83 | 0.69 | 0.83 | 0.54* | 104.32 | 12.45 | 0.33 | 0.47 |

## EXAMPLE 7

### IN VITRO ASSAYS AND SURFACE PLASMON RESONANCE (SPR) ANALYSIS

**[00658]** In vitro assays and SPR were performed to further characterize an illustrative compound, Compound C:




Ac-Cyclo-[[Abu]-QTWQC]-[Phe[4-(2-aminoethoxy)]-W-[α-MeLys]-ENG-$NH_2$

Compound C (SEQ ID NO: 280).

**[00659]** Assays described in previous examples were performed to demonstrate that Compound C is a potent, selective and competitive inhibitor of IL-23R, showing potent inhibition of IL-23-dependent upregulation of phosphor-STAT3 (pSTAT3) in human DB cells and IFNγ production in human peripheral blood natural killer (PB NK) cells. In adition, Compound C was selective, showing little inhibition in a cell free ELISA for human IL6R, or in IL-12-dependent production of IFNg in PBMC. Data is shown below in Table 18A. Compound C also cross-reacted with cynomolgus IL-23R (IC50 7 nM) and rat IL-23R (IC50 17 nM), and inhibited IL-23-dependent IL-17A production in rat splenocytes (IC50 130 nM) (data not shown).

Table 18A. In vitro Characterization of Compound C

| | IC50 | KD |
|---|---|---|

# CLAIMS

What is claimed is:

1. A peptide inhibitor of an interleukin-23 receptor, or a pharmaceutically acceptable salt or solvate thereof, wherein the peptide inhibitor comprises an amino acid sequence of Formula (Xa):

X1-X2-X3-X4-X5-X6-X7-X8-X9-X10-X11-X12-X13-X14-X15-X16-X17-X18-X19-X20 (Xa)

wherein

X1 is any amino acid or absent;

X2 is any amino acid or absent;

X3 is any amino acid or absent;

X4 is any amino acid or chemical moiety capable of forming a bond with X9;

X5 is any amino acid;

X6 is any amino acid;

X7 is any amino acid;

X8 is any amino acid;

X9 is any amino acid or chemical moiety capable of forming a bond with X4;

X10 is any amino acid;

X11 is any amino acid;

X12 is any amino acid;

X13 is any amino acid;

X14 is any amino acid;

X15 is any amino acid,

X16 is any amino acid or absent;

X17 is any amino acid or absent;

X18 is any amino acid or absent;

X19 is any amino acid or absent; and

X20 is any amino acid or absent,

wherein the peptide inhibitor is cyclized via a bond between X4 and X9, and

wherein the peptide inhibitor inhibits the binding of an interleukin-23 (IL-23) to an IL-23 receptor.

2. The peptide inhibitor of claim 1, wherein:

X1 is absent;

X2 is absent;

X3 is absent;

X4 is Cys, Abu or Pen;

X5 is Ala, α-MeOrn, α-MeSer, Cit, Dap, Dab, Dap(Ac), Gly, Lys, Asn, N-MeGln, N-MeArg, Orn, Gln, Arg, Ser or Thr;

X6 is Asp or Thr;

X7 is Trp or 6-Chloro-Trp;

X8 is Glu, Gln or Val;

X9 is Cys, Abu or Pen;

X10 is 2-Nal, a Phe analog, Tyr, or a Tyr analog;

X11 is 1-Nal, 2-Nal, Phe(3,4-dimethoxy), 5-HydroxyTrp, Phe(3,4-$Cl_2$), Trp or Tyr(3-tBu);

X12 is 3-Pal, Acpc, Acbc, Acvc, Achc, Agp, Aib, α-DiethylGly, α-MeLys, α-MeLys(Ac), α-MeLeu, a- α-MeOrn, α-MeSer, α-MeVal, Cav, Cha, Cit, Cpa, D-Asn, Glu, His, hLeu, hArg, Lys, Leu, Octgly, Orn, 4-amino-4-carboxy-piperidine, Arg, Ser, Thr or THP;

X13 is Cit, Asp, Dab, Dap, Phe, His, Dap(Peg2-Ac), Dap(pyroglutaric acid), Glu, HArg, Lys, Lys(Ac), Lys(Benzoic acid), Lys(glutaric acid), Lys(IVA), Lys(Peg4-isoGlu-Palm), Lys(pyroglutaric acid), Lys(succinic acid), Asn, Orn,Gln, Arg, Thr or Val;

X14 is Asp, Dab(Ac), Dap(Ac), Phe, His, Lys(Ac), Met, Asn(isobutyl), Gln, Arg, Tyr or Asp(1,4-diaminobutane); and

X15 is Ala, βAla, Glu, Gly, Asn, Gln, Arg or Ser.

3. The peptide inhibitor of claim1, wherein:

X1 is absent;

X2 is absent;

X3 is absent;

X4 is Cys, Abu or Pen;

X5 is Ala, α-MeOrn, α-MeSer, Cit, Dap, Dab, Dap(Ac), Gly, Lys, Asn, Orn, Gln, Arg, Ser or Thr;

X6 is Asp or Thr;

X7 is Trp or 6-Chloro-Trp;

X8 is Gln or Val;

X9 is Cys, Abu or Pen;

X10 is 2-Nal, a Phe analog, Tyr, or a Tyr analog,;

X11 is 1-Nal, 2-Nal, Phe(3,4-dimethoxy), 5-HydroxyTrp, Phe(3,4-$Cl_2$), Trp or Tyr(3-tBu);

X12 is 3-Pal, Acpc, Acbc, Acvc, Achc, Agp, Aib, α-DiethylGly, α-MeLys, α-MeLys(Ac), α-MeLeu, α-MeOrn, α-MeSer, α-MeVal, Cav, Cha, Cit, Cpa, D-Asn, His, hLeu, hArg, Lys, Leu, Octgly, Orn, 4-amino-4-carboxy-piperidine, or THP;

X13 is Cit, Asp, Dab, Dap, Phe, His, Dap(Peg2-Ac), Dap(pyroglutaric acid), Glu, hArg, Lys, Lys(Ac), Lys(Benzoic acid), Lys(glutaric acid), Lys(IVA), Lys(Peg4-isoGlu-Palm), Lys(pyroglutaric acid), Lys(succinic acid), Asn, Orn,Gln, Arg, Thr or Val;

X14 is Dab(Ac), Dap(Ac), Phe, His, Lys(Ac), Met, Asn, Gln, Arg, or Tyr; and

X15 is Ala, βAla, Gly, Asn, Gln, or Ser.

4. The peptide inhibitor of claim 1, wherein:

X1 is absent;

X2 is absent;

X3 is absent;

X4 is Cys, Abu or Pen;

X5 is Dap, Dap(Ac), Gly, Lys, Gln, Arg, Ser,Thr or Asn;

X6 is Thr;

X7 is Trp or 6-Chloro-Trp;

X8 is Gln;

X9 is Cys, Abu or Pen;

X10 is 2-Nal, a Phe analog, Tyr, or a Tyr analog;

X11 is 1-Nal, 2-Nal, Phe(3,4-dimethoxy), Phe(3,4-$Cl_2$), or Trp;

X12 is Acpc, Acbc, Acvc, Achc, Aib, α-MeGly(diethyl), α-MeLys, α-MeLys(Ac), α-MeLeu, α-MeOrn, α-MeSer, α-MeVal, Cha, Cit, homoLeu, Lys, Leu, Arg or THP;

X13 is Cit, Asp, Dap, Dap(Peg2-Ac), Dap(pyroglutaric acid), Glu, HArg, Lys, Lys(Ac), Lys(Benzoic acid), Lys(glutaric acid), Lys(IVA), Lys(Peg4-isoGlu-Palm), Lys(pyroglutaric acid), Lys-succinic acid, Asn, Orn,Gln, Arg, or Val;

X14 is Dab(Ac), Dap(Ac), His, Lys(Ac), Asn, Gln, or Tyr; and

X15 is Ala, βAla, Gly, Asn, Gln, or Ser.

5. The peptide inhibitor of claim 1, wherein:

X1 is absent;

X2 is absent;

X3 is absent;

X4 is Cys, Abu or Pen;

X5 is Dap, Dap(Ac), Gln, Ser, Thr or Asn;

X6 is Thr;

X7 is Trp;

X8 is Gln;

X9 is Cys, Abu or Pen;

X10 is a Phe analog, Tyr, or a Tyr analog;

X11 is 2-Nal or Trp;

X12 is Acpc, Acbc, Acvc, Achc, Aib, α-DiethylGly, α-MeLys, α-MeLys(Ac), α-MeLeu, α-MeOrn, α-MeSer, α-MeVal, hLeu, Leu, or THP;

X13 is Cit, Asp, Glu, Lys, Lys(Ac), Asn, or Gln;

X14 is Dab(Ac), Asn, or His; and

X15 is Ala, betaAla, Gly, Asn, or Gln.

6. The peptide inhibitor of claim 1, wherein

X4 is Cys, Pen, hCys, D-Pen, D-Cys, D-hCys, Met, Glu, Asp, Lys, Orn, Dap, Dab, D-Dap, D-Dab, D-Asp, D-Glu, D-Lys, Sec, 2-chloromethylbenzoic acid, mercapto-propanoic acid,

mercapto-butyric acid, 2-chloro-acetic acid, 3-choro-propanoic acid, 4-chloro-butyric acid, 3-chloro-isobutyric acid, Abu, β-azido-Ala-OH, propargylglycine, 2-(3'-butenyl)glycine, 2-allylglycine, 2-(3'-butenyl)glycine, 2-(4'-pentenyl)glycine, 2-(5'-hexenyl)glycine, or Abu;

X7 is Trp, Glu, Gly, Ile, Asn, Pro, Arg, Thr or OctGly, or a corresponding α-methyl amino acid form of any of the foregoing;

X9 is Cys, Pen, hCys, D-Pen, D-Cys, D-hCys, Glu, Lys, Orn, Dap, Dab, D-Dap, D-Dab, D-Asp, D-Glu, D-Lys, Asp, Leu, Val, Phe, or Ser, Sec, Abu, β-azido-Ala-OH, propargylglycine, 2-2-allylglycine, 2-(3'-butenyl)glycine, 2-(4'-pentenyl)glycine, Ala, hCys, Abu, Met, MeCys, (D)Tyr or 2-(5'-hexenyl)glycine;

X10 is Tyr, Phe(4-OMe), 1-Nal, 2-Nal, Aic, α-MePhe, Bip, (D)Cys, Cha, DMT, (D)Tyr, Glu, His, hPhe(3,4-dimethoxy), hTyr, N-Me-Tyr, Trp, Phe(4-$CONH_2$), Phe(4-phenoxy), Thr, Tic, Tyr(3-tBu), Phe(4-tBu), Phe(4-CN), Phe(4-Br), Phe(4-$NH_2$), Phe(4-F), Phe(3,5-$F_2$), Phe(4-$CH_2CO_2H$), Phe(penta-F), Phe(3,4-$Cl_2$), Phe(4-$CF_3$), Phe(4-$OCH_3$), Bip, Cha, 4-PyridylAlanine, βhTyr, OctGly, Phe(4-$N_3$), Phe(4-Br), Phe[4-(2-aminoethoxy)] or Phe, a Phe analog, a Tyr analog, or a corresponding α-methyl amino acid form of any of the foregoing;

X11 is 2-Nal, 1-Nal, 2,4-dimethylPhe, Bip, Phe(3,4-$Cl_2$), Phe (3,4-$F_2$), Phe(4-$CO_2H$), βhPhe(4-F), α-Me-Trp, 4-phenylcyclohexyl, Phe(4-$CF_3$), α-MePhe, βhNal, βhPhe, βhTyr, βhTrp, Nva(5-phenyl), Phe, His, hPhe, Tic, Tqa, Trp, Tyr, Phe(4-OMe), Phe(4-Me), Trp(2,5,7-tri-tert-Butyl), Phe(4-Oallyl), Tyr(3-tBu), Phe(4-tBu), Phe(4-guanidino, Phe(4-OBzl), Octgly, Glu(Bzl), 4-Phenylbenzylalanine, Phe[4-(2-aminoethoxy)], 5-Hydroxy-Trp, 6-Chloro-Trp, N-MeTrp, 1,2,3,4-tetrahydro-norharman, Phe(4-$CONH_2$), Phe(3,4-Dimethoxy), Phe(2,3-$Cl_2$), Phe(2,3-$F_2$), Phe(4-F), 4-phenylcyclohexylalanine, Bip, or a corresponding α-methyl amino acid form of any of the foregoing;

X12 is His, Phe, Arg, N-Me-His, Val, Cav, Cpa, Leu, Cit, hLeu, 3-Pal, t-butyl-Ala, 4-amino-4-carboxy-tetrahydropyran, Achc Acpc, Acbc, Acvc, Agp, Aib, α-DiethylGly, α-MeLys, α-MeLys(Ac), α-Me-Leu, α-MeOrn, α-MeSer, α-MeVal, Aib,, D-Ala, (D)Asn, (D)Asp, (D)Leu, (D)Phe, (D)Tyr, Aib, α-MeLeu, α-MeOrn, β-Aib, β-Ala, βhAla, βhArg, βhLeu, βhVal, β-spiro-pip, Glu, hArg, Ile, Lys, N-MeLeu, N-MeArg, Ogl, Orn, Pro, Gln, Ser, Thr, Tle, t-butyl-Gly, or a corresponding α-methyl amino acid form of any of the foregoing;

X13 is Thr, Sarc, Glu, Phe, Arg, Leu, Lys, Arg, Orn, Val, βhAla, Lys(Ac), (D)Asn, (D)Leu, (D)Phe, (D)Thr, Ala, α-MeLeu, Aib, β-Ala, β-Glu, βhLeu, βhVal, β-spiro-pip, Cha, Chg, Asp, Dab, Dap, α-DiethylGly, hLeu, Asn, Ogl, Pro, Gln, Ser, β-spiro-pip, Thr, Tba, Tle or Aib, Cit, hArg, Lys, Asn, Orn, Gln or a corresponding α-methyl amino acid form of any of the foregoing;
X14 is Phe, Tyr, Glu, Gly, His, Lys, Leu, Met, Asn, Pro, Gln, Arg, Ser, Thr, TicβhPhe, Arg, Lys(Ac), His; Dap(Ac), Dab(Ac), Asp or a corresponding α-methyl amino acid form of any of the foregoing;
X15 is Gly, Ser, Thr, Gln, Ala, (D)Ala, (D)Asn, (D)Asp, (D)Leu, (D)Phe, (D)Thr, Aea, Asp, Asn, Glu, Phe, Gly, Lys, Leu, Pro, Arg, β-Ala, Sarc, or a corresponding α-methyl amino acid form of any of the foregoing;
X16 is Asp, Glu, Ala, AEA, AEP, βhAla, Gaba, Gly, Ser, Pro, Asn, Thr or absent, or a corresponding α-methyl amino acid form of any of the foregoing; and
X17 is Leu, Lys, Arg, Glu, Ser, Gly, Gln or absent, or a corresponding α-methyl amino acid form of any of the foregoing.

7. The peptide inhibitor of claim 1 or claim 6, wherein the bond between X4 and X9, is a disulfide bond, a thioether bond, a lactam bond, a triazole ring, a selenoether bond, a diselenide bond, or an olefin bond.

8. The peptide inhibitor of any one of claims 1-7, wherein X4 is Cys and X9 is Cys, and the bond is a disulfide bond.

9. The peptide inhibitor of any one of claims 1-7, wherein X4 is Pen and X9 is Pen, and the bond is a disulfide bond.

10. The peptide inhibitor of claim 8 or claim 9, wherein
X7 is Trp;
X10 is Phe, Tyr, a Phe analog, or a Tyr analog;
X11 is Trp, 1-Nal or 2-Nal; and
X12 is Aib, α-Me-Lys, α-Me-Val α-Me-Leu; Achc, Acvc, Acpc, Acpc or THP,.

11. The peptide inhibitor of claim 10, wherein the peptide inhibitor comprises any of the following the amino acid sequences:

Ac-[Pen]-Q-T-W-Q-[Pen]-[Phe(4-OMe)]-[2-Nal]-[α-Me-Lys]-ENG-$NH_2$;

Ac-[Pen]-N-T-W-Q-[Pen]-[Phe[4-(2-aminoethoxy)]-[2-Nal]-[Aib]-[Lys(Ac)]-NN-$NH_2$;

Ac-[Pen]-Q-T-W-Q-[Pen]-[Phe[4-(2-aminoethoxy)]-[2-Nal]-[α-MeLeu]-[Lys(Ac)]-NN-$NH_2$;

Ac-[Pen]-QTWQ-[Pen]-[Phe(4-$CONH_2$)]-[2-Nal]-[α-MeLys]-[Lys(Ac)]-NN-$NH_2$;

Ac-[Pen]-QTWQ-[Pen]-[Phe[4-(2-aminoethoxy)]-[2-Nal]-[α-MeLeu]-QNN-$NH_2$;

Ac-[Pen]-Q-T-W-Q-[Pen]-[Phe(4-$CONH_2$)]-[2-Nal]-[α-MeLys]-[Lys(Ac)]-NN-$NH_2$;

Ac-[Pen]-QTWQ-[Pen]-[Phe[4-(2-aminoethoxy)]-[2-Nal]-[α-MeLys]-[Lys(Ac)]-NG-$NH_2$;

Ac-[Pen]-QTWQ-[Pen]-[Phe[4-(2-aminoethoxy)]-[2-Nal]-[α-MeLys]-[Lys(Ac)]-NN-$NH_2$;

Ac-[Pen]-QTWQ-[Pen]-[Phe[4-(2-aminoethoxy)]-[2-Nal]-[α-MeLys]-ENA-$NH_2$;

Ac-[Pen]-QTWQ-[Pen]-[Phe[4-(2-aminoethoxy)]-[2-Nal]-[α-MeLeu]-[Lys(Ac)]-NN-$NH_2$;

Ac-[Pen]-QTWQ-[Pen]-[Phe[4-(2-aminoethoxy)]-[2-Nal]-[α-MeLeu]-QNN-$NH_2$;

Ac-[Pen]-QTWQ-[Pen]-[Phe[4-(2-aminoethoxy)]-[2-Nal]-[Aib]-ENN-$NH_2$;

Ac-[Pen]-QTWQ-[Pen]-[Phe[4-(2-aminoethoxy)]-[2-Nal]-Aib-[Lys(Ac)]-NN-$NH_2$;

Ac-[Pen]-QTWQ-[Pen]-[Phe[4-(2-aminoethoxy)]-[2-Nal]-[Aib]-[Lys(Ac)]-NQ-$NH_2$;

Ac-[Pen]-QTWQ-[Pen]-[Phe[4-(2-acetylaminoethoxy)]-[2-Nal]-[α-MeLeu]-[Lys(Ac)]-NN-$NH_2$;

Ac-[Pen]-QTWQ-[Pen]-[Phe[4-(2-acetylaminoethoxy)]-[2-Nal]-[α-MeLeu]-QNN-$NH_2$;

Ac-[Pen]-NTWQ-[Pen]-[Phe[4-(2-aminoethoxy)]-[2-Nal]-[Aib]-[Lys(Ac)]-N-[βAla]-$NH_2$;

Ac-[Pen]-NTWQ-[Pen]-[Phe[4-(2-aminoethoxy)]-[2-Nal]-[hLeu]-[Lys(Ac)]-N-[βAla]-$NH_2$;

Ac-[Pen]-QTWQ-[Pen]-[Phe[4-(2-acetylaminoethoxy)]-[2-Nal]-[Aib]-[Lys(Ac)]-NN-$NH_2$;

Ac-[Pen]-NTWQ-[Pen]-[Phe[4-(2-aminoethoxy)]-[2-Nal]-[Aib]-[Lys(Ac)]-NN-$NH_2$;

Ac-[Pen]-QTWQ-[Pen]-[Phe[4-(2-acetylaminoethoxy)]-[2-Nal]-[Aib]-[Lys(Ac)]-NQ-$NH_2$; or

Ac-[Pen]-QTWQ-[Pen]-[Phe(4-OMe)]-[2-Nal]-[Aib]-[Lys(Ac)]-NQ-$NH_2$,

wherein the peptide inhibitor comprises a disulfide bond between the two Pen amino acids.

12. The peptide inhibitor of claim 1 or claim 6, wherein

X4 is an amino acid, aliphatic acid, alicyclic acid or modified 2- methyl aromatic acid having a carbon side chain capable of forming a thioether bind with X9;

X9 is a sulfur-containing amino acid capable of forming a thioether bond with X4, and the bond between X4 and X9 is a thioether bond.

13. The peptide inhibitor of claim 12, wherein
X4 is Abu, 2-chloromethylbenzoic acid, mercapto-propanoic acid, mercapto-butyric acid, 2-chloro-acetic acid, 3-chloro-propanoic acid, 4-chloro-butyric acid, 3-chloro-isobutyric acid; and
X9 is Abu, Cys, Pen, hCys, D-Pen, D-Cys, or D-hCys.

14. The peptide inhibitor of claim 13, wherein
(a) X4 is Abu and X9 is Cys; or
(b) X4 is Cys and X9 is Abu.
wherein the peptide inhibitor is cyclized via a thioether bond between X4 and X9.

15. The peptide inhibitor of claim 13 or claim 14, wherein
X7 is Trp;
X10 is Phe, Tyr, a Phe analog, or a Tyr analog;
X11 is Trp, 1-Nal or 2-Nal; and
X12 is α-Me-Lys, α-Me-Leu, α-Me-Ser, α-Me-Val, Achc, Acvc, Acpc, Acbc or 4-amino-4-carboxy-tetrahydropyran.

16. The peptide inhibitor of claim 15, wherein the peptide inhibitor comprises any of the following amino acid sequences:
Ac-Cyclo-[[Abu]-QTWQC]]-[Phe(4-OMe)]-[2-Nal]-[α-MeLys]-E-N-G;
Ac-Cyclo-[[Abu]-QTWQC]]-[Phe(4-OMe)]-[2-Nal]-[α-MeOrn]-ENG-$NH_2$;
Ac-Cyclo-[[Abu]-QTWQC]]-[Phe(4-$CO_2H$)]-[2-Nal]-[α-MeLys]-[Lys(Ac)]-NG-$NH_2$;
Ac-Cyclo-[[Abu]-QTWQC]]-[Phe(4-OMe)]-[2-Nal]-[α-MeLys]-[Lys(Ac)]-NG-$NH_2$;
Ac-Cyclo-[[Abu]-QTWQC]]-[Phe(4-$CONH_2$)]-[2-Nal]-[α-MeLys]-[Lys(Ac)]NG-$NH_2$;
Ac-Cyclo-[[Abu]-QTWQC]]-[Phe(4-OMe)]-[2-Nal]-[α-MeLys]-[Lys(Ac)]-NA-$NH_2$;
Ac-Cyclo-[[Abu]-QTWQC]]-[Phe(4-OMe)]-[2-Nal]-[α-MeLys]-[Lys(Ac)]-NAE-$NH_2$;
Ac-Cyclo-[[Abu]-QTWQC]]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[α-MeLys]-ENG-$NH_2$;

Ac-Cyclo-[[Abu]-QTWQC]]-[Phe(4-(2-aminoethoxy))]-W-[α-MeLys]-E-N-G;
Ac-Cyclo-[[Abu]-QTWQC]]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[α-MeLys]-DNG-$NH_2$;
Ac-Cyclo-[[Abu]-QTWQC]]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[α-MeLys]-[Lys(succinic acid)]-NG-$NH_2$;
Ac-Cyclo-[[Abu]-QTWQC]]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[α-MeLys]-[Lys(glutaric acid)]-NG-$NH_2$;
Ac-Cyclo-[[Abu]-QTWQC]]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[α-MeLys]-[Lys(pyroglutamic acid)]-NG-$NH_2$;
Ac-Cyclo-[[Abu]-QTWQC]]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[α-MeLys]-[Lys(isovaleric acid)]-NG-$NH_2$;
Ac-Cyclo-[[Abu]-QTWQC]]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[α-MeLys]-[Lys(Ac)]-NG-[(D)Lys]-$NH_2$;
Ac-Cyclo-[[Abu]-QTWQC]]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[α-MeLys]-[Lys(Ac)]-NG-[AEA]-$NH_2$;
Ac-Cyclo-[[Abu]-QTWQC]]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[Aib]-QNG-$NH_2$;
Ac-Cyclo-[[Abu]-QTWQC]]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[Aib]-[Lys(Ac)]-NA-$NH_2$;
Ac-Cyclo-[[Abu]-QTWQC]]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[Aib]-KNG-$NH_2$;
Ac-Cyclo-[[Abu]-QTWQC]]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[α-MeLys]-[Lys(Ac)]-NG-$NH_2$;
Ac-Cyclo-[[Abu]-QTWQC]]-[Phe[4-(2-(acetyl-aminoethoxy)]]-[2-Nal]-[α-MeLys(Ac)]-[Lys(Ac)]-NG-$NH_2$;
Ac-Cyclo-[[Abu]-QTWQC]]-[Phe[4-(2-(acetyl-aminoethoxy)]]-[2-Nal]-[α-MeLys(Ac)]-ENG-$NH_2$;

Ac-Cyclo-[[Abu]-QTWQC]]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[4-amino-4-carboxy-tetrahydropyran]-ENN-$NH_2$;
Ac-Cyclo-[[Abu]-QTWQC]]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[α-MeLys]-ENQ-$NH_2$;
Ac-Cyclo-[[Abu]-QTWQC]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[α-MeLys]-ENN-$NH_2$;
Ac-Cyclo-[[Abu]-QTWQC]]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[α-MeVal]-[Lys(Ac)]-NG-$NH_2$;
Ac-Cyclo-[[Abu]-QTWQC]]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[hLeu]-[Lys(Ac)]-N-[βAla]-$NH_2$;

Ac-Cyclo-[[Abu]-QTWQC]]-[Phe[4-(2-(acetyl-aminoethoxy)]]-[2-Nal]-[α-MeLys(Ac)]-ENQ-$NH_2$;

Ac-Cyclo-[[Abu]-QTWQC]]-[Phe[4-(2-(acetyl-aminoethoxy)]]-[2-Nal]-[α-MeLys(Ac)]-ENN-$NH_2$;

Ac-Cyclo-[[Abu]-QTWQC]]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[α-MeLeu]-ENN-$NH_2$;

Ac-Cyclo-[[Abu]-QTWQC]]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[α-MeLeu)-[Cit]-NN-$NH_2$;

Ac-Cyclo-[[Abu]-QTWQC]]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[α-MeLeu]-[Lys(Ac)]-NN-$NH_2$;

Ac-Cyclo-[[Abu]-QTWQC]]-[ Phe[4-(2-aminoethoxy)]]-[2-Nal]-[Aib]-[Lys(Ac)]-NG-$NH_2$;

Ac-E-Cyclo-[[Abu]-QTWQC]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[α-MeLys]-ENN-$NH_2$;

Ac-(D)Glu-[Cyclo-[[Abu]-QTWQC]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[α-MeLys]-ENN-$NH_2$;

Ac-Arg-Cyclo-[[Abu]-QTWQC]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[α-MeLys]-ENN-$NH_2$;

Ac-[(D)Arg-Cyclo-[[Abu]-QTWQC]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[α-MeLys]-ENN-$NH_2$;

Ac-F-Cyclo-[[Abu]-QTWQC]]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[α-MeLys]-ENN-$NH_2$;

Ac-[(D)Phe]-Cyclo-[[Abu]-QTWQC]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[α-MeLys]-ENN-$NH_2$;

Ac-[2-Nal]-Cyclo-[[Abu]-QTWQC]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[α-MeLys]-ENN-$NH_2$;

Ac-Leu-Cyclo-[[Abu]-QTWQC]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[α-MeLys]-ENN-$NH_2$;

Ac-[(D)Qln]-Cyclo-[[Abu]-QTWQC]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[α-MeLys]-ENN-$NH_2$;

Ac-Cyclo-[[Abu]-QTWQC]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[α-MeLeu]-ENG-$NH_2$;

Ac-T-Cyclo-[[Abu]-QTWQC]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[α-MeLys]-ENN-$NH_2$;

Ac-Cyclo-[[Abu]-QTWQC]]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[α-MeLeu]-QN-[βAla]-$NH_2$;

Ac-Cyclo-[[Abu]-QTWQC]]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[Acbc]-ENN-$NH_2$;

Ac-Cyclo-[[Abu]-QTWQC]]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[Achc]- ENN-$NH_2$;

Ac-Cyclo-[[Abu]-QTWQC]]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[Acvc]-ENN-$NH_2$;

Ac-Cyclo-[[Abu]-QTWQC]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[4-amino-4-carboxy-piperidine]-ENN-$NH_2$; or

Ac-Cyclo-[[Abu]-QTWQC]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[4-amino-4-carboxy-tetrahydropyran]-ENN-$NH_2$,

wherein the peptide inhibitor comprises a thioether bond between the Abu and the C.

17. The peptide inhibitor of claim 1,

wherein

X4 is Pen, Cys or homo-Cys;

X5 is any amino acid;

X6 is any amino acid;

X7 is Trp, Bip, Gln, His, Glu(Bzl), 4-Phenylbenzylalanine, Tic, Phe[4-(2-aminoethoxy)], Phe(3,4-$Cl_2$), Phe(4-OMe), 5-Hydroxy-Trp, 6-Chloro-Trp, N-MeTrp, α-Me-Trp, 1,2,3,4 -tetrahydro-norharman, Phe(4-$CO_2H$), Phe(4-$CONH_2$), Phe(3,4-Dimethoxy), Phe(4-$CF_3$), Phe(4-tBu), ββ-diPheAla, Glu, Gly, Ile, Asn, Pro, Arg, Thr or Octgly, or a corresponding α-methyl amino acid form of any of the foregoing;

X8 is any amino acid;

X9 is Pen, Cys or hCys;

X10 is 1-Nal, 2-Nal, Aic, Bip, (D)Cys, Cha, DMT, (D)Tyr, Glu, Phe, His, Trp, Thr, Tic, Tyr, 4-pyridylAla, Octgly, a Phe analog or a Tyr analog (optionally, Phe(3,4-$F_2$), Phe(3,4-$Cl_2$), F(3-Me), Phe[4-(2-aminoethoxy)], Phe[4-(2-(acetyl-aminoethoxy)], Phe(4-Br), Phe(4-$CONH_2$), Phe(4-Cl), Phe(4-CN), Phe(4-guanidino), Phe(4-Me), Phe(4-$NH_2$), Phe(4-$N_3$), Phe(4-OMe), or Phe(4-OBzl)), or a corresponding α-methyl amino acid form of any of the foregoing;

X11 is 2-Nal, 1-Nal, 2,4-dimethylPhe, Bip, Phe(3,4-$Cl_2$), Phe (3,4-$F_2$), Phe(4-$CO_2H$), βhPhe(4-F), α-Me-Trp, 4-phenylcyclohexyl, Phe(4-$CF_3$), α-MePhe, βhNal, βhPhe, βhTyr, βhTrp, Nva(5-phenyl), Phe, His, hPhe, Tic, Tqa, Trp, Tyr, Phe(4-OMe), Phe(4-Me), Trp(2,5,7-tri-tert-Butyl), Phe(4-Oallyl), Tyr(3-tBu), Phe(4-tBu), Phe(4-guanidino, Phe(4-OBzl), Octgly, Glu(Bzl), 4-Phenylbenzylalanine, Phe[4-(2-aminoethoxy)], 5-Hydroxy-Trp, 6-Chloro-Trp, N-MeTrp, 1,2,3,4-tetrahydro-norharman, Phe(4-$CONH_2$), Phe(3,4-$OMe_2$) Phe(2,3-$Cl_2$), Phe(2,3-$F_2$), Phe(4-F), 4-phenylcyclohexylalanine or Bip, or a corresponding α-methyl amino acid form of any of the foregoing;

X12 is α-MeLys, α-MeOrn, α-MeLeu, α-MeVal, 4-amino-4-carboxy-tetrahydropyran, Achc Acpc, Acbc, Acvc, MeLeu, Aib, (D)Ala, (D)Asn, (D)Leu, (D)Asp, (D)Phe, (D)Thr, 3-Pal, Aib, β-Ala, βhGlu, βhAla, βhLeu, βhVal, β-spiro-pip, Cha, Chg, Asp, Dab, Dap, α-diethylGly, Glu, Phe, hLeu, hArg, hLeu, Ile, Lys, Leu, Asn, N-MeLeu, N-MeArg, Ogl, Orn, Pro, Gln, Arg, Ser, Thr or Tle, or a corresponding α-methyl amino acid form of any of the foregoing;

X13 is Lys(Ac), (D)Asn, (D)Leu, (D)Thr, (D)Phe, Ala, Aib, α-MeLeu, β-Ala, βhGlu, βhAla, βhLeu, βhVal, β-spiro-pip, Cha, Chg, Asp, Lys, Arg, Orn, Dab, Dap, α-diethylGly, Glu, Phe, hLeu, Lys, Leu, Asn, Ogl, Pro, Gln, Asp, Arg, Ser, spiro-pip, Thr, Tba, Tlc, Val or Tyr, or a corresponding α-methyl amino acid form of any of the foregoing;
X14 is Asn, Glu, Phe, Gly, His, Lys, Leu, Met, Asn, Pro, Gln, Arg, Ser, Thr, Tic or Tyr, Lys(Ac), Orn or a corresponding α-methyl amino acid form of any of the foregoing;
X15 is Gly, (D)Ala, (D)Asn, (D)Asp, Asn, (D)Leu, (D)Phe, (D)Thr, Ala, Asn, Ser, AEA, Asp, Glu, Phe, Gly, Lys, Leu, Pro, Gln, Arg or Ser, β-Ala, Arg or a corresponding α-methyl amino acid form of any of the foregoing;
X16 is absent, Gly, Ala, Asp, Ser, Pro, Asn or Thr, or a corresponding α-methyl amino acid form of any of the foregoing;
X17 is absent, Glu, Ser, Gly or Gln, or a corresponding α-methyl amino acid form of any of the foregoing;
X18 is absent or any amino acid;
X19 is absent or any amino acid; and
X20 is absent or any amino acid.

18. The peptide inhibitor of claim 17, wherein the bond between X4 and X9 is a disulfide bond.

19. The peptide inhibitor of any one of claims 1-18, wherein one or more of X1, X2, and X3 are absent.

20. The peptide inhibitor of any one of claims 1-19, wherein one or more of X17, X19 and X20 are absent.

21. The peptide inhibitor of any one of claims 17-20, wherein one or both of X4 or X9 is Pen.

22. The peptide inhibitor of claim 21, wherein both X4 and X9 are Pen.

23. The peptide inhibitor of any one of claims 17-22, wherein X18 is (D)-Lys.

24. The peptide inhibitor of any one of claims 17-23, comprising one or more, two or more, three or more, or four of the following:
X5 is Arg, Asn, Gln, Dap, Orn;
X6 is Thr or Ser;
X7 is Trp, 2-Nal, 1-Nal, Phe(4-OAllyl), Tyr(3-tBu), Phe(4-tBu), Phe(4-guanidino), Phe(Bzl) or Phe(4-Me), 5-Hydroxy-Trp, 6-Chloro-Trp, N-MeTrp, α-MeTrp or 1,2,3,4 -tetrahydro-norharman; and
X8 is Gln, Val, Phe, Glu, Lys.

25. The peptide inhibitor of any one of claims 17-24, comprising one or more, two or more, three or more, four or more, five or more, six or more, or seven of the following:
X10 is Tyr, Phe(4-OBzl), Phe(4-OMe), Phe(4-$CONH_2$), Phe(3,4-$Cl_2$), Phe(4-tBu), Phe(4-$NH_2$), Phe(4-Br), Phe(4-CN), Phe(4-$CO_2H$), Phe(4-(2aminoethoxy)) or Phe(4-guanidino) ;
X11 is Trp, 2-Nal, 1-Nal, Phe(4-OAllyl), Tyr(3-tBu), Phe(4-tBu), Phe(4-guanidino), Phe(Bzl) or Phe(4-Me), 5-Hydroxy-Trp, 6-Chloro-Trp, N-MeTrp, α-MeTrp or 1,2,3,4 -tetrahydro-norharman;
X12 is Arg, α-MeLys α-MeLeu, Aib or α-MeOrn;
X13 is Lys, Glu or Lys(Ac);
X14 is Phe or Asn;
X15 is Asn, Gly, Ser βAla, or Ala; and
X16 is absent or AEA.

26. The peptide inhibitor of claim 25, wherein X4 and X9 are Pen; X5 is Gln; X6 is Thr; X7 is Trp; X8 is Gln; X10 is Tyr, Phe(4-OMe) or 2-Nal; X11 is Trp, 2-Nal or 1-Nal; X12 is Arg, αMeLys or α-MeOrn; X13 is Lys, Glu or Lys(Ac); X14 is Phe or Asn; X15 is Gly; and X16 is absent.

27. The peptide inhibitor of claim 26, wherein one or more of X1, X2 and X3 are absent; and one or more, two or more, three or more, or four of X17, X18, X19 and X20 are absent.

28. The peptide inhibitor of claim 1,

wherein

X4 is Abu, Pen, or Cys;

X7 is Trp, Bip, Gln, His, Glu(Bzl), 4-Phenylbenzylalanine, Tic, Phe[4-(2-aminoethoxy)], Phe(3,4-$Cl_2$), Phe(4-OMe), 5-Hydroxy-Trp, 6-Chloro-Trp, N-MeTrp, α-MeTrp, 1,2,3,4 -tetrahydro-norharman, Phe(4-$CO_2H$), Phe(4-$CONH_2$), Phe(3,4-Dimethoxy), Phe(4-$CF_3$), ββ-diPheAla, Phe(4-tBu), Glu, Gly, Ile, Asn, Pro, Arg, Thr or Octgly, or a corresponding α-methyl amino acid form of any of the foregoing;

X9 is Abu, Pen, or Cys;

X10 is 1-Nal, 2-Nal, Aic, Bip, (D)Cys, Cha, DMT, (D)Tyr, Glu, Phe, His, Trp, Thr, Tic, Tyr, 4-pyridylAla, Octgly a Phe analog or a Tyr analog, or a corresponding α-methyl amino acid form of any of the foregoing;

X11 is 2-Nal, 1-Nal, 2,4-dimethylPhe, Bip, 4-phenylcyclohexyl, Glu(Bzl), 4-Phenylbenzylalanine, Tic, Phe[4-(2-aminoethoxy)], Phe(3,4-$Cl_2$), Phe(3,4-$F_2$), βhPhe(4-F), Phe(4-OMe), 5-Hydroxy-Trp, 6-Chloro-Trp, N-MeTrp, α-MeTrp, 1,2,3,4 -tetrahydro-norharman, Phe(4-$CO_2H$), Phe(4-$CONH_2$), Phe(3,4-Dimethoxy), Phe(4-$CF_3$), Phe(2,3-$Cl_2$), Phe(2,3-$F_2$),Phe(4-F), 4-phenylcyclohexylalanine, α-MePhe, βhNal, βhPhe, βhTyr, βhTrp, Bip, Nva(5-phenyl), Phe, His, hPhe, Tqa, Trp, Tyr, Phe(4-Me), Trp(2,5,7-tri-tertButyl), Phe(4-OAllyl), Tyr(3-tBu), Phe(4-tBu), Phe(4-guanidino), Phe(4-OBzl), or Octgly, or a corresponding α-methyl amino acid form of any of the foregoing;

X12 is α-MeLys, α-MeOrn, α-MeLeu, MeLeu, Aib, Achc, Acvc, Acpc, Acpc, THP, (D)Ala, (D)Asn, (D)Leu, (D)Asp, (D)Phe, (D)Thr, 3-Pal, Aib, β-Ala, βhGlu, βhAla, βhLeu, βhVal, β-spiro-pip, Cha, Chg, Asp, Dab, Dap, α-DiethylGly, Glu, Phe, hLeu, hArg, hLeu, Ile, Lys, Leu, Asn, N-MeLeu, N-MeArg, Ogl, Orn, Pro, Gln, Arg, Ser, Thr or Tle, or a corresponding α-methyl amino acid form of any of the foregoing;

X13 is Lys(Ac), (D)Asn, (D)Leu, (D)Thr, (D)Phe, Ala, Aib, α-MeLeu, βAla, βhGlu, βhAla, βhLeu, βhVal, β-spiro-pip, Cha, Chg, Asp, Arg, Orn, Dab, Dap, α-DiethylGly, Glu, Phe, hLeu, Lys, Leu, Asn, Ogl, Pro, Gln, Asp, Arg, Ser, spiro-pip, Thr, Tba, Tlc, Val or Tyr, or a corresponding α-methyl amino acid form of any of the foregoing;

X14 is Asn, Glu, Phe, Gly, His, Lys, Leu, Met, Asn, Pro, Gln, Arg, Ser, Thr, Tic or Tyr, or a corresponding α-methyl amino acid form of any of the foregoing;
X15 is Gly, (D)Ala, (D)Asn, (D)Asp, Asn, (D)Leu, (D)Phe, (D)Thr, Ala, AEA, Asp, Glu, Phe, Gly, Lys, Leu, Pro, Gln, Arg or Ser, or a corresponding α-methyl amino acid form of any of the foregoing;
X16 is absent, Gly, Ala, Asp, Ser, Pro, Asn or Thr, or a corresponding α-methyl amino acid form of any of the foregoing; and
X17 is absent, Glu, Ser, Gly or Gln, or a corresponding α-methyl amino acid form of any of the foregoing.

29. The peptide inhibitor of claim 28, wherein the peptide inhibitor is cyclized via an intramolecular bond between X4 and X9.

30. The peptide inhibitor of claim 28 or claim 29, wherein one or more of X1, X2, and X3 are absent.

31. The peptide inhibitor of any one of claims 28-30, wherein one or more of X17, X19 and X20 are absent.

32. The peptide inhibitor of any one of claims 28-31, wherein one of X4 or X9 is Abu, and the other of X4 or X9 is not Abu.

33. The peptide inhibitor of any one of claims 28-32, comprising one or more, two or more, three or more, or four of the following:
X5 is Arg, Gln, Dap or Orn;
X6 is Thr or Ser;
X7 is Trp, 2-Nal, 1-Nal, Phe(4-OAllyl), Tyr(3-tBu), Phe(4-tBu), Phe(4-guanidino), Phe(4-OBzl), Phe(4-Me), 5-Hydroxy-Trp, 6-Chloro-Trp, N-MeTrp, or α-MeTrp, 1,2,3,4 -tetrahydro-norharman; and
X8 is Gln, Val, Phe, Glu or Lys.

34. The peptide inhibitor of any one of claims 28-33, comprising one or more, two or more, three or more, four or more, five or more, six or more, or seven of the following:
X10 is Tyr, Phe(4-OBzl), Phe(4-OMe), Phe(4-$CONH_2$), Phe(3,4-$Cl_2$), Phe(4-tBu), Phe(4-$NH_2$), Phe(4-Br), Phe(4-CN), Phe(4-$CO_2H$), Phe(4-(2aminoethoxy)) or Phe(4-guanadino);
X11 is Trp, 2-Nal, 1-Nal, Phe(4-OAllyl), Tyr(3-tBu), Phe(4-tBu), Phe(4-guanidino), Phe(Bzl) or Phe(4-Me), 5-Hydroxy-Trp, 6-Chloro-Trp, N-MeTrp, α-MeTrp or 1,2,3,4 -tetrahydro-norharman;
X12 is Arg, hLeu, (D)Asn, Aib, α-MeLys, α-MeLeu, α-Me-Val, α-MeOrn, Achc, Acvc, Acpc, Acpc, or THP;
X13 is Lys, Glu or Lys(Ac);
X14 is Phe or Asn;
X15 is Gly, Ser, Asn, βAla or Ala; and
X16 is absent or AEA.

35. The peptide inhibitor of any one of claims 1-34, wherein the peptide inhibitor comprises the structure of Formula I:

$$R^1\text{-}X\text{-}R^2 \quad (I)$$

or a pharmaceutically acceptable salt or solvate thereof, wherein
$R^1$ is a bond, hydrogen, a C1-C6 alkyl, a C6-C12 aryl, a C6-C12 aryl, a C1-C6 alkyl, a C1-C20 alkanoyl, and including PEGylated versions alone or as spacers of any of the foregoing; X is the amino acid sequence; and
$R^2$ is OH or $NH_2$.

36. A peptide dimer inhibitor of an interleukin-23 receptor, wherein the peptide dimer inhibitor comprises two peptide monomer subunits connected via one or more linker moieties, wherein each peptide monomer subunit has a sequence or structure set forth in any one of claims 1-35.

37. The peptide dimer inhibitor of claim 36, wherein one or both peptide monomer subunit is cyclized via an intramolecular bond between X4 and X9.

38. The peptide dimer inhibitor of claim 37, wherein one or both intramolecular bond is a disulfide bond, a thioether bond, a lactam bond, a selenoether, diselenide, or an olefin bond.

39. The peptide dimer inhibitor of any one of claims 36-38, wherein the linker moiety is a diethylene glycol linker, an iminodiacetic acid (IDA) linker, a β-Ala-iminodiaceticacid (β-Ala-IDA) linker, or a PEG linker.

40. The peptide dimer inhibitor of any one of claims 36-39, wherein the N-terminus of each peptide monomer subunit is connected by the linker moiety or wherein the C-terminus of each peptide monomer subunit is connected by the linker moiety.

41. The peptide dimer inhibitor of claim 36, wherein the peptide dimer inhibitor comprises one of the following amino acid sequences:
[Ac-Cyclo-[[Abu]-QTWQC]-[Phe(4-OMe)]-[2-Nal]-[α-MeLys]-ENG-NH2]$_2$ DIG;
[Ac-[Pen]-QTWQ-[Pen]-[Phe(4-OMe)]-[2-Nal]-[α-MeVal]-[Lys(Ac)]-NN-[D)Lys]$_2$ DIG;
[Ac-[Pen]-QTWQ-[Pen]-[Phe[4-(2-acetylaminoethoxy)]-[2-Nal]- [α-MeVal]-[Lys(Ac)]-NN-[D)Lys]]$_2$ DIG;
[Ac-[Pen]-QTWQ[Pen]-[Phe[4-(2-acetylaminoethoxy)]]-[2-Nal]-[α-MeVal]-KNN-$NH_2$]$_2$ DIG;
[Ac-[Pen]-QTWQ[Pen]-[Phe[4-(2-acetylaminoethoxy)]]-[2-Nal]-K-[Lys(Ac)]-NN-$NH_2$]$_2$ DIG;
[Ac-[Pen]-QTWQ-[Pen]-[Phe(4-OMe)]-[2-Nal]-[α-MeLys]-[Lys(Ac)]-NN-$NH_2$]$_2$ DIG;
[Ac-Cyclo-[[Abu]-QTWQC]-[Phe(4-OMe)]-[2-Nal]-[α-MeLys]-ENG-NH2]$_2$ DIG; or
[Ac-[Pen]-QTWQ-[Pen]-[Phe(4-$CONH_2$)]-[2-Nal]-[α-MeLys]-[Lys(Ac)]-NN-$NH_2$]$_2$ DIG.

42. A polynucleotide comprising a sequence encoding the peptide inhibitor of any one of claims 1-35 or one or both peptide monomer subunit of the peptide dimer inhibitor of any one of claims 36-41.

43. A vector comprising the polynucelotide of claim 42.

44. A pharmaceutical composition comprising the peptide inhibitor of any one of claims 1-35 or the peptide dimer inhibitor of any one of claims 36-41, and a pharmaceutically acceptable carrier, excipient, or diluent.

45. The pharmaceutical composition of claim 44, further comprising an enteric coating.

46. The pharmaceutical composition of claim 45, wherein the enteric coating protects and releases the pharmaceutical composition within a subject's lower gastrointestinal system.

47. A method for treating an Inflammatory Bowel Disease (IBD), ulcerative colitis, Crohn's disease, Celiac disease (*nontropical Sprue)*, enteropathy associated with seronegative arthropathies, microscopic colitis, collagenous colitis, eosinophilic gastroenteritis, colitis associated with radio- or chemo-therapy, colitis associated with disorders of innate immunity as in leukocyte adhesion deficiency-1, chronic granulomatous disease, glycogen storage disease type 1b, Hermansky-Pudlak syndrome, Chediak-Higashi syndrome, and Wiskott-Aldrich Syndrome, pouchitis resulting after proctocolectomy and ileoanal anastomosis, gastrointestinal cancer, pancreatitis, insulin-dependent diabetes mellitus, mastitis, cholecystitis, cholangitis, pericholangitis, chronic bronchitis, chronic sinusitis, asthma, psoriasis, psoriatic arthritis, or graft versus host disease in a subject, comprising providing to the subject an effective amount of the pharmaceutical composition of any one of claims 44-46.

48. The method of claim 47, wherein the pharmaceutical composition is provided to the subject by an oral, parenteral, intravenous, peritoneal, intradermal, subcutaneous, intramuscular, intrathecal, inhalation, vaporization, nebulization, sublingual, buccal, parenteral, rectal, intraocular, inhalation, topically, vaginal, or topical route of administration.

49. The method of claim 47 for treating Inflammatory Bowel Disease (IBD), ulcerative colitis, Crohn's disease, wherein the pharmaceutical composition is provided to the subject orally.

50. The method of claim 47 for treating psoriasis, wherein the pharmaceutical composition is provided to the subject orally, topically, parenterally, intravenously, subcutaneously, peritonealy, or intravenously.

51. The method of any one claims 47-50, wherein the peptide inhibitor or the peptide dimer inhibitor inhibits binding of an interleukin-23 (IL-23) to the interleukin-23 receptor (IL-23R).

52. A method of assessing the ability of a candidate compound to inhibit or reduce an inflammatory disease or disorder, comprising:

(a) providing to a rat an amount of dextran sulfate sodium (DSS) or 2,4,6-Trinitrobenzenesulfonic acid (TNBS) sufficient to induce an inflammatory bowel disease (IBD);

(b) providing to the rat an amount of a candidate compound; and

(c) measuring an amount of IBD symptoms present in the rat after being provided with the DSS and the candidate compound;

wherein if the amount of IBD symptoms measured in (c) are significantly lower than the amount measured in a control rat provided with the amount of DSS or TNBS and either an amount of a control compound or no peptide (e.g., vehicle control), the candidate compound inhibits or reduces the inflammatory disease or disorder.

53. The method of claim 52, wherein an anti-IL-23p19 antibody is used as a positive control.

54. The method of claim 52, wherein the candidate compound inhibits or reduces the inflammatory disease or disorder in a human.

## CLAIMS

What is claimed is:

1. A peptide inhibitor of an interleukin-23 receptor, or a pharmaceutically acceptable salt or solvate thereof, wherein the peptide inhibitor comprises an amino acid sequence of Formula (Xa):

X1-X2-X3-X4-X5-X6-X7-X8-X9-X10-X11-X12-X13-X14-X15-X16-X17-X18-X19-X20 (Xa)

wherein

X1 is any amino acid or absent;

X2 is any amino acid or absent;

X3 is any amino acid or absent;

X4 is any amino acid or chemical moiety capable of forming a bond with X9;

X5 is any amino acid;

X6 is any amino acid;

X7 is any amino acid;

X8 is any amino acid;

X9 is any amino acid or chemical moiety capable of forming a bond with X4;

X10 is any amino acid;

X11 is any amino acid;

X12 is any amino acid;

X13 is any amino acid;

X14 is any amino acid;

X15 is any amino acid,

X16 is any amino acid or absent;

X17 is any amino acid or absent;

X18 is any amino acid or absent;

X19 is any amino acid or absent; and

X20 is any amino acid or absent,

wherein the peptide inhibitor is cyclized via a bond between X4 and X9, and

wherein the peptide inhibitor inhibits the binding of an interleukin-23 (IL-23) to an IL-23 receptor.

2. The peptide inhibitor of claim 1, wherein:

X1 is absent;

X2 is absent;

X3 is absent;

X4 is Cys, Abu or Pen;

X5 is Ala, α-MeOrn, α-MeSer, Cit, Dap, Dab, Dap(Ac), Gly, Lys, Asn, N-MeGln, N-MeArg, Orn, Gln, Arg, Ser or Thr;

X6 is Asp or Thr;

X7 is Trp or 6-Chloro-Trp;

X8 is Glu, Gln or Val;

X9 is Cys, Abu or Pen;

X10 is 2-Nal, a Phe analog, Tyr, or a Tyr analog;

X11 is 1-Nal, 2-Nal, Phe(3,4-dimethoxy), 5-HydroxyTrp, Phe(3,4-$Cl_2$), Trp or Tyr(3-tBu);

X12 is 3-Pal, Acpc, Acbc, Acvc, Achc, Agp, Aib, α-DiethylGly, α-MeLys, α-MeLys(Ac), α-MeLeu, a- α-MeOrn, α-MeSer, α-MeVal, Cav, Cha, Cit, Cpa, D-Asn, Glu, His, hLeu, hArg, Lys, Leu, Octgly, Orn, 4-amino-4-carboxy-piperidine, Arg, Ser, Thr or THP;

X13 is Cit, Asp, Dab, Dap, Phe, His, Dap(Peg2-Ac), Dap(pyroglutaric acid), Glu, HArg, Lys, Lys(Ac), Lys(Benzoic acid), Lys(glutaric acid), Lys(IVA), Lys(Peg4-isoGlu-Palm), Lys(pyroglutaric acid), Lys(succinic acid), Asn, Orn,Gln, Arg, Thr or Val;

X14 is Asp, Dab(Ac), Dap(Ac), Phe, His, Lys(Ac), Met, Asn(isobutyl), Gln, Arg, Tyr or Asp(1,4-diaminobutane); and

X15 is Ala, βAla, Glu, Gly, Asn, Gln, Arg or Ser.

3. The peptide inhibitor of claim1, wherein:

X1 is absent;

X2 is absent;

X3 is absent;

X4 is Cys, Abu or Pen;

X5 is Ala, α-MeOrn, α-MeSer, Cit, Dap, Dab, Dap(Ac), Gly, Lys, Asn, Orn, Gln, Arg, Ser or Thr;

X6 is Asp or Thr;

X7 is Trp or 6-Chloro-Trp;

X8 is Gln or Val;

X9 is Cys, Abu or Pen;

X10 is 2-Nal, a Phe analog, Tyr, or a Tyr analog,;

X11 is 1-Nal, 2-Nal, Phe(3,4-dimethoxy), 5-HydroxyTrp, Phe(3,4-$Cl_2$), Trp or Tyr(3-tBu);

X12 is 3-Pal, Acpc, Acbc, Acvc, Achc, Agp, Aib, α-DiethylGly, α-MeLys, α-MeLys(Ac), α-MeLeu, α-MeOrn, α-MeSer, α-MeVal, Cav, Cha, Cit, Cpa, D-Asn, His, hLeu, hArg, Lys, Leu, Octgly, Orn, 4-amino-4-carboxy-piperidine, or THP;

X13 is Cit, Asp, Dab, Dap, Phe, His, Dap(Peg2-Ac), Dap(pyroglutaric acid), Glu, hArg, Lys, Lys(Ac), Lys(Benzoic acid), Lys(glutaric acid), Lys(IVA), Lys(Peg4-isoGlu-Palm), Lys(pyroglutaric acid), Lys(succinic acid), Asn, Orn,Gln, Arg, Thr or Val;

X14 is Dab(Ac), Dap(Ac), Phe, His, Lys(Ac), Met, Asn, Gln, Arg, or Tyr; and

X15 is Ala, βAla, Gly, Asn, Gln, or Ser.

4. The peptide inhibitor of claim 1, wherein:

X1 is absent;

X2 is absent;

X3 is absent;

X4 is Cys, Abu or Pen;

X5 is Dap, Dap(Ac), Gly, Lys, Gln, Arg, Ser,Thr or Asn;

X6 is Thr;

X7 is Trp or 6-Chloro-Trp;

X8 is Gln;

X9 is Cys, Abu or Pen;

X10 is 2-Nal, a Phe analog, Tyr, or a Tyr analog;

X11 is 1-Nal, 2-Nal, Phe(3,4-dimethoxy), Phe(3,4-$Cl_2$), or Trp;

X12 is Acpc, Acbc, Acvc, Achc, Aib, α-MeGly(diethyl), α-MeLys, α-MeLys(Ac), α-MeLeu, α-MeOrn, α-MeSer, α-MeVal, Cha, Cit, homoLeu, Lys, Leu, Arg or THP;

X13 is Cit, Asp, Dap, Dap(Peg2-Ac), Dap(pyroglutaric acid), Glu, HArg, Lys, Lys(Ac), Lys(Benzoic acid), Lys(glutaric acid), Lys(IVA), Lys(Peg4-isoGlu-Palm), Lys(pyroglutaric acid), Lys-succinic acid, Asn, Orn,Gln, Arg, or Val;

X14 is Dab(Ac), Dap(Ac), His, Lys(Ac), Asn, Gln, or Tyr; and

X15 is Ala, βAla, Gly, Asn, Gln, or Ser.

5. The peptide inhibitor of claim 1, wherein:

X1 is absent;

X2 is absent;

X3 is absent;

X4 is Cys, Abu or Pen;

X5 is Dap, Dap(Ac), Gln, Ser, Thr or Asn;

X6 is Thr;

X7 is Trp;

X8 is Gln;

X9 is Cys, Abu or Pen;

X10 is a Phe analog, Tyr, or a Tyr analog;

X11 is 2-Nal or Trp;

X12 is Acpc, Acbc, Acvc, Achc, Aib, α-DiethylGly, α-MeLys, α-MeLys(Ac), α-MeLeu, α-MeOrn, α-MeSer, α-MeVal, hLeu, Leu, or THP;

X13 is Cit, Asp, Glu, Lys, Lys(Ac), Asn, or Gln;

X14 is Dab(Ac), Asn, or His; and

X15 is Ala, betaAla, Gly, Asn, or Gln.

6. The peptide inhibitor of claim 1, wherein

X4 is Cys, Pen, hCys, D-Pen, D-Cys, D-hCys, Met, Glu, Asp, Lys, Orn, Dap, Dab, D-Dap, D-Dab, D-Asp, D-Glu, D-Lys, Sec, 2-chloromethylbenzoic acid, mercapto-propanoic acid,

mercapto-butyric acid, 2-chloro-acetic acid, 3-choro-propanoic acid, 4-chloro-butyric acid, 3-chloro-isobutyric acid, Abu, β-azido-Ala-OH, propargylglycine, 2-(3'-butenyl)glycine, 2-allylglycine, 2-(3'-butenyl)glycine, 2-(4'-pentenyl)glycine, 2-(5'-hexenyl)glycine, or Abu;

X7 is Trp, Glu, Gly, Ile, Asn, Pro, Arg, Thr or OctGly, or a corresponding α-methyl amino acid form of any of the foregoing;

X9 is Cys, Pen, hCys, D-Pen, D-Cys, D-hCys, Glu, Lys, Orn, Dap, Dab, D-Dap, D-Dab, D-Asp, D-Glu, D-Lys, Asp, Leu, Val, Phe, or Ser, Sec, Abu, β-azido-Ala-OH, propargylglycine, 2-2-allylglycine, 2-(3'-butenyl)glycine, 2-(4'-pentenyl)glycine, Ala, hCys, Abu, Met, MeCys, (D)Tyr or 2-(5'-hexenyl)glycine;

X10 is Tyr, Phe(4-OMe), 1-Nal, 2-Nal, Aic, α-MePhe, Bip, (D)Cys, Cha, DMT, (D)Tyr, Glu, His, hPhe(3,4-dimethoxy), hTyr, N-Me-Tyr, Trp, Phe(4-$CONH_2$), Phe(4-phenoxy), Thr, Tic, Tyr(3-tBu), Phe(4-tBu), Phe(4-CN), Phe(4-Br), Phe(4-$NH_2$), Phe(4-F), Phe(3,5-$F_2$), Phe(4-$CH_2CO_2H$), Phe(penta-F), Phe(3,4-$Cl_2$), Phe(4-$CF_3$), Phe(4-$OCH_3$), Bip, Cha, 4-PyridylAlanine, βhTyr, OctGly, Phe(4-$N_3$), Phe(4-Br), Phe[4-(2-aminoethoxy)] or Phe, a Phe analog, a Tyr analog, or a corresponding α-methyl amino acid form of any of the foregoing;

X11 is 2-Nal, 1-Nal, 2,4-dimethylPhe, Bip, Phe(3,4-$Cl_2$), Phe (3,4-$F_2$), Phe(4-$CO_2H$), βhPhe(4-F), α-Me-Trp, 4-phenylcyclohexyl, Phe(4-$CF_3$), α-MePhe, βhNal, βhPhe, βhTyr, βhTrp, Nva(5-phenyl), Phe, His, hPhe, Tic, Tqa, Trp, Tyr, Phe(4-OMe), Phe(4-Me), Trp(2,5,7-tri-tert-Butyl), Phe(4-Oallyl), Tyr(3-tBu), Phe(4-tBu), Phe(4-guanidino, Phe(4-OBzl), Octgly, Glu(Bzl), 4-Phenylbenzylalanine, Phe[4-(2-aminoethoxy)], 5-Hydroxy-Trp, 6-Chloro-Trp, N-MeTrp, 1,2,3,4-tetrahydro-norharman, Phe(4-$CONH_2$), Phe(3,4-Dimethoxy), Phe(2,3-$Cl_2$), Phe(2,3-$F_2$), Phe(4-F), 4-phenylcyclohexylalanine, Bip, or a corresponding α-methyl amino acid form of any of the foregoing;

X12 is His, Phe, Arg, N-Me-His, Val, Cav, Cpa, Leu, Cit, hLeu, 3-Pal, t-butyl-Ala, 4-amino-4-carboxy-tetrahydropyran, Achc Acpc, Acbc, Acvc, Agp, Aib, α-DiethylGly, α-MeLys, α-MeLys(Ac), α-Me-Leu, α-MeOrn, α-MeSer, α-MeVal, Aib,, D-Ala, (D)Asn, (D)Asp, (D)Leu, (D)Phe, (D)Tyr, Aib, α-MeLeu, α-MeOrn, β-Aib, β-Ala, βhAla, βhArg, βhLeu, βhVal, β-spiro-pip, Glu, hArg, Ile, Lys, N-MeLeu, N-MeArg, Ogl, Orn, Pro, Gln, Ser, Thr, Tle, t-butyl-Gly, or a corresponding α-methyl amino acid form of any of the foregoing;

X13 is Thr, Sarc, Glu, Phe, Arg, Leu, Lys, Arg, Orn, Val, βhAla, Lys(Ac), (D)Asn, (D)Leu, (D)Phe, (D)Thr, Ala, α-MeLeu, Aib, β-Ala, β-Glu, βhLeu, βhVal, β-spiro-pip, Cha, Chg, Asp, Dab, Dap, α-DiethylGly, hLeu, Asn, Ogl, Pro, Gln, Ser, β-spiro-pip, Thr, Tba, Tle or Aib, Cit, hArg, Lys, Asn, Orn, Gln or a corresponding α-methyl amino acid form of any of the foregoing;
X14 is Phe, Tyr, Glu, Gly, His, Lys, Leu, Met, Asn, Pro, Gln, Arg, Ser, Thr, TicβhPhe, Arg, Lys(Ac), His; Dap(Ac), Dab(Ac), Asp or a corresponding α-methyl amino acid form of any of the foregoing;
X15 is Gly, Ser, Thr, Gln, Ala, (D)Ala, (D)Asn, (D)Asp, (D)Leu, (D)Phe, (D)Thr, Aea, Asp, Asn, Glu, Phe, Gly, Lys, Leu, Pro, Arg, β-Ala, Sarc, or a corresponding α-methyl amino acid form of any of the foregoing;
X16 is Asp, Glu, Ala, AEA, AEP, βhAla, Gaba, Gly, Ser, Pro, Asn, Thr or absent, or a corresponding α-methyl amino acid form of any of the foregoing; and
X17 is Leu, Lys, Arg, Glu, Ser, Gly, Gln or absent, or a corresponding α-methyl amino acid form of any of the foregoing.

7. The peptide inhibitor of claim 1 or claim 6, wherein the bond between X4 and X9, is a disulfide bond, a thioether bond, a lactam bond, a triazole ring, a selenoether bond, a diselenide bond, or an olefin bond.

8. The peptide inhibitor of any one of claims 1-7, wherein X4 is Cys and X9 is Cys, and the bond is a disulfide bond.

9. The peptide inhibitor of any one of claims 1-7, wherein X4 is Pen and X9 is Pen, and the bond is a disulfide bond.

10. The peptide inhibitor of claim 8 or claim 9, wherein
X7 is Trp;
X10 is Phe, Tyr, a Phe analog, or a Tyr analog;
X11 is Trp, 1-Nal or 2-Nal; and
X12 is Aib, α-Me-Lys, α-Me-Val α-Me-Leu; Achc, Acvc, Acpc, Acpc or THP,.

11. The peptide inhibitor of claim 10, wherein the peptide inhibitor comprises any of the following the amino acid sequences:

Ac-[Pen]-Q-T-W-Q-[Pen]-[Phe(4-OMe)]-[2-Nal]-[α-Me-Lys]-ENG-$NH_2$ (SEQ ID NO: 282);

Ac-[Pen]-N-T-W-Q-[Pen]-[Phe[4-(2-aminoethoxy)]-[2-Nal]-[Aib]-[Lys(Ac)]-NN-$NH_2$ (SEQ ID NO: 283);

Ac-[Pen]-Q-T-W-Q-[Pen]-[Phe[4-(2-aminoethoxy)]-[2-Nal]-[α-MeLeu]-[Lys(Ac)]-NN-$NH_2$ (SEQ ID NO: 285);

Ac-[Pen]-QTWQ-[Pen]-[Phe(4-$CONH_2$)]-[2-Nal]-[α-MeLys]-[Lys(Ac)]-NN-$NH_2$(SEQ ID NO: 668);

Ac-[Pen]-QTWQ-[Pen]-[Phe[4-(2-aminoethoxy)]-[2-Nal]-[α-MeLeu]-QNN-$NH_2$ (SEQ ID NO: 603);

Ac-[Pen]-Q-T-W-Q-[Pen]-[Phe(4-$CONH_2$)]-[2-Nal]-[α-MeLys]-[Lys(Ac)]-NN-$NH_2$ (SEQ ID NO: 286);

Ac-[Pen]-QTWQ-[Pen]-[Phe[4-(2-aminoethoxy)]-[2-Nal]-[α-MeLys]-[Lys(Ac)]-NG-$NH_2$ (SEQ ID NO: 598);

Ac-[Pen]-QTWQ-[Pen]-[Phe[4-(2-aminoethoxy)]-[2-Nal]-[α-MeLys]-[Lys(Ac)]-NN-$NH_2$ (SEQ ID NO: 1034);

Ac-[Pen]-QTWQ-[Pen]-[Phe[4-(2-aminoethoxy)]-[2-Nal]-[α-MeLys]-ENA-$NH_2$ (SEQ ID NO: 601);

Ac-[Pen]-QTWQ-[Pen]-[Phe[4-(2-aminoethoxy)]-[2-Nal]-[α-MeLeu]-[Lys(Ac)]-NN-$NH_2$ (SEQ ID NO: 602);

Ac-[Pen]-QTWQ-[Pen]-[Phe[4-(2-aminoethoxy)]-[2-Nal]-[α-MeLeu]-QNN-$NH_2$ (SEQ ID NO: 603);

Ac-[Pen]-QTWQ-[Pen]-[Phe[4-(2-aminoethoxy)]-[2-Nal]-[Aib]-ENN-$NH_2$ (SEQ ID NO: 604);

Ac-[Pen]-QTWQ-[Pen]-[Phe[4-(2-aminoethoxy)]-[2-Nal]-Aib-[Lys(Ac)]-NN-$NH_2$ (SEQ ID NO: 605);

Ac-[Pen]-QTWQ-[Pen]-[Phe[4-(2-aminoethoxy)]-[2-Nal]-[Aib]-[Lys(Ac)]-NQ-$NH_2$ (SEQ ID NO: 606);

Ac-[Pen]-QTWQ-[Pen]-[Phe[4-(2-acetylaminoethoxy)]-[2-Nal]-[α-MeLeu]-[Lys(Ac)]-NN-$NH_2$ (SEQ ID NO: 613);
Ac-[Pen]-QTWQ-[Pen]-[Phe[4-(2-acetylaminoethoxy)]-[2-Nal]-[α-MeLeu]-QNN-$NH_2$ (SEQ ID NO: 614);
Ac-[Pen]-NTWQ-[Pen]-[Phe[4-(2-aminoethoxy)]-[2-Nal]-[Aib]-[Lys(Ac)]-N-[βAla]-$NH_2$ (SEQ ID NO: 639);
Ac-[Pen]-NTWQ-[Pen]-[Phe[4-(2-aminoethoxy)]-[2-Nal]-[hLeu]-[Lys(Ac)]-N-[βAla]-$NH_2$ (SEQ ID NO: 641);
Ac-[Pen]-QTWQ-[Pen]-[Phe[4-(2-acetylaminoethoxy)]-[2-Nal]-[Aib]-[Lys(Ac)]-NN-$NH_2$ (SEQ ID NO: 616);
Ac-[Pen]-NTWQ-[Pen]-[Phe[4-(2-aminoethoxy)]-[2-Nal]-[Aib]-[Lys(Ac)]-NN-$NH_2$ (SEQ ID NO: 632);
Ac-[Pen]-QTWQ-[Pen]-[Phe[4-(2-acetylaminoethoxy)]-[2-Nal]-[Aib]-[Lys(Ac)]-NQ-$NH_2$ (SEQ ID NO: 617); or
Ac-[Pen]-QTWQ-[Pen]-[Phe(4-OMe)]-[2-Nal]-[Aib]-[Lys(Ac)]-NQ-$NH_2$ (SEQ ID NO: 623),
wherein the peptide inhibitor comprises a disulfide bond between the two Pen amino acids.

12. The peptide inhibitor of claim 1 or claim 6, wherein
X4 is an amino acid, aliphatic acid, alicyclic acid or modified 2- methyl aromatic acid having a carbon side chain capable of forming a thioether bind with X9;
X9 is a sulfur-containing amino acid capable of forming a thioether bond with X4,
and the bond between X4 and X9 is a thioether bond.

13. The peptide inhibitor of claim 12, wherein
X4 is Abu, 2-chloromethylbenzoic acid, mercapto-propanoic acid, mercapto-butyric acid, 2-chloro-acetic acid, 3-chloro-propanoic acid, 4-chloro-butyric acid, 3-chloro-isobutyric acid; and
X9 is Abu, Cys, Pen, hCys, D-Pen, D-Cys, or D-hCys.

14. The peptide inhibitor of claim 13, wherein
(a) X4 is Abu and X9 is Cys; or

(b) X4 is Cys and X9 is Abu.

wherein the peptide inhibitor is cyclized via a thioether bond between X4 and X9.

15. The peptide inhibitor of claim 13 or claim 14, wherein

X7 is Trp;

X10 is Phe, Tyr, a Phe analog, or a Tyr analog;

X11 is Trp, 1-Nal or 2-Nal; and

X12 is α-Me-Lys, α-Me-Leu, α-Me-Ser, α-Me-Val, Achc, Acvc, Acpc, Acbc or 4-amino-4-carboxy-tetrahydropyran.

16. The peptide inhibitor of claim 15, wherein the peptide inhibitor comprises any of the following amino acid sequences:

Ac-Cyclo-[[Abu]-QTWQC]]-[Phe(4-OMe)]-[2-Nal]-[α-MeLys]-E-N-G (SEQ ID NO: 430);

Ac-Cyclo-[[Abu]-QTWQC]]-[Phe(4-OMe)]-[2-Nal]-[α-MeOrn]-ENG-$NH_2$ (SEQ ID NO: 431);

Ac-Cyclo-[[Abu]-QTWQC]]-[Phe(4-$CO_2H$)]-[2-Nal]-[α-MeLys]-[Lys(Ac)]-NG-$NH_2$ (SEQ ID NO: 432);

Ac-Cyclo-[[Abu]-QTWQC]]-[Phe(4-OMe)]-[2-Nal]-[α-MeLys]-[Lys(Ac)]-NG-$NH_2$ (SEQ ID NO: 433);

Ac-Cyclo-[[Abu]-QTWQC]]-[Phe(4-$CONH_2$)]-[2-Nal]-[α-MeLys]-[Lys(Ac)]NG-$NH_2$ (SEQ ID NO: 434);

Ac-Cyclo-[[Abu]-QTWQC]]-[Phe(4-OMe)]-[2-Nal]-[α-MeLys]-[Lys(Ac)]-NA-$NH_2$ (SEQ ID NO: 435);

Ac-Cyclo-[[Abu]-QTWQC]]-[Phe(4-OMe)]-[2-Nal]-[α-MeLys]-[Lys(Ac)]-NAE-$NH_2$ (SEQ ID NO: 436);

Ac-Cyclo-[[Abu]-QTWQC]]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[α-MeLys]-ENG-$NH_2$ (SEQ ID NO: 437);

Ac-Cyclo-[[Abu]-QTWQC]]-[Phe(4-(2-aminoethoxy))]-W-[α-MeLys]-E-N-G (SEQ ID NO: 438);

Ac-Cyclo-[[Abu]-QTWQC]]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[α-MeLys]-DNG-$NH_2$ (SEQ ID NO: 439);

Ac-Cyclo-[[Abu]-QTWQC]]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[α-MeLys]-[Lys(succinic acid)]-NG-$NH_2$ (SEQ ID NO: 440);

Ac-Cyclo-[[Abu]-QTWQC]]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[α-MeLys]-[Lys(glutaric acid)]-NG-$NH_2$ (SEQ ID NO: 441);

Ac-Cyclo-[[Abu]-QTWQC]]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[α-MeLys]-[Lys(pyroglutamic acid)]-NG-$NH_2$ (SEQ ID NO: 442);

Ac-Cyclo-[[Abu]-QTWQC]]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[α-MeLys]-[Lys(isovaleric acid)]-NG-$NH_2$ (SEQ ID NO: 443);

Ac-Cyclo-[[Abu]-QTWQC]]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[α-MeLys]-[Lys(Ac)]-NG-[(D)Lys]-$NH_2$ (SEQ ID NO: 444);

Ac-Cyclo-[[Abu]-QTWQC]]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[α-MeLys]-[Lys(Ac)]-NG-[AEA]-$NH_2$ (SEQ ID NO: 445);

Ac-Cyclo-[[Abu]-QTWQC]]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[Aib]-QNG-$NH_2$ (SEQ ID NO: 446);

Ac-Cyclo-[[Abu]-QTWQC]]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[Aib]-[Lys(Ac)]-NA-$NH_2$ (SEQ ID NO: 447);

Ac-Cyclo-[[Abu]-QTWQC]]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[Aib]-KNG-$NH_2$ (SEQ ID NO: 448);

Ac-Cyclo-[[Abu]-QTWQC]]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[α-MeLys]-[Lys(Ac)]-NG-$NH_2$ (SEQ ID NO: 449);

Ac-Cyclo-[[Abu]-QTWQC]]-[Phe[4-(2-(acetyl-aminoethoxy)]]-[2-Nal]-[α-MeLys(Ac)]-[Lys(Ac)]-NG-$NH_2$ (SEQ ID NO: 656);

Ac-Cyclo-[[Abu]-QTWQC]]-[Phe[4-(2-(acetyl-aminoethoxy)]]-[2-Nal]-[α-MeLys(Ac)]-ENG-$NH_2$ (SEQ ID NO: 657);

Ac-Cyclo-[[Abu]-QTWQC]]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[4-amino-4-carboxy-tetrahydropyran]-ENN-$NH_2$ (SEQ ID NO: 658);

Ac-Cyclo-[[Abu]-QTWQC]]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[α-MeLys]-ENQ-$NH_2$ (SEQ ID NO: 659);

Ac-Cyclo-[[Abu]-QTWQC]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[α-MeLys]-ENN-$NH_2$ (SEQ ID NO: 912);

Ac-Cyclo-[[Abu]-QTWQC]]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[α-MeVal]-[Lys(Ac)]-NG-$NH_2$ (SEQ ID NO: 660);

Ac-Cyclo-[[Abu]-QTWQC]]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[hLeu]-[Lys(Ac)]-N-[βAla]-$NH_2$ (SEQ ID NO: 661);

Ac-Cyclo-[[Abu]-QTWQC]]-[Phe[4-(2-(acetyl-aminoethoxy)]]-[2-Nal]-[α-MeLys(Ac)]-ENQ-$NH_2$ (SEQ ID NO: 662);

Ac-Cyclo-[[Abu]-QTWQC]]-[Phe[4-(2-(acetyl-aminoethoxy)]]-[2-Nal]-[α-MeLys(Ac)]-ENN-$NH_2$ (SEQ ID NO: 663);

Ac-Cyclo-[[Abu]-QTWQC]]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[α-MeLeu]-ENN-$NH_2$ (SEQ ID NO: 664);

Ac-Cyclo-[[Abu]-QTWQC]]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[α-MeLeu)-[Cit]-NN-$NH_2$ (SEQ ID NO: 665);

Ac-Cyclo-[[Abu]-QTWQC]]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[α-MeLeu]-[Lys(Ac)]-NN-$NH_2$ (SEQ ID NO: 766);

Ac-Cyclo-[[Abu]-QTWQC]]-[ Phe[4-(2-aminoethoxy)]]-[2-Nal]-[Aib]-[Lys(Ac)]-NG-$NH_2$ (SEQ ID NO: 767);

Ac-E-Cyclo-[[Abu]-QTWQC]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[α-MeLys]-ENN-$NH_2$ (SEQ ID NO: 965);

Ac-(D)Glu-[Cyclo-[[Abu]-QTWQC]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[α-MeLys]-ENN-$NH_2$ (SEQ ID NO: 966);

Ac-Arg-Cyclo-[[Abu]-QTWQC]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[α-MeLys]-ENN-$NH_2$ (SEQ ID NO: 967);

Ac-[(D)Arg-Cyclo-[[Abu]-QTWQC]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[α-MeLys]-ENN-$NH_2$ (SEQ ID NO: 1041);

Ac-F-Cyclo-[[Abu]-QTWQC]]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[α-MeLys]-ENN-$NH_2$ (SEQ ID NO: 969);

Ac-[(D)Phe]-Cyclo-[[Abu]-QTWQC]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[α-MeLys]-ENN-$NH_2$ (SEQ ID NO: 970);

Ac-[2-Nal]-Cyclo-[[Abu]-QTWQC]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[α-MeLys]-ENN-$NH_2$ (SEQ ID NO: 971);

Ac-Leu-Cyclo-[[Abu]-QTWQC]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[α-MeLys]-ENN-$NH_2$ (SEQ ID NO: 973);

Ac-[(D)Gln]-Cyclo-[[Abu]-QTWQC]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[α-MeLys]-ENN-$NH_2$ (SEQ ID NO: 1042);

Ac-Cyclo-[[Abu]-QTWQC]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[α-MeLeu]-ENG-$NH_2$ (SEQ ID NO: 842);

Ac-T-Cyclo-[[Abu]-QTWQC]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[α-MeLys]-ENN-$NH_2$ (SEQ ID NO: 972);

Ac-Cyclo-[[Abu]-QTWQC]]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[α-MeLeu]-QN-[βAla]-$NH_2$ (SEQ ID NO: 752);

Ac-Cyclo-[[Abu]-QTWQC]]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[Acbc]-ENN-$NH_2$ (SEQ ID NO: 753);

Ac-Cyclo-[[Abu]-QTWQC]]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[Achc]- ENN-$NH_2$ (SEQ ID NO: 754);

Ac-Cyclo-[[Abu]-QTWQC]]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[Acvc]-ENN-$NH_2$ (SEQ ID NO: 755);

Ac-Cyclo-[[Abu]-QTWQC]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[4-amino-4-carboxy-piperidine]-ENN-$NH_2$ (SEQ ID NO: 979); or

Ac-Cyclo-[[Abu]-QTWQC]-[Phe[4-(2-aminoethoxy)]]-[2-Nal]-[4-amino-4-carboxy-tetrahydropyran]-ENN-$NH_2$ (SEQ ID NO: 980),

wherein the peptide inhibitor comprises a thioether bond between the Abu and the C.

17. The peptide inhibitor of claim 1,

wherein

X4 is Pen, Cys or homo-Cys;

X5 is any amino acid;

X6 is any amino acid;

X7 is Trp, Bip, Gln, His, Glu(Bzl), 4-Phenylbenzylalanine, Tic, Phe[4-(2-aminoethoxy)], Phe(3,4-$Cl_2$), Phe(4-OMe), 5-Hydroxy-Trp, 6-Chloro-Trp, N-MeTrp, α-Me-Trp, 1,2,3,4 - tetrahydro-norharman, Phe(4-$CO_2H$), Phe(4-$CONH_2$), Phe(3,4-Dimethoxy), Phe(4-$CF_3$), Phe(4-tBu), ββ-diPheAla, Glu, Gly, Ile, Asn, Pro, Arg, Thr or Octgly, or a corresponding α-methyl amino acid form of any of the foregoing;

X8 is any amino acid;

X9 is Pen, Cys or hCys;

X10 is 1-Nal, 2-Nal, Aic, Bip, (D)Cys, Cha, DMT, (D)Tyr, Glu, Phe, His, Trp, Thr, Tic, Tyr, 4-pyridylAla, Octgly, a Phe analog or a Tyr analog (optionally, Phe(3,4-$F_2$), Phe(3,4-$Cl_2$), F(3-Me), Phe[4-(2-aminoethoxy)], Phe[4-(2-(acetyl-aminoethoxy)], Phe(4-Br), Phe(4-$CONH_2$), Phe(4-Cl), Phe(4-CN), Phe(4-guanidino), Phe(4-Me), Phe(4-$NH_2$), Phe(4-$N_3$), Phe(4-OMe), or Phe(4-OBzl)), or a corresponding α-methyl amino acid form of any of the foregoing;

X11 is 2-Nal, 1-Nal, 2,4-dimethylPhe, Bip, Phe(3,4-$Cl_2$), Phe (3,4-$F_2$), Phe(4-$CO_2H$), βhPhe(4-F), α-Me-Trp, 4-phenylcyclohexyl, Phe(4-$CF_3$), α-MePhe, βhNal, βhPhe, βhTyr, βhTrp, Nva(5-phenyl), Phe, His, hPhe, Tic, Tqa, Trp, Tyr, Phe(4-OMe), Phe(4-Me), Trp(2,5,7-tri-tert-Butyl), Phe(4-Oallyl), Tyr(3-tBu), Phe(4-tBu), Phe(4-guanidino, Phe(4-OBzl), Octgly, Glu(Bzl), 4-Phenylbenzylalanine, Phe[4-(2-aminoethoxy)], 5-Hydroxy-Trp, 6-Chloro-Trp, N-MeTrp, 1,2,3,4-tetrahydro-norharman, Phe(4-$CONH_2$), Phe(3,4-$OMe_2$) Phe(2,3-$Cl_2$), Phe(2,3-$F_2$), Phe(4-F), 4-phenylcyclohexylalanine or Bip, or a corresponding α-methyl amino acid form of any of the foregoing;

X12 is α-MeLys, α-MeOrn, α-MeLeu, α-MeVal, 4-amino-4-carboxy-tetrahydropyran, Achc Acpc, Acbc, Acvc, MeLeu, Aib, (D)Ala, (D)Asn, (D)Leu, (D)Asp, (D)Phe, (D)Thr, 3-Pal, Aib, β-Ala, βhGlu, βhAla, βhLeu, βhVal, β-spiro-pip, Cha, Chg, Asp, Dab, Dap, α-diethylGly, Glu, Phe, hLeu, hArg, hLeu, Ile, Lys, Leu, Asn, N-MeLeu, N-MeArg, Ogl, Orn, Pro, Gln, Arg, Ser, Thr or Tle, or a corresponding α-methyl amino acid form of any of the foregoing;

X13 is Lys(Ac), (D)Asn, (D)Leu, (D)Thr, (D)Phe, Ala, Aib, α-MeLeu, β-Ala, βhGlu, βhAla, βhLeu, βhVal, β-spiro-pip, Cha, Chg, Asp, Lys, Arg, Orn, Dab, Dap, α-diethylGly, Glu, Phe, hLeu, Lys, Leu, Asn, Ogl, Pro, Gln, Asp, Arg, Ser, spiro-pip, Thr, Tba, Tlc, Val or Tyr, or a corresponding α-methyl amino acid form of any of the foregoing;

X14 is Asn, Glu, Phe, Gly, His, Lys, Leu, Met, Asn, Pro, Gln, Arg, Ser, Thr, Tic or Tyr, Lys(Ac), Orn or a corresponding α-methyl amino acid form of any of the foregoing;
X15 is Gly, (D)Ala, (D)Asn, (D)Asp, Asn, (D)Leu, (D)Phe, (D)Thr, Ala, Asn, Ser, AEA, Asp, Glu, Phe, Gly, Lys, Leu, Pro, Gln, Arg or Ser, β-Ala, Arg or a corresponding α-methyl amino acid form of any of the foregoing;
X16 is absent, Gly, Ala, Asp, Ser, Pro, Asn or Thr, or a corresponding α-methyl amino acid form of any of the foregoing;
X17 is absent, Glu, Ser, Gly or Gln, or a corresponding α-methyl amino acid form of any of the foregoing;
X18 is absent or any amino acid;
X19 is absent or any amino acid; and
X20 is absent or any amino acid.

18. The peptide inhibitor of claim 17, wherein the bond between X4 and X9 is a disulfide bond.

19. The peptide inhibitor of any one of claims 1-18, wherein one or more of X1, X2, and X3 are absent.

20. The peptide inhibitor of any one of claims 1-19, wherein one or more of X17, X19 and X20 are absent.

21. The peptide inhibitor of any one of claims 17-20, wherein one or both of X4 or X9 is Pen.

22. The peptide inhibitor of claim 21, wherein both X4 and X9 are Pen.

23. The peptide inhibitor of any one of claims 17-22, wherein X18 is (D)-Lys.

24. The peptide inhibitor of any one of claims 17-23, comprising one or more, two or more, three or more, or four of the following:
X5 is Arg, Asn, Gln, Dap, Orn;

X6 is Thr or Ser;
X7 is Trp, 2-Nal, 1-Nal, Phe(4-OAllyl), Tyr(3-tBu), Phe(4-tBu), Phe(4-guanidino), Phe(Bzl) or Phe(4-Me), 5-Hydroxy-Trp, 6-Chloro-Trp, N-MeTrp, α-MeTrp or 1,2,3,4 -tetrahydro-norharman; and
X8 is Gln, Val, Phe, Glu, Lys.

25. The peptide inhibitor of any one of claims 17-24, comprising one or more, two or more, three or more, four or more, five or more, six or more, or seven of the following:
X10 is Tyr, Phe(4-OBzl), Phe(4-OMe), Phe(4-$CONH_2$), Phe(3,4-$Cl_2$), Phe(4-tBu), Phe(4-$NH_2$), Phe(4-Br), Phe(4-CN), Phe(4-$CO_2H$), Phe(4-(2aminoethoxy)) or Phe(4-guanidino) ;
X11 is Trp, 2-Nal, 1-Nal, Phe(4-OAllyl), Tyr(3-tBu), Phe(4-tBu), Phe(4-guanidino), Phe(Bzl) or Phe(4-Me), 5-Hydroxy-Trp, 6-Chloro-Trp, N-MeTrp, α-MeTrp or 1,2,3,4 -tetrahydro-norharman;
X12 is Arg, α-MeLys α-MeLeu, Aib or α-MeOrn;
X13 is Lys, Glu or Lys(Ac);
X14 is Phe or Asn;
X15 is Asn, Gly, Ser βAla, or Ala; and
X16 is absent or AEA.

26. The peptide inhibitor of claim 25, wherein X4 and X9 are Pen; X5 is Gln; X6 is Thr; X7 is Trp; X8 is Gln; X10 is Tyr, Phe(4-OMe) or 2-Nal; X11 is Trp, 2-Nal or 1-Nal; X12 is Arg, αMeLys or α-MeOrn; X13 is Lys, Glu or Lys(Ac); X14 is Phe or Asn; X15 is Gly; and X16 is absent.

27. The peptide inhibitor of claim 26, wherein one or more of X1, X2 and X3 are absent; and one or more, two or more, three or more, or four of X17, X18, X19 and X20 are absent.

28. The peptide inhibitor of claim 1,
wherein
X4 is Abu, Pen, or Cys;

X7 is Trp, Bip, Gln, His, Glu(Bzl), 4-Phenylbenzylalanine, Tic, Phe[4-(2-aminoethoxy)], Phe(3,4-$Cl_2$), Phe(4-OMe), 5-Hydroxy-Trp, 6-Chloro-Trp, N-MeTrp, α-MeTrp, 1,2,3,4 -tetrahydro-norharman, Phe(4-$CO_2H$), Phe(4-$CONH_2$), Phe(3,4-Dimethoxy), Phe(4-$CF_3$), ββ-diPheAla, Phe(4-tBu), Glu, Gly, Ile, Asn, Pro, Arg, Thr or Octgly, or a corresponding α-methyl amino acid form of any of the foregoing;

X9 is Abu, Pen, or Cys;

X10 is 1-Nal, 2-Nal, Aic, Bip, (D)Cys, Cha, DMT, (D)Tyr, Glu, Phe, His, Trp, Thr, Tic, Tyr, 4-pyridylAla, Octgly a Phe analog or a Tyr analog, or a corresponding α-methyl amino acid form of any of the foregoing;

X11 is 2-Nal, 1-Nal, 2,4-dimethylPhe, Bip, 4-phenylcyclohexyl, Glu(Bzl), 4-Phenylbenzylalanine, Tic, Phe[4-(2-aminoethoxy)], Phe(3,4-$Cl_2$), Phe(3,4-$F_2$), βhPhe(4-F), Phe(4-OMe), 5-Hydroxy-Trp, 6-Chloro-Trp, N-MeTrp, α-MeTrp, 1,2,3,4 -tetrahydro-norharman, Phe(4-$CO_2H$), Phe(4-$CONH_2$), Phe(3,4-Dimethoxy), Phe(4-$CF_3$), Phe(2,3-$Cl_2$), Phe(2,3-$F_2$),Phe(4-F), 4-phenylcyclohexylalanine, α-MePhe, βhNal, βhPhe, βhTyr, βhTrp, Bip, Nva(5-phenyl), Phe, His, hPhe, Tqa, Trp, Tyr, Phe(4-Me), Trp(2,5,7-tri-tertButyl), Phe(4-OAllyl), Tyr(3-tBu), Phe(4-tBu), Phe(4-guanidino), Phe(4-OBzl), or Octgly, or a corresponding α-methyl amino acid form of any of the foregoing;

X12 is α-MeLys, α-MeOrn, α-MeLeu, MeLeu, Aib, Achc, Acvc, Acpc, Acpc, THP, (D)Ala, (D)Asn, (D)Leu, (D)Asp, (D)Phe, (D)Thr, 3-Pal, Aib, β-Ala, βhGlu, βhAla, βhLeu, βhVal, β-spiro-pip, Cha, Chg, Asp, Dab, Dap, α-DiethylGly, Glu, Phe, hLeu, hArg, hLeu, Ile, Lys, Leu, Asn, N-MeLeu, N-MeArg, Ogl, Orn, Pro, Gln, Arg, Ser, Thr or Tle, or a corresponding α-methyl amino acid form of any of the forego`ing;

X13 is Lys(Ac), (D)Asn, (D)Leu, (D)Thr, (D)Phe, Ala, Aib, α-MeLeu, βAla, βhGlu, βhAla, βhLeu, βhVal, β-spiro-pip, Cha, Chg, Asp, Arg, Orn, Dab, Dap, α-DiethylGly, Glu, Phe, hLeu, Lys, Leu, Asn, Ogl, Pro, Gln, Asp, Arg, Ser, spiro-pip, Thr, Tba, Tlc, Val or Tyr, or a corresponding α-methyl amino acid form of any of the foregoing;

X14 is Asn, Glu, Phe, Gly, His, Lys, Leu, Met, Asn, Pro, Gln, Arg, Ser, Thr, Tic or Tyr, or a corresponding α-methyl amino acid form of any of the foregoing;

X15 is Gly, (D)Ala, (D)Asn, (D)Asp, Asn, (D)Leu, (D)Phe, (D)Thr, Ala, AEA, Asp, Glu, Phe, Gly, Lys, Leu, Pro, Gln, Arg or Ser, or a corresponding α-methyl amino acid form of any of the foregoing;
X16 is absent, Gly, Ala, Asp, Ser, Pro, Asn or Thr, or a corresponding α-methyl amino acid form of any of the foregoing; and
X17 is absent, Glu, Ser, Gly or Gln, or a corresponding α-methyl amino acid form of any of the foregoing.

29. The peptide inhibitor of claim 28, wherein the peptide inhibitor is cyclized via an intramolecular bond between X4 and X9.

30. The peptide inhibitor of claim 28 or claim 29, wherein one or more of X1, X2, and X3 are absent.

31. The peptide inhibitor of any one of claims 28-30, wherein one or more of X17, X19 and X20 are absent.

32. The peptide inhibitor of any one of claims 28-31, wherein one of X4 or X9 is Abu, and the other of X4 or X9 is not Abu.

33. The peptide inhibitor of any one of claims 28-32, comprising one or more, two or more, three or more, or four of the following:
X5 is Arg, Gln, Dap or Orn;
X6 is Thr or Ser;
X7 is Trp, 2-Nal, 1-Nal, Phe(4-OAllyl), Tyr(3-tBu), Phe(4-tBu), Phe(4-guanidino), Phe(4-OBzl), Phe(4-Me), 5-Hydroxy-Trp, 6-Chloro-Trp, N-MeTrp, or α-MeTrp, 1,2,3,4 -tetrahydro-norharman; and
X8 is Gln, Val, Phe, Glu or Lys.

34. The peptide inhibitor of any one of claims 28-33, comprising one or more, two or more, three or more, four or more, five or more, six or more, or seven of the following:
X10 is Tyr, Phe(4-OBzl), Phe(4-OMe), Phe(4-$CONH_2$), Phe(3,4-$Cl_2$), Phe(4-tBu), Phe(4-$NH_2$), Phe(4-Br), Phe(4-CN), Phe(4-$CO_2H$), Phe(4-(2aminoethoxy)) or Phe(4-guanadino);
X11 is Trp, 2-Nal, 1-Nal, Phe(4-OAllyl), Tyr(3-tBu), Phe(4-tBu), Phe(4-guanidino), Phe(Bzl) or Phe(4-Me), 5-Hydroxy-Trp, 6-Chloro-Trp, N-MeTrp, α-MeTrp or 1,2,3,4 -tetrahydro-norharman;
X12 is Arg, hLeu, (D)Asn, Aib, α-MeLys, α-MeLeu, α-Me-Val, α-MeOrn, Achc, Acvc, Acpc, Acpc, or THP;
X13 is Lys, Glu or Lys(Ac);
X14 is Phe or Asn;
X15 is Gly, Ser, Asn, βAla or Ala; and
X16 is absent or AEA.

35. The peptide inhibitor of any one of claims 1-34, wherein the peptide inhibitor comprises the structure of Formula I:

$$R^1\text{-}X\text{-}R^2 \quad (I)$$

or a pharmaceutically acceptable salt or solvate thereof, wherein
$R^1$ is a bond, hydrogen, a C1-C6 alkyl, a C6-C12 aryl, a C6-C12 aryl, a C1-C6 alkyl, a C1-C20 alkanoyl, and including PEGylated versions alone or as spacers of any of the foregoing; X is the amino acid sequence; and
$R^2$ is OH or $NH_2$.

36. A peptide dimer inhibitor of an interleukin-23 receptor, wherein the peptide dimer inhibitor comprises two peptide monomer subunits connected via one or more linker moieties, wherein each peptide monomer subunit has a sequence or structure set forth in any one of claims 1-35.

37. The peptide dimer inhibitor of claim 36, wherein one or both peptide monomer subunit is cyclized via an intramolecular bond between X4 and X9.

38. The peptide dimer inhibitor of claim 37, wherein one or both intramolecular bond is a disulfide bond, a thioether bond, a lactam bond, a selenoether, diselenide, or an olefin bond.

39. The peptide dimer inhibitor of any one of claims 36-38, wherein the linker moiety is a diethylene glycol linker, an iminodiacetic acid (IDA) linker, a β-Ala-iminodiaceticacid (β-Ala-IDA) linker, or a PEG linker.

40. The peptide dimer inhibitor of any one of claims 36-39, wherein the N-terminus of each peptide monomer subunit is connected by the linker moiety or wherein the C-terminus of each peptide monomer subunit is connected by the linker moiety.

41. The peptide dimer inhibitor of claim 36, wherein the peptide dimer inhibitor comprises one of the following amino acid sequences:
[Ac-Cyclo-[[Abu]-QTWQC]-[Phe(4-OMe)]-[2-Nal]-[α-MeLys]-ENG-NH2]$_2$ DIG (SEQ ID NO: 996);
[Ac-[Pen]-QTWQ-[Pen]-[Phe(4-OMe)]-[2-Nal]-[α-MeVal]-[Lys(Ac)]-NN-[D)Lys]$_2$ DIG (SEQ ID NO: 756);
[Ac-[Pen]-QTWQ-[Pen]-[Phe[4-(2-acetylaminoethoxy)]-[2-Nal]- [α-MeVal]-[Lys(Ac)]-NN-[D)Lys]]$_2$ DIG (SEQ ID NO: 757);
[Ac-[Pen]-QTWQ[Pen]-[Phe[4-(2-acetylaminoethoxy)]]-[2-Nal]-[α-MeVal]-KNN-$NH_2$]$_2$ DIG (SEQ ID NO: 758);
[Ac-[Pen]-QTWQ[Pen]-[Phe[4-(2-acetylaminoethoxy)]]-[2-Nal]-K-[Lys(Ac)]-NN-$NH_2$]$_2$ DIG (SEQ ID NO: 759);
[Ac-[Pen]-QTWQ-[Pen]-[Phe(4-OMe)]-[2-Nal]-[α-MeLys]-[Lys(Ac)]-NN-$NH_2$]$_2$ DIG (SEQ ID NO: 532);
[Ac-Cyclo-[[Abu]-QTWQC]-[Phe(4-OMe)]-[2-Nal]-[α-MeLys]-ENG-NH2]$_2$ DIG (SEQ ID NO: 996); or
[Ac-[Pen]-QTWQ-[Pen]-[Phe(4-$CONH_2$)]-[2-Nal]-[α-MeLys]-[Lys(Ac)]-NN-$NH_2$]$_2$ DIG (SEQ ID NO: 534).

42. A polynucleotide comprising a sequence encoding the peptide inhibitor of any one of claims 1-35 or one or both peptide monomer subunit of the peptide dimer inhibitor of any one of claims 36-41.

43. A vector comprising the polynucelotide of claim 42.

44. A pharmaceutical composition comprising the peptide inhibitor of any one of claims 1-35 or the peptide dimer inhibitor of any one of claims 36-41, and a pharmaceutically acceptable carrier, excipient, or diluent.

45. The pharmaceutical composition of claim 44, further comprising an enteric coating.

46. The pharmaceutical composition of claim 45, wherein the enteric coating protects and releases the pharmaceutical composition within a subject's lower gastrointestinal system.

47. Use of an effective amount of the pharmaceutical composition of any one of claims 44-46 in the manufacture of a medicament for treating an Inflammatory Bowel Disease (IBD), ulcerative colitis, Crohn's disease, Celiac disease (*nontropical Sprue)*, enteropathy associated with seronegative arthropathies, microscopic colitis, collagenous colitis, eosinophilic gastroenteritis, colitis associated with radio- or chemo-therapy, colitis associated with disorders of innate immunity as in leukocyte adhesion deficiency-1, chronic granulomatous disease, glycogen storage disease type 1b, Hermansky-Pudlak syndrome, Chediak-Higashi syndrome, and Wiskott-Aldrich Syndrome, pouchitis resulting after proctocolectomy and ileoanal anastomosis, gastrointestinal cancer, pancreatitis, insulin-dependent diabetes mellitus, mastitis, cholecystitis, cholangitis, pericholangitis, chronic bronchitis, chronic sinusitis, asthma, psoriasis, psoriatic arthritis, or graft versus host disease in a subject.

48. The use of claim 47, wherein the pharmaceutical composition is provided

to the subject by an oral, parenteral, intravenous, peritoneal, intradermal, subcutaneous, intramuscular, intrathecal, inhalation, vaporization, nebulization, sublingual, buccal, parenteral, rectal, intraocular, inhalation, topically, vaginal, or topical route of administration.

49. The use of claim 47 for treating Inflammatory Bowel Disease (IBD), ulcerative colitis, Crohn's disease, wherein the pharmaceutical composition is provided to the subject orally.

50. The use of claim 47 for treating psoriasis, wherein the pharmaceutical composition is provided to the subject orally, topically, parenterally, intravenously, subcutaneously, peritonealy, or intravenously.

51. The use of any one claims 47-50, wherein the peptide inhibitor or the peptide dimer inhibitor inhibits binding of an interleukin-23 (IL-23) to the interleukin-23 receptor (IL-23R).

52. A method of assessing the ability of a candidate compound to inhibit or reduce an inflammatory disease or disorder, comprising:

(a) providing to a rat an amount of dextran sulfate sodium (DSS) or 2,4,6-Trinitrobenzenesulfonic acid (TNBS) sufficient to induce an inflammatory bowel disease (IBD);

(b) providing to the rat an amount of a candidate compound; and

(c) measuring an amount of IBD symptoms present in the rat after being provided with the DSS and the candidate compound;

wherein if the amount of IBD symptoms measured in (c) are significantly lower than the amount measured in a control rat provided with the amount of DSS or TNBS and either an amount of a control compound or no peptide (e.g., vehicle control), the candidate compound inhibits or reduces the inflammatory disease or disorder.

53. The method of claim 52, wherein an anti-IL-23p19 antibody is used as a positive control.

54. The method of claim 52, wherein the candidate compound inhibits or reduces the inflammatory disease or disorder in a human.

SEQUENCE LISTING

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<210> 37
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<400> 37
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<210> 38
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<400> 38
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<210> 39
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<400> 40
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<210> 41
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<400> 41
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<223> Beta-Ala

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<400> 42
Cys Ala Asp Trp Val Cys Tyr Trp Xaa Lys Phe Gly Ala Lys
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<210> 43
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<210> 44
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<210> 45
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<400> 45
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<210> 46
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<400> 46
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<210> 47
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<400> 47
Cys Gln Thr Trp Gln Cys Tyr Trp Asn Val Phe Gly Xaa Lys
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<210> 48
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<223> (2-aminoethoxy)acetic acid

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<400> 48
Cys Gln Thr Trp Gln Cys Tyr Trp Thr Val Phe Gly Xaa Lys
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<210> 49
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<223> (2-aminoethoxy)acetic acid

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<400> 49
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<210> 51
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<210> 52
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<223> (2-aminoethoxy)acetic acid

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<400> 53
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<210> 54
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<400> 54
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<210> 55
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<210> 56
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<210> 57
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<210> 58
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<400> 58
Cys Gln Thr Trp Gln Cys Tyr Trp Xaa Xaa Asn Gly Xaa Lys
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<210> 59
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1 5 10

<210> 62
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<400> 62
Cys Gln Thr Trp Gln Cys Tyr Trp Xaa Val Phe Asn Xaa Lys
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<210> 63
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<400> 63
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<210> 64
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<223> (2-aminoethoxy)acetic acid

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<210> 65
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<223> (2-aminoethoxy)acetic acid

<220>
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<400> 65
Cys Arg Thr Trp Gln Cys Tyr Trp Arg Val Phe Gly Xaa Lys
1 5 10

<210> 66
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<400> 66
Cys Gln Thr Trp Gln Cys Tyr Trp Arg Val Phe Gly Xaa Lys
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<210> 67
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<400> 67

Cys Xaa Thr Trp Gln Cys Tyr Trp Arg Val Phe Gly Xaa Lys
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<210> 68
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<210> 69
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<400> 69
Cys Ala Asp Trp Val Cys Tyr Xaa Xaa Xaa Phe Gly Xaa Lys
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<210> 70
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<222> (13)..(13)
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<400> 70
Cys Ala Asp Trp Val Cys Tyr Trp Xaa Xaa Phe Gly Xaa Lys
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<210> 71
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<223> (2-aminoethoxy)acetic acid

<220>
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<222> (14)..(14)
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<400> 71
Cys Ala Asp Trp Val Cys Tyr Phe Xaa Xaa Phe Gly Xaa Lys
1 5 10

<210> 72
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<400> 72
Cys Ala Asp Trp Val Cys Tyr Xaa Xaa Xaa Phe Gly Xaa Lys
1 5 10

<210> 73
<211> 14
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<400> 73
Cys Ala Asp Trp Val Cys Tyr Phe Xaa Xaa Phe Gly Xaa Lys
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<210> 74
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<400> 74
Cys Ala Asp Trp Val Cys Tyr Phe Xaa Xaa Phe Gly Xaa Lys
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<210> 75
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<212> PRT
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<220>
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<222> (14)..(14)
<223> D-Lys

<400> 75
Cys Ala Asp Trp Val Cys Tyr Phe Xaa Xaa Phe Gly Xaa Lys
1 5 10

<210> 76
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<220>
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<220>
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<223> Dap

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Cys Ala Asp Trp Val Cys Tyr Phe Xaa Xaa Phe Gly Xaa Lys
1 5 10

<210> 77
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<400> 77
Cys Met Thr Trp Gln Cys Tyr Trp Leu Tyr Gly Arg Xaa Lys
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<210> 78
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<220>
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<223> (2-aminoethoxy)acetic acid

<220>
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<222> (14)..(14)
<223> D-Lys

<400> 78
Cys Ala Asp Trp Val Cys Tyr Trp Xaa Xaa Phe Gly Xaa Lys
1 5 10

<210> 79
<211> 14
<212> PRT
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<220>
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Cys Ala Asp Trp Val Cys Tyr Trp Xaa Leu Phe Gly Xaa Lys
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<210> 80
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<220>
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<400> 80
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<210> 81
<211> 14
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<220>
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<222> (10)..(10)
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<223> (2-aminoethoxy)acetic acid

<220>
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<222> (14)..(14)
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<400> 81
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<210> 82
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<223> (2-aminoethoxy)acetic acid

<220>
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<222> (14)..(14)
<223> D-Lys

<400> 82
Cys Ala Asp Trp Val Cys Tyr Trp Xaa Xaa Phe Gly Xaa Lys
1 5 10

<210> 83
<211> 14
<212> PRT
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<220>
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<222> (10)..(10)
<223> Diethyl-Gly

<220>
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<222> (13)..(13)
<223> (2-aminoethoxy)acetic acid

<220>
<221> MOD_RES
<222> (14)..(14)
<223> D-Lys

<400> 83
Cys Ala Asp Trp Val Cys Tyr Trp Xaa Gly Phe Gly Xaa Lys
1 5 10

<210> 84
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

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<223> Beta-MePhe(4-F)

<220>
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<223> Orn

<220>
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<222> (10)..(10)
<223> Dap

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<222> (13)..(13)
<223> (2-aminoethoxy)acetic acid

<220>
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<222> (14)..(14)
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<400> 84
Cys Ala Asp Trp Val Cys Tyr Phe Xaa Xaa Phe Gly Xaa Lys
1 5 10

<210> 85
<211> 14
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<220>
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<220>
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<222> (14)..(14)
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<210> 86
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<220>

<223> Description of Artificial Sequence: Synthetic peptide

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<220>
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<223> (2-aminoethoxy)acetic acid

<220>
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<222> (14)..(14)
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<400> 86
Cys Gln Thr Trp Gln Cys Tyr Xaa Arg Val Asn Gly Xaa Lys
1 5 10

<210> 87
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 87
Cys Ser Asp Trp Glu Cys Tyr Trp His Ile Phe Gly
1 5 10

<210> 88
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 88
Cys Glu Thr Trp Glu Cys Tyr Trp His Ser Phe Ser
1 5 10

<210> 89
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 89
Cys Gln Ser Trp Glu Cys Tyr Trp His Tyr Tyr Gly
1 5 10

<210> 90
<211> 12

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 90
Cys Ser Asp Trp Arg Cys Tyr Trp His Val Phe Gly
1 5 10

<210> 91
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
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<400> 91
Cys His Thr Trp Val Cys Tyr Trp His Glu Phe Ser
1 5 10

<210> 92
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 92
Cys Thr Asp Trp Val Cys Tyr Trp His Glu Tyr Ser
1 5 10

<210> 93
<211> 12
<212> PRT
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<220>
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<400> 93
Cys Gln Thr Trp Val Cys Tyr Trp His Thr Tyr Gly
1 5 10

<210> 94
<211> 12
<212> PRT
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<220>
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<400> 94
Cys Gly Asn Trp Glu Cys Tyr Trp His Val Tyr Gly
1 5 10

<210> 95
<211> 12
<212> PRT
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<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 95
Cys Lys Asp Trp Lys Cys Tyr Trp His Ile Tyr Gly
1 5 10

<210> 96
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 96
Cys Arg Thr Trp Val Cys Tyr Trp His Val Phe Gly
1 5 10

<210> 97
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (4)..(4)
<223> 1-Nal

<400> 97
Cys Ala Asp Xaa Val Cys Tyr Trp His Thr Phe Gly
1 5 10

<210> 98
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (4)..(4)
<223> 2-Nal

<400> 98
Cys Ala Asp Xaa Val Cys Tyr Trp His Thr Phe Gly
1 5 10

<210> 99
<211> 12
<212> PRT
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<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (4)..(4)
<223> 1-Bip

<400> 99
Cys Ala Asp Xaa Val Cys Tyr Trp His Thr Phe Gly
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<210> 100
<211> 12
<212> PRT
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<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (4)..(4)
<223> Tic

<400> 100
Cys Ala Asp Xaa Val Cys Tyr Trp His Thr Phe Gly
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<210> 101
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<212> PRT
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<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
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<222> (4)..(4)
<223> Beta-hTrp

<400> 101
Cys Ala Asp Trp Val Cys Tyr Trp His Thr Phe Gly
1 5 10

<210> 102
<211> 12
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<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (8)..(8)
<223> 1-Bip

<400> 102
Cys Ala Asp Trp Val Cys Tyr Xaa His Thr Phe Gly
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<210> 103
<211> 12
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<220>
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<400> 103
Cys Ala Asp Trp Val Cys Tyr Xaa His Thr Phe Gly
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<210> 104
<211> 12
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<220>
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<400> 104
Cys Ala Asp Trp Val Cys Tyr Trp His Thr Phe Gly
1 5 10

<210> 105
<211> 12
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<220>
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<400> 105
Cys Ala Asp Trp Val Cys Tyr Ala His Thr Phe Gly
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<210> 106
<211> 12

<212> PRT
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<220>
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<400> 106
Ala Cys Asp Trp Val Cys Tyr Trp His Thr Phe Gly
1 5 10

<210> 107
<211> 12
<212> PRT
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<220>
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<400> 107
Ala Cys Asp Trp Cys Cys Tyr Trp Cys Thr Phe Gly
1 5 10

<210> 108
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
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<400> 108
Ala Ala Asp Trp Cys Ala Tyr Trp Cys Thr Phe Gly
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<210> 109
<211> 12
<212> PRT
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<220>
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<400> 109
Cys Ala Asp Trp Cys Cys Tyr Trp Cys Thr Phe Gly
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<210> 110
<211> 12
<212> PRT
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<220>
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<400> 110
Cys Ala Asp Trp Cys Cys Tyr Trp Cys Thr Phe Gly
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<210> 111
<211> 12
<212> PRT
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<220>
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<400> 111
Cys Ala Asp Trp Cys Cys Tyr Trp Cys Thr Phe Gly
1 5 10

<210> 112
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
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<400> 112
Cys Ala Asp Trp Val Cys Tyr Trp His Thr Phe
1 5 10

<210> 113
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
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<400> 113
Cys Ala Asp Trp Val Cys Tyr Trp His Thr
1 5 10

<210> 114
<211> 8
<212> PRT
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<220>
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<400> 114
Cys Ala Asp Trp Val Cys Tyr Trp
1 5

<210> 115
<211> 14
<212> PRT
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<220>
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<222> (1)..(1)
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<400> 115
Ala Ser Cys Ala Asp Trp Val Cys Tyr Trp His Thr Phe Gly
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<210> 116
<211> 14
<212> PRT
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<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (1)..(1)
<223> D-Lys

<400> 116
Lys Ser Cys Ala Asp Trp Val Cys Tyr Trp His Thr Phe Gly
1 5 10

<210> 117
<211> 14
<212> PRT
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<220>
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<220>
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<222> (1)..(1)
<223> D-Lys

<220>
<221> MOD_RES
<222> (2)..(2)
<223> Beta-Ala

<400> 117
Lys Ala Cys Ala Asp Trp Val Cys Tyr Trp His Thr Phe Gly
1 5 10

<210> 118
<211> 13
<212> PRT
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<220>
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<222> (1)..(1)
<223> (2-aminoethoxy)acetic acid

<400> 118
Xaa Cys Ala Asp Trp Val Cys Tyr Trp His Thr Phe Gly
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<210> 119
<211> 13
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<220>
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<220>
<221> MOD_RES
<222> (1)..(1)
<223> D-Lys

<400> 119
Lys Cys Ala Asp Trp Val Cys Tyr Trp His Thr Phe Gly
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<210> 120
<211> 12
<212> PRT
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<220>
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<400> 120
Cys Lys Asp Trp Val Cys Tyr Trp His Thr Phe Gly
1 5 10

<210> 121
<211> 12
<212> PRT
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<220>
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<400> 121
Cys Ala Asp Trp Lys Cys Tyr Trp His Thr Phe Gly
1 5 10

<210> 122
<211> 12
<212> PRT
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<220>
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<400> 122
Cys Ala Asp Trp Val Cys Tyr Trp Lys Thr Phe Gly
1 5 10

<210> 123

<211> 12
<212> PRT
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<220>
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<400> 123
Cys Ala Asp Trp Val Cys Tyr Trp His Lys Phe Gly
1 5 10

<210> 124
<211> 12
<212> PRT
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<220>
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<400> 124
Cys Ala Asp Trp Val Cys Tyr Trp His Thr Lys Gly
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<210> 125
<211> 12
<212> PRT
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<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
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<222> (12)..(12)
<223> D-Lys

<400> 125
Cys Ala Asp Trp Val Cys Tyr Trp His Thr Phe Lys
1 5 10

<210> 126
<211> 12
<212> PRT
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<220>
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<400> 126
Cys Ala Asp Trp Val Cys Tyr Trp His Thr Phe Gly
1 5 10

<210> 127
<211> 11
<212> PRT
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<220>
<223> Description of Artificial Sequence: Synthetic

peptide

<220>
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<222> (8)..(8)
<223> 1-Nal

<400> 127
Cys Ala Asp Trp Val Cys Tyr Xaa His Thr Phe
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<210> 128
<211> 11
<212> PRT
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<220>
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<223> 1-Nal

<220>
<221> MOD_RES
<222> (11)..(11)
<223> N-Me-Phe

<400> 128
Cys Ala Asp Trp Val Cys Tyr Xaa His Thr Phe
1 5 10

<210> 129
<211> 11
<212> PRT
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<220>
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<223> 1-Nal

<220>
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<222> (10)..(10)
<223> Sarc

<400> 129
Cys Ala Asp Trp Val Cys Tyr Xaa His Xaa Phe
1 5 10

<210> 130
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
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<220>
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<223> 1-Nal

<220>
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<222> (9)..(9)
<223> N-Me-His

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Cys Ala Asp Trp Val Cys Tyr Xaa His Thr Phe
1 5 10

<210> 131
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
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<400> 131
Cys Ala Asp Trp Val Cys Tyr Trp His Thr Phe Gly Lys
1 5 10

<210> 132
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
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<222> (2)..(2)
<223> Sarc

<220>
<221> MOD_RES
<222> (8)..(8)
<223> 1-Nal

<400> 132
Cys Xaa Asp Trp Val Cys Tyr Xaa His Thr Phe
1 5 10

<210> 133
<211> 11
<212> PRT
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<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
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<222> (4)..(4)
<223> N-Me-Trp

<220>
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<222> (8)..(8)
<223> 1-Nal

<400> 133
Cys Ala Asp Trp Val Cys Tyr Xaa His Thr Phe
1 5 10

<210> 134
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
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<222> (5)..(5)
<223> Sarc

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<221> MOD_RES
<222> (8)..(8)
<223> 1-Nal

<400> 134
Cys Ala Asp Trp Xaa Cys Tyr Xaa His Thr Phe
1 5 10

<210> 135
<211> 11
<212> PRT
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<220>
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<223> 1-Nal

<220>
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<222> (11)..(11)
<223> D-Phe

<400> 135
Cys Ala Asp Trp Val Cys Tyr Xaa His Thr Phe
1 5 10

<210> 136
<211> 12

<212> PRT
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<220>
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<220>
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<220>
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<400> 136
Cys Ala Asp Trp Val Cys Tyr Xaa His Thr Phe Xaa
1 5 10

<210> 137
<211> 12
<212> PRT
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<220>
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<400> 137
Cys Ala Thr Trp Val Cys Tyr Trp His Thr Phe Gly
1 5 10

<210> 138
<211> 12
<212> PRT
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<220>
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<400> 138
Cys Ala Asp Trp Glu Cys Tyr Trp His Thr Phe Gly
1 5 10

<210> 139
<211> 16
<212> PRT
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<220>
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<400> 139
Cys Ala Asp Trp Val Cys Tyr Trp His Arg Cys Gly Trp Trp Gly Cys
1 5 10 15

<210> 140
<211> 12
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<220>
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<222> (8)..(8)
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<220>
<221> MOD_RES
<222> (10)..(10)
<223> D-Ala

<400> 140
Cys Ala Asp Trp Val Cys Tyr Xaa His Ala Phe Gly
1 5 10

<210> 141
<211> 12
<212> PRT
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<220>
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<220>
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<220>
<221> MOD_RES
<222> (10)..(10)
<223> Aib

<400> 141
Cys Ala Asp Trp Val Cys Tyr Xaa His Xaa Phe Gly
1 5 10

<210> 142
<211> 12
<212> PRT
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<220>
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<222> (8)..(8)
<223> 1-Nal

<220>
<221> MOD_RES
<222> (10)..(10)
<223> beta-Ala

<400> 142

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Cys Ala Asp Trp Val Cys Tyr Xaa His Ala Phe Gly
1 5 10

<210> 143
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (8)..(8)
<223> 1-Nal

<400> 143
Cys Ala Asp Trp Val Cys Tyr Xaa Phe Thr Phe Gly
1 5 10

<210> 144
<211> 12
<212> PRT
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<220>
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<220>
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<220>
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<222> (9)..(9)
<223> D-Ala

<400> 144
Cys Ala Asp Trp Val Cys Tyr Xaa Ala Thr Phe Gly
1 5 10

<210> 145
<211> 12
<212> PRT
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<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
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<223> 1-Nal

<220>
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<223> Aib

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<222> (11)..(11)
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<400> 145
Cys Ala Asp Trp Val Cys Tyr Xaa His Xaa Phe Gly
1 5 10

<210> 146
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<220>
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<220>
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<223> 1-Nal

<220>
<221> MOD_RES
<222> (12)..(12)
<223> Aib

<400> 146
Cys Ala Asp Trp Val Cys Tyr Xaa His Thr Phe Xaa
1 5 10

<210> 147
<211> 12
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<213> Artificial Sequence

<220>
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<220>
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<223> N-Me-His

<220>
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<223> D-Ala

<220>
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<223> Aib

<400> 147
Cys Ala Asp Trp Val Cys Tyr Xaa His Ala Phe Xaa

1 5 10

<210> 148
<211> 11
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<220>
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<223> AEP

<400> 148
Cys Ala Asp Trp Val Cys Tyr Xaa His Xaa Gly
1 5 10

<210> 149
<211> 14
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<220>
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<223> (2-aminoethoxy)acetic acid

<220>
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<223> D-Lys

<400> 149
Cys Ala Asp Trp Val Cys Tyr Trp His Thr Phe Gly Xaa Lys
1 5 10

<210> 150
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<220>
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<220>
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<222> (14)..(14)
<223> D-Lys

<400> 150
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1 5 10

<210> 151
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<220>
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<222> (13)..(13)
<223> (2-aminoethoxy)acetic acid

<220>
<221> MOD_RES
<222> (14)..(14)
<223> D-Lys

<400> 151
Cys Ala Asp Trp Val Cys Tyr Xaa His Thr Phe Gly Xaa Lys
1 5 10

<210> 152
<211> 14
<212> PRT
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<220>
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<220>
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<220>
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<223> (2-aminoethoxy)acetic acid

<220>
<221> MOD_RES
<222> (14)..(14)
<223> D-Lys

<400> 152
Cys Gln Thr Trp Gln Cys Tyr Trp Arg Glu Asn Gly Xaa Lys
1 5 10

<210> 153
<211> 14
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<220>
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<220>
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<400> 153
Cys Gln Thr Trp Gln Cys Tyr Trp Arg Arg Asn Gly Xaa Lys
1 5 10

<210> 154
<211> 14
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<220>
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<400> 154

Cys Gln Thr Trp Gln Cys Tyr Trp Arg Lys Asn Gly Xaa Lys
1 5 10

<210> 155
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<220>
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<220>
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<222> (13)..(13)
<223> (2-aminoethoxy)acetic acid

<220>
<221> MOD_RES
<222> (14)..(14)
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<400> 155
Cys Gln Thr Trp Gln Cys Tyr Trp Arg Xaa Asn Gly Xaa Lys
1 5 10

<210> 156
<211> 14
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<220>
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<222> (13)..(13)
<223> (2-aminoethoxy)acetic acid

<220>
<221> MOD_RES
<222> (14)..(14)
<223> D-Lys

<400> 156
Cys Gln Thr Trp Gln Cys Tyr Trp Arg Glu Asn Gly Xaa Lys
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<210> 157
<211> 14
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<220>
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<223> D-Arg

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<222> (13)..(13)
<223> (2-aminoethoxy)acetic acid

<220>
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<222> (14)..(14)
<223> D-Lys

<400> 157
Cys Gln Thr Trp Gln Cys Tyr Trp Arg Glu Asn Gly Xaa Lys
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<210> 158
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<212> PRT
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<220>
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<223> (2-aminoethoxy)acetic acid

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<400> 158
Cys Gln Thr Trp Gln Cys Tyr Trp Arg Glu Asn Gly Xaa Lys
1 5 10

<210> 159
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<220>
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<220>
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<222> (12)..(12)
<223> (2-aminoethoxy)acetic acid

<220>
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<222> (13)..(13)
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<400> 159
Cys Gln Thr Trp Gln Cys Tyr Trp Glu Asn Gly Xaa Lys
1 5 10

<210> 160
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<212> PRT
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<220>
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<400> 160
Cys Ala Asp Trp Val Cys
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<210> 161
<211> 14
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<220>
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<220>
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<222> (14)..(14)
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<400> 161
Cys Arg Asp Trp Gln Cys Tyr Trp Arg Lys Phe Gly Xaa Lys
1 5 10

<210> 162

<211> 14
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<220>
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<223> AEP

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<400> 162
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<222> (14)..(14)
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Cys Arg Asp Trp Gln Cys Tyr Trp Arg Lys Phe Gly Xaa Lys
1 5 10

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<222> (14)..(14)
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<400> 165
Cys Gln Thr Trp Gln Cys Tyr Trp Arg Glu Asn Gly Xaa Lys
1 5 10

<210> 166
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 166
Cys Thr Asp Trp Lys Cys Tyr Trp His Glu Phe Gly
1 5 10

<210> 167
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
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<400> 167
Cys Arg Thr Trp Thr Cys Tyr Trp His Val Tyr Gly
1 5 10

<210> 168
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 168
Cys Pro Asn Trp Glu Cys Tyr Trp His Arg Phe Gly
1 5 10

<210> 169
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 169
Cys Ala Asp Trp Val Cys Tyr Trp His Thr Phe Gly
1 5 10

<210> 170
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
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<400> 170
Cys Ala Asp Trp Met Cys Tyr Trp His Glu Tyr Gly
1 5 10

<210> 171
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<400> 171

Cys Thr Thr Trp Lys Cys Tyr Trp His Gln Tyr Gly
1 5 10

<210> 172
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<220>
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<400> 172
Cys Ser Asn Trp Glu Cys Tyr Trp His His Tyr Gly
1 5 10

<210> 173
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
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<400> 173
Cys Ser Asp Trp Val Cys Tyr Trp His Val Tyr Gly
1 5 10

<210> 174
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 174
Cys Asp Thr Trp Lys Cys Tyr Trp His Arg Gln Ser
1 5 10

<210> 175
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
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<220>
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<223> 1-Nal

<400> 175
Cys Ala Asp Trp Val Cys Tyr Xaa His Thr Phe Gly
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<210> 176
<211> 12

<212> PRT
<213> Artificial Sequence

<220>
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<220>
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<222> (8)..(8)
<223> 2-Nal

<400> 176
Cys Ala Asp Trp Val Cys Tyr Xaa His Thr Phe Gly
1 5 10

<210> 177
<211> 12
<212> PRT
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<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 177
Cys Ala Asp Trp Val Cys Tyr Trp His Thr Phe Gly
1 5 10

<210> 178
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (13)..(13)
<223> D-Lys

<400> 178
Cys Ala Asp Trp Val Cys Tyr Trp His Thr Phe Gly Lys
1 5 10

<210> 179
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (15)..(15)
<223> D-Lys

<400> 179

Cys Ala Asp Trp Val Cys Tyr Trp His Thr Phe Gly Ala Pro Lys
1 5 10 15

<210> 180
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 180
Cys Thr Asp Trp Lys Cys Tyr Trp His Thr Phe Gly
1 5 10

<210> 181
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 181
Cys Arg Asp Trp Val Cys Tyr Trp His Thr Phe Gly
1 5 10

<210> 182
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 182
Cys Ala Asp Trp Val Cys Tyr Trp His Glu Phe Gly
1 5 10

<210> 183
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 183
Cys Ala Asp Trp Val Cys Tyr Trp His Phe His Gln Leu Arg Asp Ala
1 5 10 15

<210> 184
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 184
Cys Ala Asp Trp Val Cys Tyr Trp His Glu His Ser Glu Arg Val Gly
1 5 10 15

<210> 185
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 185
Cys Ala Asp Trp Val Cys Tyr Trp His Asn His Ser Glu Gly Ser Gly
1 5 10 15

<210> 186
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 186
Cys Ala Asp Trp Val Cys Tyr Trp His Arg Ser Thr Gly Gly Gln His
1 5 10 15

<210> 187
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
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<220>
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<223> D-Lys

<220>
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<222> (9)..(9)
<223> 1-Nal

<220>
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<223> Sarc

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<222> (14)..(14)
<223> AEP

<220>
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<222> (15)..(15)
<223> D-Arg

<400> 187
Lys Cys Arg Asp Trp Gln Cys Tyr Xaa His Thr His Xaa Xaa Arg
1 5 10 15

<210> 188
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 188
Thr Gln Phe Asp Cys Arg Thr Trp Glu Cys Tyr Trp His Thr Phe Gly
1 5 10 15

<210> 189
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 189
Gly Gly Val Glu Cys Asn Asp Trp Gln Cys Tyr Trp His Thr Phe Gly
1 5 10 15

<210> 190
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 190
Arg Glu Gly Thr Cys Ser Thr Trp Lys Cys Tyr Trp His Thr Phe Gly
1 5 10 15

<210> 191
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 191
Asp Thr Pro Arg Cys Arg Thr Trp Glu Cys Tyr Trp His Thr Phe Gly
1 5 10 15

<210> 192
<211> 16
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 192
Gly Gly Gly Glu Cys Glu Asn Trp Glu Cys Tyr Trp His Thr Phe Gly
1 5 10 15

<210> 193
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 193
Gly Asp His Lys Cys Ser Ser Trp Glu Cys Tyr Trp His Thr Phe Gly
1 5 10 15

<210> 194
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 194
Gly Ser Val His Cys Met Thr Trp Glu Cys Tyr Trp His Thr Phe Gly
1 5 10 15

<210> 195
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (8)..(8)
<223> 1-Nal

<400> 195
Cys Ala Asp Trp Val Cys Tyr Xaa Val Thr Phe Gly
1 5 10

<210> 196
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
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<220>
<221> MOD_RES

<222> (9)..(9)
<223> D-His

<220>
<221> MOD_RES
<222> (13)..(13)
<223> (2-aminoethoxy)acetic acid

<220>
<221> MOD_RES
<222> (14)..(14)
<223> D-Lys

<400> 196
Cys Ala Asp Trp Val Cys Tyr Trp His Thr Phe Gly Xaa Lys
1 5 10

<210> 197
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 197
Cys Arg Asp Trp Gln Cys Tyr Trp His Lys Phe Gly
1 5 10

<210> 198
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 198
Cys Ser Asn Trp Val Cys Tyr Trp His Thr Tyr Gly
1 5 10

<210> 199
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
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<222> (13)..(13)
<223> Beta-Ala

<220>
<221> MOD_RES
<222> (14)..(14)
<223> D-Lys

<400> 199
Cys Ala Asp Trp Val Cys Tyr Trp His Thr Phe Gly Ala Lys

1 5 10

<210> 200
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

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<222> (13)..(13)
<223> (2-aminoethoxy)acetic acid

<220>
<221> MOD_RES
<222> (14)..(14)
<223> D-Lys

<400> 200
Cys Ala Asp Trp Val Cys Tyr Trp His Thr Phe Gly Xaa Lys
1 5 10

<210> 201
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 201
Cys Ala Asp Trp Val Cys Tyr Trp His Thr Phe Gly
1 5 10

<210> 202
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
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<220>
<221> MOD_RES
<222> (13)..(13)
<223> AEP

<220>
<221> MOD_RES
<222> (14)..(14)
<223> D-Arg

<400> 202
Cys Ala Asp Trp Val Cys Tyr Trp His Thr Phe Gly Xaa Arg
1 5 10

<210> 203

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

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (13)..(13)
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<400> 203
Cys Ala Asp Trp Val Cys Tyr Trp His Thr Phe Gly Xaa Lys
1 5 10

<210> 204
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (13)..(13)
<223> Gaba

<220>
<221> MOD_RES
<222> (14)..(14)
<223> D-Lys

<400> 204
Cys Ala Asp Trp Val Cys Tyr Trp His Thr Phe Gly Xaa Lys
1 5 10

<210> 205
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (13)..(13)
<223> Hexanoic-D-Lys

<400> 205
Cys Ala Asp Trp Val Cys Tyr Trp His Thr Phe Gly Lys
1 5 10

<210> 206
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (13)..(13)
<223> (PEG)2-D-Lys

<400> 206
Cys Ala Asp Trp Val Cys Tyr Trp His Thr Phe Gly Lys
1 5 10

<210> 207
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (14)..(14)
<223> D-Lys

<400> 207
Cys Ala Asp Trp Val Cys Tyr Trp His Thr Phe Gly Pro Lys
1 5 10

<210> 208
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (13)..(13)
<223> Azt

<220>
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<222> (14)..(14)
<223> D-Lys

<400> 208
Cys Ala Asp Trp Val Cys Tyr Trp His Thr Phe Gly Xaa Lys
1 5 10

<210> 209
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<212> PRT
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<220>
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peptide

<220>
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<222> (14)..(14)
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<400> 209
Cys Ala Asp Trp Val Cys Tyr Trp His Thr Phe Gly Ala Lys
1 5 10

<210> 210
<211> 15
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<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
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<400> 210
Cys Ala Asp Trp Val Cys Tyr Trp His Thr Phe Gly Ala Pro Lys
1 5 10 15

<210> 211
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<220>
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<220>
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<222> (15)..(15)
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<400> 211
Cys Ala Asp Trp Val Cys Tyr Trp His Thr Phe Gly Ala Xaa Lys
1 5 10 15

<210> 212
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<220>
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<220>
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<223> D-Lys

<400> 212
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<210> 213
<211> 14
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<220>
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<220>
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<223> AEP

<220>
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<222> (14)..(14)
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<400> 213
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1 5 10

<210> 214
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
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<400> 214
Cys Ala Thr Trp Gln Cys Tyr Trp His Glu Tyr Gly
1 5 10

<210> 215
<211> 12
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<213> Artificial Sequence

<220>
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<400> 215
Cys Lys Thr Trp Thr Cys Tyr Trp His Glu Phe Gly
1 5 10

<210> 216
<211> 12
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<220>
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<400> 216
Cys Thr Thr Trp Thr Cys Tyr Trp His Gln Tyr Gly
1 5 10

<210> 217
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<220>
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<400> 217
Cys Arg Thr Trp Glu Cys Tyr Trp His Glu Phe Gly
1 5 10

<210> 218
<211> 12
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<220>
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<400> 218
Cys Arg Thr Trp Gln Cys Tyr Trp His Glu Tyr Gly
1 5 10

<210> 219
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<220>
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<400> 219
Cys Gln Thr Trp Gln Cys Tyr Trp Arg Glu Asn Gly
1 5 10

<210> 220
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<220>
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<400> 220
Cys Arg Thr Trp Glu Cys Tyr Trp His Glu Tyr Gly
1 5 10

<210> 221
<211> 12
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<220>
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<400> 221
Cys Thr Thr Trp Glu Cys Tyr Trp His Glu Tyr Gly
1 5 10

<210> 222
<211> 12
<212> PRT
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<220>
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<210> 223
<211> 12
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<220>
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<400> 223
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<210> 224
<211> 12
<212> PRT
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<220>
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<400> 224
Cys Thr Thr Trp Glu Cys Tyr Trp His Glu Phe Gly
1 5 10

<210> 225
<211> 12
<212> PRT
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<220>
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<400> 225
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<210> 226

<211> 12
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<220>
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<400> 226
Cys Glu Asp Trp Lys Cys Tyr Trp His Lys Tyr Gly
1 5 10

<210> 227
<211> 12
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<220>
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<400> 227
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1 5 10

<210> 228
<211> 12
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<220>
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<400> 228
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1 5 10

<210> 229
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<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 229
Cys Ala Asp Trp Val Cys Tyr Trp His Arg His Ala Asp Arg Val Lys
1 5 10 15

<210> 230
<211> 14
<212> PRT
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<220>
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<400> 230
Cys Ala Asp Trp Val Cys Tyr Trp His Thr Phe Gly Glu Arg
1 5 10

<210> 231
<211> 14
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<220>
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<400> 231
Cys Ala Asp Trp Val Cys Tyr Trp His Thr His Gly Glu Arg
1 5 10

<210> 232
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<220>
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<400> 232
Asp Thr Pro Arg Cys Arg Thr Trp Glu Cys Tyr Trp His Thr Phe Gly
1 5 10 15

<210> 233
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<212> PRT
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<220>
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<220>
<221> MOD_RES
<222> (14)..(14)
<223> D-Lys

<400> 233
Cys Gln Thr Trp Val Cys Tyr Trp Arg Glu Asn Gly Xaa Lys
1 5 10

<210> 234
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
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<223> (2-aminoethoxy)acetic acid

<220>
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<222> (14)..(14)
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<400> 234
Cys Gln Thr Trp Gln Cys Tyr Trp Arg Glu Asn Gly Xaa Lys
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<210> 235
<211> 14
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<220>
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<223> (2-aminoethoxy)acetic acid

<220>
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<222> (14)..(14)
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<400> 235
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1 5 10

<210> 236
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<220>
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<220>
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<222> (14)..(14)
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<400> 236
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<210> 237
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<220>
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peptide

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<223> (2-aminoethoxy)acetic acid

<220>
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<222> (14)..(14)
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1 5 10

<210> 238
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<400> 238
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1 5 10

<210> 239
<211> 14
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<220>
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<400> 239
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<222> (14)..(14)
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<400> 240
Cys Arg Thr Trp Gln Cys Tyr Trp Arg Lys Phe Gly Xaa Lys
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<210> 241
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<220>
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<210> 242
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<222> (14)..(14)
<223> D-Lys

<400> 242
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1 5 10

<210> 243
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<223> (2-aminoethoxy)acetic acid

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<222> (14)..(14)
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<223> (2-aminoethoxy)acetic acid

<220>
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<222> (14)..(14)
<223> D-Lys

<400> 244
Cys Gln Thr Trp Gln Cys Tyr Trp Arg Glu Asn Gly Xaa Lys
1 5 10

<210> 245

<211> 14
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<220>
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<223> (2-aminoethoxy)acetic acid

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<222> (14)..(14)
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<400> 245
Cys Gln Thr Trp Gln Cys Tyr Trp Arg Thr Asn Gly Xaa Lys
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<210> 246
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<220>
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<222> (14)..(14)
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<400> 246
Cys Gln Thr Trp Val Cys Tyr Trp Arg Glu Asn Gly Xaa Lys
1 5 10

<210> 247
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<220>
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<220>
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<222> (14)..(14)
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<400> 247
Cys Gln Thr Trp Gln Cys Tyr Trp Arg Lys Asn Gly Xaa Lys
1 5 10

<210> 248
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<220>
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1 5 10

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<400> 249
Cys Gln Thr Trp Gln Cys Tyr Trp Xaa Glu Asn Gly
1 5 10

<210> 250
<211> 12
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<220>
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<400> 250
Cys Gln Thr Trp Gln Cys Tyr Trp Leu Glu Asn Gly
1 5 10

<210> 251
<211> 12
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<223> Description of Artificial Sequence: Synthetic peptide

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<400> 251
Cys Gln Thr Trp Gln Cys Tyr Trp Leu Glu Asn Gly
1 5 10

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<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (10)..(10)
<223> Lys-Ac

<400> 252
Cys Gln Thr Trp Gln Cys Tyr Trp Arg Lys Asn Gly
1 5 10

<210> 253
<211> 12
<212> PRT
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<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 253
Cys Arg Thr Trp Gln Cys Tyr Trp Arg Lys Phe Gly
1 5 10

<210> 254
<211> 12
<212> PRT
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<220>
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<222> (7)..(7)
<223> Phe(4-OMe)

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<222> (8)..(8)
<223> 2-Nal

<220>
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<222> (9)..(9)
<223> alpha-Me-Lys

<400> 254
Xaa Gln Thr Trp Gln Xaa Phe Xaa Lys Glu Asn Gly
1 5 10

<210> 255
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<220>
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<222> (6)..(6)
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<222> (7)..(7)
<223> Phe[4-(2-aminoethoxy)]

<220>
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<222> (8)..(8)
<223> 2-Nal

<220>
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<222> (9)..(9)
<223> Aib

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<222> (10)..(10)
<223> Lys(Ac)

<400> 255
Xaa Asn Thr Trp Gln Xaa Phe Xaa Xaa Lys Asn Asn
1 5 10

<210> 256
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<212> PRT
<213> Artificial Sequence

<220>
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<222> (10)..(10)
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<400> 256
Xaa Gln Thr Trp Gln Xaa Phe Xaa Leu Lys Asn Asn
1 5 10

<210> 257
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<222> (6)..(6)
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<222> (7)..(7)
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<223> 2-Nal

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1 5 10

<210> 258
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<220>
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<220>
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<222> (7)..(7)
<223> Phe(4-OMe)

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<223> 2-Nal

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<222> (9)..(9)
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<400> 258
Xaa Gln Thr Trp Gln Cys Phe Xaa Lys Glu Asn Gly
1 5 10

<210> 259
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<220>
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<220>
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<222> (9)..(9)
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<400> 259
Xaa Gln Thr Trp Gln Cys Phe Trp Lys Glu Asn Gly
1 5 10

<210> 260
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<220>
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<222> (7)..(7)
<223> Phe[4-(2-aminoethoxy)]

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1 5 10

<210> 261
<211> 20
<212> PRT
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<400> 261
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1 5 10 15

Thr Gly Lys Arg
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<210> 262
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<220>
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<220>
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<222> (10)..(10)
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<400> 262
Xaa Gln Thr Trp Gln Xaa Phe Xaa Lys Lys Asn Gly
1 5 10

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<220>
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<223> Phe(4-OMe)

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<223> 2-Nal

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<220>
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<222> (10)..(10)
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<400> 263
Xaa Gln Thr Trp Gln Xaa Phe Xaa Lys Lys Asn Gly
1 5 10

<210> 264
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<220>
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<223> Any amino acid

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<222> (3)..(3)
<223> Any amino acid

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<222> (5)..(5)
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<400> 264
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<210> 265
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<220>
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<223> alpha-MeLys

<400> 265
Lys Glu Asn Gly
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<210> 266

<211> 4
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<220>
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<222> (2)..(2)
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<400> 266
Lys Lys Asn Asn
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<210> 267
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<220>
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<222> (2)..(2)
<223> Lys(Ac)

<400> 267
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<210> 268
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<212> PRT
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<220>
<223> Description of Artificial Sequence: Synthetic peptide

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<400> 268
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<210> 269
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<220>
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<400> 269
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<210> 270
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<212> PRT
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<220>
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<210> 271
<211> 6
<212> PRT
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<220>
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<222> (5)..(5)
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<220>
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<222> (6)..(6)
<223> alpha-MeLys

<400> 271
Trp Gln Cys Tyr Xaa Lys
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<210> 272
<211> 6

<212> PRT
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<220>
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<220>
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<222> (6)..(6)
<223> alpha-MeLys

<400> 272
Trp Gln Cys Phe Xaa Lys
1 5

<210> 273
<211> 6
<212> PRT
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<220>
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<220>
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<222> (6)..(6)
<223> Aib

<400> 273
Trp Gln Cys Phe Xaa Xaa
1 5

<210> 274
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
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<222> (3)..(3)
<223> Pen

<220>
<221> MOD_RES
<222> (4)..(4)
<223> Phe(4-OMe)

<220>
<221> MOD_RES
<222> (5)..(5)
<223> 2-Nal

<220>
<221> MOD_RES
<222> (6)..(6)
<223> alpha-MeLys

<400> 274
Trp Gln Xaa Phe Xaa Lys
1 5

<210> 275
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
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<220>
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<222> (2)..(2)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (3)..(3)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (5)..(5)
<223> Any amino acid

<220>
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<222> (10)..(10)
<223> Any amino acid

<220>
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<222> (12)..(12)
<223> Any amino acid

<220>
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<222> (13)..(13)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (14)..(14)

<223> D-Lys

<400> 275
Cys Xaa Xaa Trp Xaa Cys Tyr Trp His Xaa Phe Xaa Xaa Lys
1 5 10

<210> 276
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Abu

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Tyr(OMe)

<220>
<221> MOD_RES
<222> (8)..(8)
<223> 2-Nal

<220>
<221> MOD_RES
<222> (9)..(9)
<223> alpha-MeLys

<400> 276
Xaa Gln Thr Trp Gln Cys Tyr Xaa Lys Glu Asn Gly
1 5 10

<210> 277
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 277
Phe Pro Thr Trp Glu Trp Tyr Trp Cys Asn Arg Asp
1 5 10

<210> 278
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 278
Ala Leu Thr Trp Glu Phe Tyr Trp Leu Cys Arg Glu
1 5 10

<210> 279
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
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<223> Pen

<220>
<221> MOD_RES
<222> (6)..(6)
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<220>
<221> MOD_RES
<222> (7)..(7)
<223> Tyr(OMe)

<220>
<221> MOD_RES
<222> (8)..(8)
<223> 2-Nal

<220>
<221> MOD_RES
<222> (9)..(9)
<223> alpha-MeLys

<400> 279
Xaa Gln Thr Trp Gln Xaa Tyr Xaa Lys Glu Asn Gly
1 5 10

<210> 280
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Abu

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Phe[4-(2-aminoethoxy)]

<220>
<221> MOD_RES
<222> (9)..(9)
<223> alpha-MeLys

<400> 280

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Xaa Gln Thr Trp Gln Cys Phe Trp Lys Glu Asn Gly
1 5 10

<210> 281
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 281
Lys Met Thr Trp Gln Asp Tyr Trp Leu Tyr Gly Arg
1 5 10

<210> 282
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
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<223> Pen

<220>
<221> MOD_RES
<222> (6)..(6)
<223> Pen

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Phe(4-OMe)

<220>
<221> MOD_RES
<222> (8)..(8)
<223> 2-Nal

<220>
<221> MOD_RES
<222> (9)..(9)
<223> alpha-Me-Lys

<400> 282
Xaa Gln Thr Trp Gln Xaa Phe Xaa Lys Glu Asn Gly
1 5 10

<210> 283
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
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<223> Pen

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<222> (6)..(6)
<223> Pen

<220>
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<222> (7)..(7)
<223> Phe[4-(2-aminoethoxy)]

<220>
<221> MOD_RES
<222> (8)..(8)
<223> 2-Nal

<220>
<221> MOD_RES
<222> (9)..(9)
<223> Aib

<220>
<221> MOD_RES
<222> (10)..(10)
<223> Lys(Ac)

<400> 283
Xaa Asn Thr Trp Gln Xaa Phe Xaa Xaa Lys Asn Asn
1 5 10

<210> 284
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 284
Ala Met Thr Trp Gln Asp Tyr Trp Leu Tyr Gly Lys
1 5 10

<210> 285
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Pen

<220>
<221> MOD_RES
<222> (6)..(6)
<223> Pen

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Phe[4-(2-aminoethoxy)]

<220>
<221> MOD_RES
<222> (8)..(8)
<223> 2-Nal

<220>
<221> MOD_RES
<222> (9)..(9)
<223> alpha-MeLeu

<220>
<221> MOD_RES
<222> (10)..(10)
<223> Lys(Ac)

<400> 285
Xaa Gln Thr Trp Gln Xaa Phe Xaa Leu Lys Asn Asn
1 5 10

<210> 286
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
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<223> Pen

<220>
<221> MOD_RES
<222> (6)..(6)
<223> Pen

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Phe(4-CONH2)

<220>
<221> MOD_RES
<222> (8)..(8)
<223> 2-Nal

<220>
<221> MOD_RES
<222> (9)..(9)
<223> alpha-MeLys

<220>
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<222> (10)..(10)
<223> Lys(Ac)

<400> 286
Xaa Gln Thr Trp Gln Xaa Phe Xaa Lys Lys Asn Asn

1 5 10

<210> 287

<400> 287
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<210> 288

<400> 288
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<210> 289

<400> 289
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<400> 290
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<210> 291
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Beta-Ala

<400> 291
Ala Ser Cys Ala Asp Trp Val Cys Tyr Trp His Thr Phe Gly
1 5 10

<210> 292
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (1)..(1)
<223> D-Lys

<400> 292
Lys Ser Cys Ala Asp Trp Val Cys Tyr Trp His Thr Phe Gly
1 5 10

<210> 293

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

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (1)..(1)
<223> D-Lys

<220>
<221> MOD_RES
<222> (2)..(2)
<223> Beta-Ala

<400> 293
Lys Ala Cys Ala Asp Trp Val Cys Tyr Trp His Thr Phe Gly
1 5 10

<210> 294
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (1)..(1)
<223> (2-aminoethoxy)acetic acid

<400> 294
Xaa Cys Ala Asp Trp Val Cys Tyr Trp His Thr Phe Gly
1 5 10

<210> 295
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (1)..(1)
<223> D-Lys

<400> 295
Lys Cys Ala Asp Trp Val Cys Tyr Trp His Thr Phe Gly
1 5 10

<210> 296
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 296
Cys Lys Asp Trp Val Cys Tyr Trp His Thr Phe Gly
1 5 10

<210> 297
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 297
Cys Ala Asp Trp Lys Cys Tyr Trp His Thr Phe Gly
1 5 10

<210> 298
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 298
Cys Ala Asp Trp Val Cys Tyr Trp Lys Thr Phe Gly
1 5 10

<210> 299
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 299
Cys Ala Asp Trp Val Cys Tyr Trp His Lys Phe Gly
1 5 10

<210> 300
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 300
Cys Ala Asp Trp Val Cys Tyr Trp His Thr Lys Gly
1 5 10

<210> 301
<211> 13

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 301
Cys Ala Asp Trp Val Cys Tyr Trp His Thr Phe Asp Lys
1 5 10

<210> 302
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 302
Cys Ala Asp Trp Val Cys Tyr Trp His Thr Phe Gly Asp Lys
1 5 10

<210> 303
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (13)..(13)
<223> Beta-Ala

<220>
<221> MOD_RES
<222> (14)..(14)
<223> D-Lys

<400> 303
Cys Ala Asp Trp Val Cys Tyr Trp His Thr Phe Gly Ala Lys
1 5 10

<210> 304
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (13)..(13)
<223> (2-aminoethoxy)acetic acid

<220>
<221> MOD_RES

<222> (14)..(14)
<223> D-Lys

<400> 304
Cys Ala Asp Trp Val Cys Tyr Trp His Thr Phe Gly Xaa Lys
1 5 10

<210> 305
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 305
Cys Ala Asp Trp Val Cys Tyr Trp His Thr Phe Gly Lys
1 5 10

<210> 306
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Beta-Ala

<400> 306
Ala Ser Cys Ala Asp Trp Val Cys Tyr Trp His Thr Phe Gly
1 5 10

<210> 307
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (1)..(1)
<223> D-Lys

<400> 307
Lys Ser Cys Ala Asp Trp Val Cys Tyr Trp His Thr Phe Gly
1 5 10

<210> 308
<211> 14
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (1)..(1)
<223> D-Lys

<220>
<221> MOD_RES
<222> (2)..(2)
<223> Beta-Ala

<400> 308
Lys Ala Cys Ala Asp Trp Val Cys Tyr Trp His Thr Phe Gly
1 5 10

<210> 309
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (1)..(1)
<223> (2-aminoethoxy)acetic acid

<400> 309
Xaa Cys Ala Asp Trp Val Cys Tyr Trp His Thr Phe Gly
1 5 10

<210> 310
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (1)..(1)
<223> D-Lys

<400> 310
Lys Cys Ala Asp Trp Val Cys Tyr Trp His Thr Phe Gly
1 5 10

<210> 311
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 311
Cys Lys Asp Trp Val Cys Tyr Trp His Thr Phe Gly
1 5 10

<210> 312
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 312
Cys Ala Asp Trp Lys Cys Tyr Trp His Thr Phe Gly
1 5 10

<210> 313
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 313
Cys Ala Asp Trp Val Cys Tyr Trp Lys Thr Phe Gly
1 5 10

<210> 314
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 314
Cys Ala Asp Trp Val Cys Tyr Trp His Lys Phe Gly
1 5 10

<210> 315
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 315
Cys Ala Asp Trp Val Cys Tyr Trp His Thr Lys Gly
1 5 10

<210> 316
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

peptide

<220>
<221> MOD_RES
<222> (12)..(12)
<223> D-Lys

<400> 316
Cys Ala Asp Trp Val Cys Tyr Trp His Thr Phe Lys
1 5 10

<210> 317
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (13)..(13)
<223> D-Lys

<400> 317
Cys Ala Asp Trp Val Cys Tyr Trp His Thr Phe Gly Lys
1 5 10

<210> 318
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (13)..(13)
<223> Beta-Ala

<220>
<221> MOD_RES
<222> (14)..(14)
<223> D-Lys

<400> 318
Cys Ala Asp Trp Val Cys Tyr Trp His Thr Phe Gly Ala Lys
1 5 10

<210> 319
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (13)..(13)
<223> (2-aminoethoxy)acetic acid

<220>
<221> MOD_RES
<222> (14)..(14)
<223> D-Lys

<400> 319
Cys Ala Asp Trp Val Cys Tyr Trp His Thr Phe Gly Xaa Lys
1 5 10

<210> 320
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 320
Cys Ala Asp Trp Val Cys Tyr Trp His Thr Phe Gly Lys
1 5 10

<210> 321
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (8)..(8)
<223> Beta-hTyr

<220>
<221> MOD_RES
<222> (13)..(13)
<223> (2-aminoethoxy)acetic acid

<220>
<221> MOD_RES
<222> (14)..(14)
<223> D-Lys

<400> 321
Cys Gln Thr Trp Gln Cys Tyr Tyr Arg Val Asn Gly Xaa Lys
1 5 10

<210> 322
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (8)..(8)
<223> Beta-hPhe(4-F)

<220>
<221> MOD_RES
<222> (13)..(13)
<223> (2-aminoethoxy)acetic acid

<220>
<221> MOD_RES
<222> (14)..(14)
<223> D-Lys

<400> 322
Cys Gln Thr Trp Gln Cys Tyr Phe Arg Val Asn Gly Xaa Lys
1 5 10

<210> 323
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (8)..(8)
<223> Beta-Nva(5-Phenyl)

<220>
<221> MOD_RES
<222> (13)..(13)
<223> (2-aminoethoxy)acetic acid

<220>
<221> MOD_RES
<222> (14)..(14)
<223> D-Lys

<400> 323
Cys Gln Thr Trp Gln Cys Tyr Xaa Arg Val Asn Gly Xaa Lys
1 5 10

<210> 324
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (8)..(8)
<223> Phe(3,4-Cl2)

<220>
<221> MOD_RES

<222> (13)..(13)
<223> (2-aminoethoxy)acetic acid

<220>
<221> MOD_RES
<222> (14)..(14)
<223> D-Lys

<400> 324
Cys Gln Thr Trp Gln Cys Tyr Phe Arg Val Asn Gly Xaa Lys
1 5 10

<210> 325
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (8)..(8)
<223> Tqa

<220>
<221> MOD_RES
<222> (13)..(13)
<223> (2-aminoethoxy)acetic acid

<220>
<221> MOD_RES
<222> (14)..(14)
<223> D-Lys

<400> 325
Cys Gln Thr Trp Gln Cys Tyr Xaa Arg Val Asn Gly Xaa Lys
1 5 10

<210> 326
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (10)..(10)
<223> Beta-hLeu

<220>
<221> MOD_RES
<222> (13)..(13)
<223> (2-aminoethoxy)acetic acid

<220>
<221> MOD_RES
<222> (14)..(14)
<223> D-Lys

<400> 326
Cys Gln Thr Trp Gln Cys Tyr Trp Arg Leu Asn Gly Xaa Lys
1 5 10

<210> 327
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
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<222> (10)..(10)
<223> Aib

<220>
<221> MOD_RES
<222> (13)..(13)
<223> (2-aminoethoxy)acetic acid

<220>
<221> MOD_RES
<222> (14)..(14)
<223> D-Lys

<400> 327
Cys Gln Thr Trp Gln Cys Tyr Trp Arg Xaa Asn Gly Xaa Lys
1 5 10

<210> 328
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (10)..(10)
<223> Beta-hAla

<220>
<221> MOD_RES
<222> (13)..(13)
<223> (2-aminoethoxy)acetic acid

<220>
<221> MOD_RES
<222> (14)..(14)
<223> D-Lys

<400> 328
Cys Gln Thr Trp Gln Cys Tyr Trp Arg Ala Asn Gly Xaa Lys
1 5 10

<210> 329
<211> 14
<212> PRT

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (10)..(10)
<223> Beta-hVal

<220>
<221> MOD_RES
<222> (13)..(13)
<223> (2-aminoethoxy)acetic acid

<220>
<221> MOD_RES
<222> (14)..(14)
<223> D-Lys

<400> 329
Cys Gln Thr Trp Gln Cys Tyr Trp Arg Val Asn Gly Xaa Lys
1 5 10

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

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (10)..(10)
<223> Beta-spiral-pip

<220>
<221> MOD_RES
<222> (13)..(13)
<223> (2-aminoethoxy)acetic acid

<220>
<221> MOD_RES
<222> (14)..(14)
<223> D-Lys

<400> 330
Cys Gln Thr Trp Gln Cys Tyr Trp Arg Xaa Asn Gly Xaa Lys
1 5 10

<210> 331
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>

<221> MOD_RES
<222> (10)..(10)
<223> Beta-Glu

<220>
<221> MOD_RES
<222> (13)..(13)
<223> (2-aminoethoxy)acetic acid

<220>
<221> MOD_RES
<222> (14)..(14)
<223> D-Lys

<400> 331
Cys Gln Thr Trp Gln Cys Tyr Trp Arg Glu Asn Gly Xaa Lys
1 5 10

<210> 332
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (9)..(9)
<223> Beta-hLeu

<220>
<221> MOD_RES
<222> (13)..(13)
<223> (2-aminoethoxy)acetic acid

<220>
<221> MOD_RES
<222> (14)..(14)
<223> D-Lys

<400> 332
Cys Gln Thr Trp Gln Cys Tyr Trp Leu Val Asn Gly Xaa Lys
1 5 10

<210> 333
<211> 14
<212> PRT
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<220>
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<220>
<221> MOD_RES
<222> (9)..(9)
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<220>
<221> MOD_RES
<222> (13)..(13)
<223> (2-aminoethoxy)acetic acid

<220>
<221> MOD_RES
<222> (14)..(14)
<223> D-Lys

<400> 333
Cys Gln Thr Trp Gln Cys Tyr Trp Xaa Val Asn Gly Xaa Lys
1 5 10

<210> 334
<211> 14
<212> PRT
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<220>
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<220>
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<220>
<221> MOD_RES
<222> (13)..(13)
<223> (2-aminoethoxy)acetic acid

<220>
<221> MOD_RES
<222> (14)..(14)
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<400> 334
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1 5 10

<210> 335
<211> 14
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<220>
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<223> Beta-hVal

<220>
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<222> (13)..(13)
<223> (2-aminoethoxy)acetic acid

<220>
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<222> (14)..(14)
<223> D-Lys

<400> 335
Cys Gln Thr Trp Gln Cys Tyr Trp Val Val Asn Gly Xaa Lys

1 5 10

<210> 336
<211> 14
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<220>
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<223> Beta-spiral-pip

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<222> (13)..(13)
<223> (2-aminoethoxy)acetic acid

<220>
<221> MOD_RES
<222> (14)..(14)
<223> D-Lys

<400> 336
Cys Gln Thr Trp Gln Cys Tyr Trp Xaa Val Asn Gly Xaa Lys
1 5 10

<210> 337
<211> 14
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<220>
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<223> Beta-hArg

<220>
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<223> (2-aminoethoxy)acetic acid

<220>
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<222> (14)..(14)
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<400> 337
Cys Gln Thr Trp Gln Cys Tyr Trp Arg Val Asn Gly Xaa Lys
1 5 10

<210> 338
<211> 14
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<220>
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<220>
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<223> MeCys

<220>
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<222> (13)..(13)
<223> (2-aminoethoxy)acetic acid

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<222> (14)..(14)
<223> D-Lys

<400> 338
Met Arg Thr Trp Gln Cys Tyr Trp Arg Lys Phe Gly Xaa Lys
1 5 10

<210> 339
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<220>
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<222> (13)..(13)
<223> (2-aminoethoxy)acetic acid

<220>
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<222> (14)..(14)
<223> D-Lys

<400> 339
Ala Cys Asp Trp Val Cys Tyr Trp Arg Lys Phe Gly Xaa Lys
1 5 10

<210> 340
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<223> D-Lys

<400> 340
Ser Arg Thr Trp Gln Ser Tyr Trp Arg Lys Phe Gly Xaa Lys
1 5 10

<210> 341
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<220>
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<223> (2-aminoethoxy)acetic acid

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<222> (13)..(13)
<223> D-Lys

<400> 341
Cys Asp Trp Val Cys Tyr Trp Arg Lys Phe Gly Xaa Lys
1 5 10

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<223> MeCys

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<222> (13)..(13)
<223> (2-aminoethoxy)acetic acid

<220>
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<222> (14)..(14)
<223> D-Lys

<400> 342
Ala Arg Thr Trp Gln Cys Tyr Trp Arg Lys Phe Gly Xaa Lys
1 5 10

<210> 343
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<223> D-Lys

<400> 343
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1 5 10

<210> 344
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<223> (2-aminoethoxy)acetic acid

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<222> (13)..(13)
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<400> 344
Cys Gln Thr Trp Gln Cys Tyr Trp Leu Glu Asn Xaa Lys
1 5 10

<210> 345
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<220>
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<400> 345
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<210> 346
<211> 14
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<220>
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<220>
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<222> (14)..(14)
<223> D-Lys

<400> 346
Cys Ser Thr Trp Glu Cys Tyr Trp Arg Val Tyr Gly Xaa Lys
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<210> 347
<211> 14
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<220>
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<220>
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<223> Orn

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<222> (13)..(13)
<223> (2-aminoethoxy)acetic acid

<220>
<221> MOD_RES
<222> (14)..(14)
<223> D-Lys

<400> 347
Cys Xaa Thr Trp Gln Cys Tyr Trp Arg Val Phe Gly Xaa Lys
1 5 10

<210> 348
<211> 14

<212> PRT
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<220>
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<223> Orn

<220>
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<222> (10)..(10)
<223> Dap

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<223> (2-aminoethoxy)acetic acid

<220>
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<222> (14)..(14)
<223> D-Lys

<400> 348
Cys Gln Thr Trp Gln Cys Tyr Trp Xaa Xaa Phe Gly Xaa Lys
1 5 10

<210> 349
<211> 14
<212> PRT
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<220>
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<223> N-MeAsn

<220>
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<222> (13)..(13)
<223> (2-aminoethoxy)acetic acid

<220>
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<222> (14)..(14)
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<400> 349
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<220>
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<400> 350
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<220>
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<222> (14)..(14)
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<400> 351
Cys Xaa Thr Trp Gln Cys Tyr Trp Arg Val Phe Gly Xaa Lys
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<210> 352
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<220>
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<223> (2-aminoethoxy)acetic acid

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<400> 352
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<210> 353
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<223> (2-aminoethoxy)acetic acid

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Cys Ser Thr Trp Gln Cys Tyr Trp Xaa Xaa Tyr Gly Xaa Lys
1 5 10

<210> 354
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<220>
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<220>
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<222> (14)..(14)
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<400> 354
Cys Ser Thr Trp Glu Cys Tyr Trp Xaa Xaa Tyr Gly Xaa Lys
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<210> 355
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<223> (2-aminoethoxy)acetic acid

<220>
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<222> (14)..(14)
<223> D-Lys

<400> 355
Cys Gln Thr Trp Gln Cys Phe Phe Xaa Xaa Phe Gly Xaa Lys
1 5 10

<210> 356
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<220>
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<223> (2-aminoethoxy)acetic acid

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<222> (14)..(14)
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<400> 356
Cys Pro Thr Trp Gln Cys Tyr Trp Arg Val Phe Gly Xaa Lys
1 5 10

<210> 357
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<223> (2-aminoethoxy)acetic acid

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<222> (14)..(14)
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<400> 357
Cys Ser Thr Trp Glu Cys Tyr Trp Xaa Xaa Tyr Gly Xaa Lys
1 5 10

<210> 358
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<220>
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<223> (2-aminoethoxy)acetic acid

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<222> (14)..(14)
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<400> 358
Cys Ser Thr Trp Glu Cys Tyr Trp Arg Val Phe Gly Xaa Lys
1 5 10

<210> 359
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<223> (2-aminoethoxy)acetic acid

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<400> 359
Cys Leu Thr Trp Gln Cys Tyr Trp Arg Val Phe Gly Xaa Lys
1 5 10

<210> 360
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<223> (2-aminoethoxy)acetic acid

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<222> (14)..(14)
<223> D-Lys

<400> 360
Cys Gln Thr Trp Gln Cys Tyr Phe Xaa Xaa Phe Gly Xaa Lys
1 5 10

<210> 361
<211> 14
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<220>
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<220>
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<222> (13)..(13)
<223> (2-aminoethoxy)acetic acid

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<222> (14)..(14)
<223> D-Lys

<400> 361
Cys Asn Thr Trp Gln Cys Tyr Trp Arg Val Phe Gly Xaa Lys
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<210> 362
<211> 14
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<222> (13)..(13)
<223> (2-aminoethoxy)acetic acid

<220>
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<222> (14)..(14)
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<400> 362
Cys Xaa Thr Trp Gln Cys Tyr Trp Arg Val Phe Gly Xaa Lys
1 5 10

<210> 363
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<223> N-Me-Ala

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<222> (13)..(13)
<223> (2-aminoethoxy)acetic acid

<220>
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<222> (14)..(14)
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<400> 363
Cys Ala Thr Trp Gln Cys Tyr Trp Arg Val Phe Gly Xaa Lys
1 5 10

<210> 364
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<222> (14)..(14)
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<400> 364
Cys Lys Thr Trp Gln Cys Tyr Trp Arg Val Phe Gly Xaa Lys
1 5 10

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<222> (14)..(14)
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<400> 365

Cys Gln Asp Trp Gln Cys Tyr Trp Arg Xaa Phe Gly Xaa Lys
1 5 10

<210> 366
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<400> 366
Cys Gln Thr Trp Gln Cys Tyr Trp Arg Xaa Phe Gly Xaa Lys
1 5 10

<210> 367
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<222> (14)..(14)
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<400> 367
Cys Gln Thr Trp Gln Cys Tyr Trp Lys Xaa Phe Gly Xaa Lys
1 5 10

<210> 368
<211> 14
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<222> (13)..(13)
<223> (2-aminoethoxy)acetic acid

<220>
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<222> (14)..(14)
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<400> 368
Cys Gln Thr Trp Gln Cys Tyr Trp His Xaa Phe Gly Xaa Lys
1 5 10

<210> 369
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<220>
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<222> (14)..(14)
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<400> 369
Cys Gln Thr Trp Gln Cys Tyr Trp Arg Leu Phe Gly Xaa Lys
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<210> 370
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<223> (2-aminoethoxy)acetic acid

<220>
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<222> (14)..(14)
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<400> 370
Cys Gln Thr Trp Gln Cys Tyr Trp Arg Xaa Phe Gly Xaa Lys
1 5 10

<210> 371
<211> 12
<212> PRT
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<220>
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<400> 371
Cys Ser Thr Trp Glu Cys Tyr Trp Arg Thr Phe Gly
1 5 10

<210> 372
<211> 12
<212> PRT
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<220>
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<400> 372
Cys Asp Ser Trp Glu Cys Tyr Trp Arg Thr Tyr Gly
1 5 10

<210> 373
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
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<400> 373
Cys Ser Thr Trp Glu Cys Tyr Trp His Thr Tyr Gly
1 5 10

<210> 374
<211> 12
<212> PRT
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<220>
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<400> 374
Cys Lys Thr Trp Thr Cys Tyr Trp His Thr Tyr Gly
1 5 10

<210> 375
<211> 12
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<220>
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<400> 375
Cys Arg Thr Trp Glu Cys Tyr Trp His Glu Tyr Ser
1 5 10

<210> 376
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<220>
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<400> 376
Cys Arg Thr Trp Thr Cys Tyr Trp His Glu Tyr Gly
1 5 10

<210> 377
<211> 12
<212> PRT
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<220>
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<400> 377
Cys Phe Thr Trp Gln Cys Tyr Trp His Glu Tyr Ser
1 5 10

<210> 378
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<220>
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<400> 378
Cys Gln Thr Trp Gln Cys Tyr Trp Xaa Glu Asn Gly
1 5 10

<210> 379
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<220>
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<400> 379
Cys Gln Thr Trp Gln Cys
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<210> 380
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<220>
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<400> 380
Cys Arg Thr Trp Gln Cys
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<210> 381
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<220>
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<400> 381
Cys Ala Asp Trp Val Cys Tyr
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<210> 382
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<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 382
Cys Ala Asp Trp Val Cys Tyr Trp
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<210> 383
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<212> PRT
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<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 383
Cys Ala Asp Trp Val Cys Tyr Trp His
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<210> 384
<211> 10
<212> PRT
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<220>
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<400> 384
Cys Ala Asp Trp Val Cys Tyr Trp His Thr
1 5 10

<210> 385
<211> 11
<212> PRT
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<220>
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<400> 385
Cys Ala Asp Trp Val Cys Tyr Trp His Thr Phe
1 5 10

<210> 386
<211> 12
<212> PRT
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<220>
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<400> 386
Cys Met Thr Trp Gln Cys Tyr Trp Leu Tyr Gly Arg
1 5 10

<210> 387
<211> 12
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<220>
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<400> 387
Cys Arg Thr Trp Gln Cys Tyr Trp His Glu Phe Gly
1 5 10

<210> 388
<211> 12
<212> PRT
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<220>
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<400> 388

Cys Arg Thr Trp Glu Cys Tyr Trp His Thr Phe Gly
1 5 10

<210> 389
<211> 12
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<220>
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<400> 389
Cys Gln Thr Trp Gln Cys Tyr Trp His Glu Phe Gly
1 5 10

<210> 390
<211> 14
<212> PRT
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<220>
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<400> 390
Cys Arg Thr Trp Gln Cys Tyr Trp Gln Gln Phe Gly Gly Glu
1 5 10

<210> 391
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 391
Cys Arg Ser Trp Gln Cys Tyr Trp Leu Asn Phe Gly Pro Asp
1 5 10

<210> 392
<211> 14
<212> PRT
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<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 392
Cys Arg Thr Trp Gln Cys Tyr Trp Leu Lys Met Gly Asp Ser
1 5 10

<210> 393
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 393
Cys Gln Thr Trp Gln Cys Tyr Trp Ile Lys Arg Asp Gln Gly
1 5 10

<210> 394
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 394
Cys Ser Thr Trp Gln Cys Tyr Trp Leu Lys His Gly Gly Glu
1 5 10

<210> 395
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 395
Cys Ser Thr Trp Glu Cys Tyr Trp Ser Gln Arg Ala Asp Gln
1 5 10

<210> 396
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 396
Cys Gln Thr Trp Glu Cys Tyr Trp Arg Thr Phe Gly Pro Ser
1 5 10

<210> 397
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 397
Cys Arg Thr Trp Gln Cys Tyr Trp Gln Glu Lys Gly Thr Asp
1 5 10

<210> 398
<211> 14
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 398
Cys Gln Thr Trp Gln Cys Tyr Trp Leu Asp Ser Leu Gly Asp
1 5 10

<210> 399
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 399
Cys Arg Thr Trp Gln Cys Tyr Trp Thr Lys Phe Gly Ser Glu Pro
1 5 10 15

<210> 400
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (9)..(9)
<223> hLeu

<400> 400
Cys Gln Thr Trp Gln Cys Tyr Trp Leu Glu Pro Gly
1 5 10

<210> 401
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (9)..(9)
<223> hLeu

<400> 401
Cys Gln Thr Trp Gln Cys Tyr Trp Leu Glu Leu Gly
1 5 10

<210> 402
<211> 12
<212> PRT
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<220>

<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (9)..(9)
<223> hLeu

<400> 402
Cys Gln Thr Trp Gln Cys Tyr Trp Leu Glu Thr Gly
1 5 10

<210> 403
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (9)..(9)
<223> hLeu

<400> 403
Cys Gln Thr Trp Gln Cys Tyr Trp Leu Phe Asn Gly
1 5 10

<210> 404
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (9)..(9)
<223> hLeu

<400> 404
Cys Gln Thr Trp Gln Cys Tyr Trp Leu Pro Asn Gly
1 5 10

<210> 405
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (9)..(9)
<223> hLeu

<400> 405
Cys Gln Thr Trp Gln Cys Tyr Trp Leu Asn Asn Gly
1 5 10

<210> 406
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (9)..(9)
<223> hLeu

<400> 406
Cys Gln Thr Trp Gln Cys Tyr Trp Leu Leu Asn Gly
1 5 10

<210> 407
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (9)..(9)
<223> hLeu

<400> 407
Cys Gln Thr Trp Gln Cys Tyr Trp Leu Thr Asn Gly
1 5 10

<210> 408
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 408
Cys Gln Thr Trp Gln Cys Tyr Trp Phe Glu Asn Gly
1 5 10

<210> 409
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 409
Cys Gln Thr Trp Gln Cys Tyr Trp Pro Glu Asn Gly
1 5 10

<210> 410
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 410
Cys Gln Thr Trp Gln Cys Tyr Trp Gln Glu Asn Gly
1 5 10

<210> 411
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 411
Cys Gln Thr Trp Gln Cys Tyr Trp Thr Glu Asn Gly
1 5 10

<210> 412
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 412
Cys Gln Thr Trp Gln Cys Tyr Trp Glu Glu Asn Gly
1 5 10

<210> 413
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (9)..(9)
<223> hLeu

<400> 413
Cys Gln Thr Trp Phe Cys Tyr Trp Leu Glu Asn Gly
1 5 10

<210> 414
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (9)..(9)
<223> hLeu

<400> 414
Cys Gln Thr Trp Pro Cys Tyr Trp Leu Glu Asn Gly
1 5 10

<210> 415
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (9)..(9)
<223> hLeu

<400> 415
Cys Gln Thr Trp Asn Cys Tyr Trp Leu Glu Asn Gly
1 5 10

<210> 416
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (9)..(9)
<223> hLeu

<400> 416
Cys Gln Thr Trp Arg Cys Tyr Trp Leu Glu Asn Gly
1 5 10

<210> 417
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (9)..(9)
<223> hLeu

<400> 417
Cys Gln Thr Trp Thr Cys Tyr Trp Leu Glu Asn Gly
1 5 10

<210> 418
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (9)..(9)
<223> hLeu

<400> 418
Cys Gln Thr Trp Glu Cys Tyr Trp Leu Glu Asn Gly
1 5 10

<210> 419
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (9)..(9)
<223> hLeu

<400> 419
Cys Gln Thr Gly Gln Cys Tyr Trp Leu Glu Asn Gly
1 5 10

<210> 420
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (9)..(9)
<223> hLeu

<400> 420

Cys Gln Thr Pro Gln Cys Tyr Trp Leu Glu Asn Gly
1 5 10

<210> 421
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (9)..(9)
<223> hLeu

<400> 421
Cys Gln Thr Asn Gln Cys Tyr Trp Leu Glu Asn Gly
1 5 10

<210> 422
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (9)..(9)
<223> hLeu

<400> 422
Cys Gln Thr Arg Gln Cys Tyr Trp Leu Glu Asn Gly
1 5 10

<210> 423
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (9)..(9)
<223> hLeu

<400> 423
Cys Gln Thr Thr Gln Cys Tyr Trp Leu Glu Asn Gly
1 5 10

<210> 424
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (9)..(9)
<223> hLeu

<400> 424
Cys Gln Thr Glu Gln Cys Tyr Trp Leu Glu Asn Gly
1 5 10

<210> 425
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (9)..(9)
<223> hLeu

<400> 425
Cys Gln Phe Trp Gln Cys Tyr Trp Leu Glu Asn Gly
1 5 10

<210> 426
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (9)..(9)
<223> hLeu

<400> 426
Cys Gln Pro Trp Gln Cys Tyr Trp Leu Glu Asn Gly
1 5 10

<210> 427
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES

<222> (9)..(9)
<223> hLeu

<400> 427
Cys Gln Asn Trp Gln Cys Tyr Trp Leu Glu Asn Gly
1 5 10

<210> 428
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (9)..(9)
<223> hLeu

<400> 428
Cys Gln Arg Trp Gln Cys Tyr Trp Leu Glu Asn Gly
1 5 10

<210> 429
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (9)..(9)
<223> hLeu

<400> 429
Cys Gln Glu Trp Gln Cys Tyr Trp Leu Glu Asn Gly
1 5 10

<210> 430
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Abu

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Phe(4-OMe)

<220>
<221> MOD_RES
<222> (8)..(8)
<223> 2-Nal

<220>
<221> MOD_RES
<222> (9)..(9)
<223> alpha-MeLys

<400> 430
Xaa Gln Thr Trp Gln Cys Phe Xaa Lys Glu Asn Gly
1 5 10

<210> 431
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Abu

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Phe(4-OMe)

<220>
<221> MOD_RES
<222> (8)..(8)
<223> 2-Nal

<220>
<221> MOD_RES
<222> (9)..(9)
<223> alpha-MeOrn

<400> 431
Xaa Gln Thr Trp Gln Cys Phe Xaa Xaa Glu Asn Gly
1 5 10

<210> 432
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Abu

<220>
<221> MOD_RES
<222> (7)..(7)

<223> Phe(4-CO2H)

<220>
<221> MOD_RES
<222> (8)..(8)
<223> 2-Nal

<220>
<221> MOD_RES
<222> (9)..(9)
<223> alpha-MeLys

<220>
<221> MOD_RES
<222> (10)..(10)
<223> Lys(Ac)

<400> 432
Xaa Gln Thr Trp Gln Cys Phe Xaa Lys Lys Asn Gly
1 5 10

<210> 433
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Abu

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Phe(4-OMe)

<220>
<221> MOD_RES
<222> (8)..(8)
<223> 2-Nal

<220>
<221> MOD_RES
<222> (9)..(9)
<223> alpha-MeLys

<220>
<221> MOD_RES
<222> (10)..(10)
<223> Lys(Ac)

<400> 433
Xaa Gln Thr Trp Gln Cys Phe Xaa Lys Lys Asn Gly
1 5 10

<210> 434
<211> 12
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Abu

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Phe(4-CONH2)

<220>
<221> MOD_RES
<222> (8)..(8)
<223> 2-Nal

<220>
<221> MOD_RES
<222> (9)..(9)
<223> alpha-MeLys

<220>
<221> MOD_RES
<222> (10)..(10)
<223> Lys(Ac)

<400> 434
Xaa Gln Thr Trp Gln Cys Phe Xaa Lys Lys Asn Gly
1 5 10

<210> 435
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Abu

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Phe(4-OMe)

<220>
<221> MOD_RES
<222> (8)..(8)
<223> 2-Nal

<220>
<221> MOD_RES
<222> (9)..(9)
<223> alpha-MeLys

<220>
<221> MOD_RES
<222> (10)..(10)
<223> Lys(Ac)

<400> 435
Xaa Gln Thr Trp Gln Cys Phe Xaa Lys Lys Asn Ala
1 5 10

<210> 436
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Abu

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Phe(4-OMe)

<220>
<221> MOD_RES
<222> (8)..(8)
<223> 2-Nal

<220>
<221> MOD_RES
<222> (9)..(9)
<223> alpha-MeLys

<220>
<221> MOD_RES
<222> (10)..(10)
<223> Lys(Ac)

<400> 436
Xaa Gln Thr Trp Gln Cys Phe Xaa Lys Lys Asn Ala Glu
1 5 10

<210> 437
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Abu

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Phe[4-(2-aminoethoxy)]

<220>
<221> MOD_RES

<222> (8)..(8)
<223> 2-Nal

<220>
<221> MOD_RES
<222> (9)..(9)
<223> alpha-MeLys

<400> 437
Xaa Gln Thr Trp Gln Cys Phe Xaa Lys Glu Asn Gly
1 5 10

<210> 438
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Abu

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Phe(4-(2-aminoethoxy))

<220>
<221> MOD_RES
<222> (9)..(9)
<223> alpha-MeLys

<400> 438
Xaa Gln Thr Trp Gln Cys Phe Trp Lys Glu Asn Gly
1 5 10

<210> 439
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Abu

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Phe[4-(2-aminoethoxy)]

<220>
<221> MOD_RES
<222> (8)..(8)
<223> 2-Nal

<220>
<221> MOD_RES
<222> (9)..(9)
<223> alpha-MeLys

<400> 439
Xaa Gln Thr Trp Gln Cys Phe Xaa Lys Asp Asn Gly
1 5 10

<210> 440
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Abu

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Phe[4-(2-aminoethoxy)]

<220>
<221> MOD_RES
<222> (8)..(8)
<223> 2-Nal

<220>
<221> MOD_RES
<222> (9)..(9)
<223> alpha-MeLys

<220>
<221> MOD_RES
<222> (10)..(10)
<223> Lys(succinic acid)

<400> 440
Xaa Gln Thr Trp Gln Cys Phe Xaa Lys Lys Asn Gly
1 5 10

<210> 441
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Abu

<220>
<221> MOD_RES
<222> (7)..(7)

<223> Phe[4-(2-aminoethoxy)]

<220>
<221> MOD_RES
<222> (8)..(8)
<223> 2-Nal

<220>
<221> MOD_RES
<222> (9)..(9)
<223> alpha-MeLys

<220>
<221> MOD_RES
<222> (10)..(10)
<223> Lys(glutaric acid)

<400> 441
Xaa Gln Thr Trp Gln Cys Phe Xaa Lys Lys Asn Gly
1 5 10

<210> 442
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Abu

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Phe[4-(2-aminoethoxy)]

<220>
<221> MOD_RES
<222> (8)..(8)
<223> 2-Nal

<220>
<221> MOD_RES
<222> (9)..(9)
<223> alpha-MeLys

<220>
<221> MOD_RES
<222> (10)..(10)
<223> Lys(pyroglutamic acid) conjugated through side chain

<400> 442
Xaa Gln Thr Trp Gln Cys Phe Xaa Lys Lys Asn Gly
1 5 10

<210> 443
<211> 12
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Abu

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Phe[4-(2-aminoethoxy)]

<220>
<221> MOD_RES
<222> (8)..(8)
<223> 2-Nal

<220>
<221> MOD_RES
<222> (9)..(9)
<223> alpha-MeLys

<220>
<221> MOD_RES
<222> (10)..(10)
<223> Lys(isovaleric acid)

<400> 443
Xaa Gln Thr Trp Gln Cys Phe Xaa Lys Lys Asn Gly
1 5 10

<210> 444
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Abu

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Phe[4-(2-aminoethoxy)]

<220>
<221> MOD_RES
<222> (8)..(8)
<223> 2-Nal

<220>
<221> MOD_RES
<222> (9)..(9)
<223> alpha-MeLys

<220>
<221> MOD_RES
<222> (10)..(10)
<223> Lys(Ac)

<220>
<221> MOD_RES
<222> (13)..(13)
<223> D-Lys

<400> 444
Xaa Gln Thr Trp Gln Cys Phe Xaa Lys Lys Asn Gly Lys
1 5 10

<210> 445
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Abu

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Phe[4-(2-aminoethoxy)]

<220>
<221> MOD_RES
<222> (8)..(8)
<223> 2-Nal

<220>
<221> MOD_RES
<222> (9)..(9)
<223> alpha-MeLys

<220>
<221> MOD_RES
<222> (10)..(10)
<223> Lys(Ac)

<220>
<221> MOD_RES
<222> (13)..(13)
<223> (2-aminoethoxy)acetic acid

<400> 445
Xaa Gln Thr Trp Gln Cys Phe Xaa Lys Lys Asn Gly Xaa
1 5 10

<210> 446
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES

<222> (1)..(1)
<223> Abu

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Phe[4-(2-aminoethoxy)]

<220>
<221> MOD_RES
<222> (8)..(8)
<223> 2-Nal

<220>
<221> MOD_RES
<222> (9)..(9)
<223> Aib

<400> 446
Xaa Gln Thr Trp Gln Cys Phe Xaa Xaa Gln Asn Gly
1 5 10

<210> 447
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Abu

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Phe[4-(2-aminoethoxy)]

<220>
<221> MOD_RES
<222> (8)..(8)
<223> 2-Nal

<220>
<221> MOD_RES
<222> (9)..(9)
<223> Aib

<220>
<221> MOD_RES
<222> (10)..(10)
<223> Lys(Ac)

<400> 447
Xaa Gln Thr Trp Gln Cys Phe Xaa Xaa Lys Asn Ala
1 5 10

<210> 448
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Abu

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Phe[4-(2-aminoethoxy)]

<220>
<221> MOD_RES
<222> (8)..(8)
<223> 2-Nal

<220>
<221> MOD_RES
<222> (9)..(9)
<223> Aib

<400> 448
Xaa Gln Thr Trp Gln Cys Phe Xaa Xaa Lys Asn Gly
1 5 10

<210> 449
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
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<222> (1)..(1)
<223> Abu

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Phe[4-(2-aminoethoxy)]

<220>
<221> MOD_RES
<222> (8)..(8)
<223> 2-Nal

<220>
<221> MOD_RES
<222> (9)..(9)
<223> alpha-MeLys

<220>
<221> MOD_RES
<222> (10)..(10)
<223> Lys(Ac)

<400> 449
Xaa Gln Thr Trp Gln Cys Phe Xaa Lys Lys Asn Gly
1 5 10

<210> 450
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (9)..(9)
<223> hLeu

<400> 450
Cys Phe Thr Trp Gln Cys Tyr Trp Leu Glu Asn Gly
1 5 10

<210> 451
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (9)..(9)
<223> hLeu

<400> 451
Cys Pro Thr Trp Gln Cys Tyr Trp Leu Glu Asn Gly
1 5 10

<210> 452
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (9)..(9)
<223> hLeu

<400> 452
Cys Asn Thr Trp Gln Cys Tyr Trp Leu Glu Asn Gly
1 5 10

<210> 453
<211> 12
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<220>
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<222> (9)..(9)
<223> hLeu

<400> 453
Cys Gly Thr Trp Gln Cys Tyr Trp Leu Glu Asn Gly
1 5 10

<210> 454
<211> 12
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<220>
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<220>
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<222> (9)..(9)
<223> hLeu

<400> 454
Cys Thr Thr Trp Gln Cys Tyr Trp Leu Glu Asn Gly
1 5 10

<210> 455
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<220>
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<220>
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<222> (9)..(9)
<223> hLeu

<400> 455
Cys Glu Thr Trp Gln Cys Tyr Trp Leu Glu Asn Gly
1 5 10

<210> 456
<211> 12
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<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
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<222> (9)..(9)
<223> N-MeLeu

<400> 456
Cys Gln Thr Trp Gln Cys Tyr Trp Leu Glu Asn Gly
1 5 10

<210> 457
<211> 12
<212> PRT
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<220>
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<220>
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<222> (9)..(9)
<223> alpha-MeOrn

<400> 457
Cys Gln Thr Trp Gln Cys Tyr Trp Xaa Glu Asn Gly
1 5 10

<210> 458
<211> 12
<212> PRT
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<220>
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<220>
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<222> (9)..(9)
<223> alpha-MeOrn

<400> 458
Cys Gln Thr Trp Gln Cys Tyr Trp Xaa Glu Asn Gly
1 5 10

<210> 459
<211> 12
<212> PRT
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<220>
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<220>
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<223> alpha-MePhe

<220>
<221> MOD_RES
<222> (9)..(9)
<223> hLeu

<400> 459
Cys Gln Thr Trp Gln Cys Phe Trp Leu Glu Asn Gly

1 5 10

<210> 460
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
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<220>
<221> MOD_RES
<222> (9)..(9)
<223> Aib

<400> 460
Cys Gln Thr Trp Gln Cys Tyr Trp Xaa Glu Asn Gly
1 5 10

<210> 461
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<213> Artificial Sequence

<220>
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<220>
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<222> (7)..(7)
<223> hTyr

<220>
<221> MOD_RES
<222> (9)..(9)
<223> hLeu

<400> 461
Cys Gln Thr Trp Gln Cys Tyr Trp Leu Glu Asn Gly
1 5 10

<210> 462
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
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<220>
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<222> (7)..(7)
<223> Bip

<220>
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<222> (9)..(9)
<223> hLeu

<400> 462
Cys Gln Thr Trp Gln Cys Xaa Trp Leu Glu Asn Gly
1 5 10

<210> 463
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
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<220>
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<222> (9)..(9)
<223> Ogl

<400> 463
Cys Gln Thr Trp Gln Cys Tyr Trp Xaa Glu Asn Gly
1 5 10

<210> 464
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
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<220>
<221> MOD_RES
<222> (9)..(9)
<223> hLeu

<220>
<221> MOD_RES
<222> (10)..(10)
<223> Lys(Ac)

<400> 464
Cys Gln Thr Trp Gln Cys Tyr Trp Leu Lys Asn Gly
1 5 10

<210> 465
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (9)..(9)
<223> hLeu

<400> 465
Cys Gln Thr Trp Gln Cys Tyr Trp Leu Glu Asn Gly Gly
1 5 10

<210> 466
<211> 13
<212> PRT
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<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
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<222> (9)..(9)
<223> hLeu

<400> 466
Cys Gln Thr Trp Gln Cys Tyr Trp Leu Glu Asn Gly Pro
1 5 10

<210> 467
<211> 13
<212> PRT
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<220>
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<220>
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<400> 467
Cys Gln Thr Trp Gln Cys Tyr Trp Leu Glu Asn Gly Glu
1 5 10

<210> 468
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<213> Artificial Sequence

<220>
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<220>
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<223> hLeu

<220>
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<222> (13)..(13)
<223> D-Glu

<400> 468
Cys Gln Thr Trp Gln Cys Tyr Trp Leu Glu Asn Gly Glu
1 5 10

<210> 469

<211> 12
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<213> Artificial Sequence

<220>
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<220>
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<222> (8)..(8)
<223> alpha-MePhe

<220>
<221> MOD_RES
<222> (9)..(9)
<223> hLeu

<400> 469
Cys Gln Thr Trp Gln Cys Tyr Phe Leu Glu Asn Gly
1 5 10

<210> 470
<211> 13
<212> PRT
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<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (9)..(9)
<223> hLeu

<400> 470
Cys Gln Thr Trp Gln Cys Tyr Trp Leu Glu Asn Gly Pro
1 5 10

<210> 471
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (9)..(9)
<223> hLeu

<400> 471
Cys Gln Thr Trp Gln Cys Tyr Trp Leu Glu Asn Gly Gly
1 5 10

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

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
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<222> (9)..(9)
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<400> 472
Cys Gln Thr Trp Gln Cys Tyr Trp Leu Glu Asn Gly Leu
1 5 10

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

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
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<400> 473
Cys Gln Thr Trp Gln Cys Tyr Trp Leu Glu Asn Gly Phe
1 5 10

<210> 474
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<220>
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<220>
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<222> (9)..(9)
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<400> 474
Cys Gln Thr Trp Gln Cys Tyr Trp Leu Glu Asn Gly Glu
1 5 10

<210> 475
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<220>
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<223> hLeu

<400> 475
Cys Gln Thr Trp Gln Cys Tyr Trp Leu Glu Asn Gly Asn
1 5 10

<210> 476
<211> 13
<212> PRT
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<220>
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<220>
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<400> 476
Cys Gln Thr Trp Gln Cys Tyr Trp Leu Glu Asn Gly Thr
1 5 10

<210> 477
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<212> PRT
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<220>
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<220>
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<222> (9)..(9)
<223> hLeu

<400> 477
Cys Gln Thr Trp Gln Cys Tyr Trp Leu Glu Asn Gly Arg
1 5 10

<210> 478
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
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<220>
<221> MOD_RES
<222> (10)..(10)
<223> hLeu

<400> 478
Pro Cys Gln Thr Trp Gln Cys Tyr Trp Leu Glu Asn Gly
1 5 10

<210> 479
<211> 13
<212> PRT
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<220>
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<400> 479
Leu Cys Gln Thr Trp Gln Cys Tyr Trp Leu Glu Asn Gly
1 5 10

<210> 480
<211> 13
<212> PRT
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<220>
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<400> 480
Phe Cys Gln Thr Trp Gln Cys Tyr Trp Leu Glu Asn Gly
1 5 10

<210> 481
<211> 13
<212> PRT
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<220>
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<223> hLeu

<400> 481
Glu Cys Gln Thr Trp Gln Cys Tyr Trp Leu Glu Asn Gly
1 5 10

<210> 482
<211> 13
<212> PRT
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<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (10)..(10)
<223> hLeu

<400> 482
Asn Cys Gln Thr Trp Gln Cys Tyr Trp Leu Glu Asn Gly
1 5 10

<210> 483
<211> 13
<212> PRT
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<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (10)..(10)
<223> hLeu

<400> 483
Arg Cys Gln Thr Trp Gln Cys Tyr Trp Leu Glu Asn Gly
1 5 10

<210> 484
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
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<220>
<221> MOD_RES
<222> (8)..(8)
<223> 2-Nal

<220>
<221> MOD_RES
<222> (9)..(9)
<223> hLeu

<400> 484
Cys Gln Thr Trp Gln Cys Tyr Xaa Leu Glu Asn Gly
1 5 10

<210> 485
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>

<221> MOD_RES
<222> (8)..(8)
<223> 1-Nal

<220>
<221> MOD_RES
<222> (9)..(9)
<223> hLeu

<400> 485
Cys Gln Thr Trp Gln Cys Tyr Xaa Leu Glu Asn Gly
1 5 10

<210> 486
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
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<223> 2-Nal

<220>
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<222> (9)..(9)
<223> hLeu

<400> 486
Cys Gln Thr Trp Gln Cys Xaa Trp Leu Glu Asn Gly
1 5 10

<210> 487
<211> 12
<212> PRT
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<220>
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<223> 1-Nal

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<223> 2-Nal

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<222> (9)..(9)
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<400> 487
Cys Gln Thr Trp Gln Cys Xaa Xaa Leu Glu Asn Gly
1 5 10

<210> 488
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<220>
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<222> (8)..(8)
<223> 1-Nal

<220>
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<222> (9)..(9)
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<400> 488
Cys Gln Thr Trp Gln Cys Xaa Xaa Leu Glu Asn Gly
1 5 10

<210> 489
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
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<220>
<221> MOD_RES
<222> (7)..(7)
<223> Aic

<220>
<221> MOD_RES
<222> (9)..(9)
<223> hLeu

<400> 489
Cys Gln Thr Trp Gln Cys Xaa Trp Leu Glu Asn Gly
1 5 10

<210> 490
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES

<222> (9)..(9)
<223> hLeu

<400> 490
Cys Gln Thr Trp Gln Cys His Trp Leu Glu Asn Gly
1 5 10

<210> 491
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (9)..(9)
<223> hLeu

<400> 491
Cys Gln Thr Trp Gln Cys Tyr His Leu Glu Asn Gly
1 5 10

<210> 492
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Tyr(OMe)

<220>
<221> MOD_RES
<222> (9)..(9)
<223> hLeu

<400> 492
Cys Gln Thr Trp Gln Cys Tyr Trp Leu Glu Asn Gly
1 5 10

<210> 493
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
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<220>
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<222> (8)..(8)
<223> Bip

<220>
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<222> (9)..(9)
<223> hLeu

<400> 493
Cys Gln Thr Trp Gln Cys Tyr Xaa Leu Glu Asn Gly
1 5 10

<210> 494
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
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<220>
<221> MOD_RES
<222> (8)..(8)
<223> Tyr(OMe)

<220>
<221> MOD_RES
<222> (9)..(9)
<223> hLeu

<400> 494
Cys Gln Thr Trp Gln Cys Tyr Tyr Leu Glu Asn Gly
1 5 10

<210> 495
<211> 12
<212> PRT
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<220>
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<220>
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<222> (9)..(9)
<223> hLeu

<400> 495
Cys Gln Thr Trp Gln Cys His His Leu Glu Asn Gly
1 5 10

<210> 496
<211> 12
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<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (8)..(8)

<223> alpha-MeTrp

<220>
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<222> (9)..(9)
<223> hLeu

<400> 496
Cys Gln Thr Trp Gln Cys Tyr Trp Leu Glu Gln Gly
1 5 10

<210> 497
<211> 12
<212> PRT
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<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
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<222> (5)..(5)
<223> Lys(PEG8)

<400> 497
Cys Gln Thr Trp Lys Cys Tyr Trp Leu Glu Asn Gly
1 5 10

<210> 498
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (9)..(9)
<223> Any amino acid

<400> 498
Cys Gln Thr Trp Gln Cys Tyr Trp Xaa Leu Asn Gly
1 5 10

<210> 499
<211> 12
<212> PRT
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<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (5)..(5)
<223> Lys(PEG8)

<220>

<221> MOD_RES
<222> (9)..(9)
<223> Lys(PEG8)

<400> 499
Cys Gln Thr Trp Lys Cys Tyr Trp Lys Glu Asn Gly
1 5 10

<210> 500
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (5)..(5)
<223> Lys(Palm)

<400> 500
Cys Gln Thr Trp Lys Cys Tyr Trp Leu Glu Asn Gly
1 5 10

<210> 501
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (9)..(9)
<223> Orn

<220>
<221> MOD_RES
<222> (10)..(10)
<223> Lys(Palm)

<400> 501
Cys Gln Thr Trp Gln Cys Tyr Trp Xaa Lys Asn Gly
1 5 10

<210> 502
<211> 12
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<220>
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<220>
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<222> (2)..(2)
<223> D-Asn

<220>
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<222> (3)..(3)
<223> D-Glu

<220>
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<222> (4)..(4)
<223> D-Leu

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<222> (5)..(5)
<223> D-Trp

<220>
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<222> (6)..(6)
<223> D-Tyr

<220>
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<222> (7)..(7)
<223> D-Cys

<220>
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<222> (8)..(8)
<223> D-Gln

<220>
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<222> (9)..(9)
<223> D-Trp

<220>
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<222> (10)..(10)
<223> D-Thr

<220>
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<222> (11)..(11)
<223> D-Gln

<220>
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<222> (12)..(12)
<223> D-Cys

<400> 502
Gly Asn Glu Leu Trp Tyr Cys Gln Trp Thr Gln Cys
1 5 10

<210> 503
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
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<220>
<221> MOD_RES

<222> (9)..(9)
<223> Orn

<220>
<221> MOD_RES
<222> (10)..(10)
<223> Lys(PEG8)

<400> 503
Cys Gln Thr Trp Gln Cys Tyr Trp Xaa Lys Asn Gly
1 5 10

<210> 504
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 504
Cys Arg Thr Trp Gln Cys Tyr Trp His Glu Phe Gly
1 5 10

<210> 505
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 505
Cys Arg Thr Trp Glu Cys Tyr Trp His Thr Phe Gly
1 5 10

<210> 506
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 506
Cys Gln Thr Trp Gln Cys Tyr Trp His Glu Phe Gly
1 5 10

<210> 507
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 507
Cys Gln Thr Trp Gln Cys Tyr Trp Arg Asn Phe Gly Asp Ser
1 5 10

<210> 508
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 508
Cys Gln Thr Trp Gln Cys Tyr Trp Arg Asn Phe Glu Ser Gly
1 5 10

<210> 509
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 509
Cys Gln Asp Trp Gln Cys Tyr Trp Arg Glu Phe Gly Pro Gly
1 5 10

<210> 510
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 510
Cys Gln Asp Trp Gln Cys Tyr Trp Arg Ser Phe Gly Pro Gln
1 5 10

<210> 511
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 511
Cys Gln Thr Trp Gln Cys Tyr Trp Arg Thr Leu Gly Pro Ser
1 5 10

<210> 512
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>

<221> MOD_RES
<222> (9)..(9)
<223> D-Pro

<400> 512
Cys Gln Thr Trp Gln Cys Tyr Trp Pro Glu Asn Gly
1 5 10

<210> 513
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 513
Cys Gln Thr Trp Gln Cys Tyr Trp Glu Leu Asn Gly
1 5 10

<210> 514
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 514
Cys Gln Thr Trp Glu Cys Tyr Trp Glu Leu Asn Gly
1 5 10

<210> 515
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
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<400> 515
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<400> 516
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Cys Gln Thr Trp Gln Cys Tyr Trp Leu Glu Asn Lys
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Cys Ser Thr Trp Glu Cys Tyr Trp Arg Thr Phe Gly
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1 5 10

<210> 521
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<210> 527
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<210> 528
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<400> 553
Ala Xaa Asp Trp Val Xaa Tyr Trp Xaa Xaa Phe Gly Xaa Lys
1 5 10

<210> 554
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1 5 10

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<400> 582
Xaa Gln Thr Trp Gln Xaa Phe Xaa Lys Lys Asn Gly
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<223> 2-Nal

<220>
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<222> (10)..(10)
<223> Aib

<220>
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<223> Lys(Ac)

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1 5 10

<210> 646
<211> 13
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<220>
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<220>
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<222> (7)..(7)
<223> Pen

<220>
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<222> (8)..(8)
<223> Phe[4-(2-aminoethoxy)]

<220>
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<223> 2-Nal

<220>

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<223> Aib

<220>
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<222> (11)..(11)
<223> Lys(Ac)

<400> 646
Phe Xaa Gln Thr Trp Gln Xaa Phe Xaa Xaa Lys Asn Asn
1 5 10

<210> 647
<211> 13
<212> PRT
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<220>
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<220>
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<220>
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<223> Phe[4-(2-aminoethoxy)]

<220>
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<223> 2-Nal

<220>
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<222> (10)..(10)
<223> Aib

<220>
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<222> (11)..(11)
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<400> 647
Phe Xaa Gln Thr Trp Gln Xaa Phe Xaa Xaa Lys Asn Asn
1 5 10

<210> 648
<211> 13
<212> PRT
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<220>
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<220>
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<220>
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<223> 2-Nal

<220>
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<222> (10)..(10)
<223> Aib

<220>
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<223> Lys(Ac)

<400> 648
Xaa Xaa Gln Thr Trp Gln Xaa Phe Xaa Xaa Lys Asn Asn
1 5 10

<210> 649
<211> 13
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<220>
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<222> (8)..(8)
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<223> 2-Nal

<220>
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<222> (10)..(10)
<223> Aib

<220>
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<222> (11)..(11)
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<400> 649
Thr Xaa Gln Thr Trp Gln Xaa Phe Xaa Xaa Lys Asn Asn
1 5 10

<210> 650
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<220>
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<220>
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<222> (8)..(8)
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<220>
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<222> (9)..(9)
<223> 2-Nal

<220>
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<222> (10)..(10)
<223> Aib

<220>
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<400> 650
Leu Xaa Gln Thr Trp Gln Xaa Phe Xaa Xaa Lys Asn Asn
1 5 10

<210> 651
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<220>
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<223> Pen

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Pen

<220>
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<222> (8)..(8)
<223> Phe[4-(2-aminoethoxy)]

<220>
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<222> (9)..(9)
<223> 2-Nal

<220>
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<222> (10)..(10)
<223> Aib

<220>
<221> MOD_RES
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<400> 651
Gln Xaa Gln Thr Trp Gln Xaa Phe Xaa Xaa Lys Asn Asn
1 5 10

<210> 652
<211> 13
<212> PRT
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<220>
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<221> MOD_RES
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<223> Pen

<220>
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<222> (7)..(7)
<223> Pen

<220>
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<222> (8)..(8)
<223> Phe[4-(2-aminoethoxy)]

<220>
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<222> (9)..(9)
<223> 2-Nal

<220>
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<222> (10)..(10)
<223> Aib

<220>
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<222> (11)..(11)
<223> Lys(Ac)

<400> 652
Asn Xaa Gln Thr Trp Gln Xaa Phe Xaa Xaa Lys Asn Asn
1 5 10

<210> 653
<211> 13
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<213> Artificial Sequence

<220>
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<222> (6)..(6)
<223> Pen

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<222> (7)..(7)
<223> Phe(4-OMe)

<220>
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<222> (8)..(8)
<223> 2-Nal

<220>
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<222> (9)..(9)
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<220>

<221> MOD_RES
<222> (10)..(10)
<223> Lys(Ac)

<220>
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<222> (13)..(13)
<223> D-Lys

<400> 653
Xaa Gln Thr Trp Gln Xaa Phe Xaa Val Lys Asn Asn Lys
1 5 10

<210> 654
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
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<222> (6)..(6)
<223> Pen

<220>
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<222> (7)..(7)
<223> Phe[4-(2-acetylaminoethoxy)]

<220>
<221> MOD_RES
<222> (8)..(8)
<223> 2-Nal

<220>
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<222> (9)..(9)
<223> alpha-MeVal

<400> 654
Xaa Gln Thr Trp Gln Xaa Phe Xaa Val Lys Asn Asn
1 5 10

<210> 655
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
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<222> (6)..(6)
<223> Pen

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<222> (7)..(7)
<223> Phe[4-(2-acetylaminoethoxy)]

<220>
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<222> (8)..(8)
<223> 2-Nal

<220>
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<222> (10)..(10)
<223> Lys(Ac)

<400> 655
Xaa Gln Thr Trp Gln Xaa Phe Xaa Lys Lys Asn Asn
1 5 10

<210> 656
<211> 12
<212> PRT
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<220>
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<220>
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<220>
<221> MOD_RES
<222> (7)..(7)
<223> Phe[4-(2-(acetyl-aminoethoxy)]

<220>
<221> MOD_RES
<222> (8)..(8)
<223> 2-Nal

<220>
<221> MOD_RES
<222> (9)..(9)
<223> alpha-MeLys(Ac)

<220>
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<222> (10)..(10)
<223> Lys(Ac)

<400> 656
Xaa Gln Thr Trp Gln Cys Phe Xaa Lys Lys Asn Gly
1 5 10

<210> 657
<211> 12

<212> PRT
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<220>
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<220>
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<222> (7)..(7)
<223> Phe[4-(2-(acetyl-aminoethoxy)]

<220>
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<222> (8)..(8)
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<220>
<221> MOD_RES
<222> (9)..(9)
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Xaa Gln Thr Trp Gln Cys Phe Xaa Lys Glu Asn Gly
1 5 10

<210> 658
<211> 12
<212> PRT
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<220>
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<223> Abu

<220>
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<222> (7)..(7)
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<220>
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<222> (8)..(8)
<223> 2-Nal

<220>
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<222> (9)..(9)
<223> 4-amino-4-carboxy-tetrahydropyran

<400> 658
Xaa Gln Thr Trp Gln Cys Phe Xaa Xaa Glu Asn Asn
1 5 10

<210> 659
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
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<220>
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<223> Abu

<220>
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<222> (7)..(7)
<223> Phe[4-(2-aminoethoxy)]

<220>
<221> MOD_RES
<222> (8)..(8)
<223> 2-Nal

<220>
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<222> (9)..(9)
<223> alpha-MeLys

<400> 659
Xaa Gln Thr Trp Gln Cys Phe Xaa Lys Glu Asn Gln
1 5 10

<210> 660
<211> 12
<212> PRT
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<220>
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<220>
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<220>
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<222> (7)..(7)
<223> Phe[4-(2-aminoethoxy)]

<220>
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<222> (8)..(8)
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<220>
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<222> (9)..(9)
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<220>
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<223> Lys(Ac)

<400> 660
Xaa Gln Thr Trp Gln Cys Phe Xaa Val Lys Asn Gly
1 5 10

<210> 661
<211> 12
<212> PRT
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<220>
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<220>
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<220>
<221> MOD_RES
<222> (7)..(7)
<223> Phe[4-(2-aminoethoxy)]

<220>
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<222> (8)..(8)
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<220>
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<222> (9)..(9)
<223> hLeu

<220>
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<222> (10)..(10)
<223> Lys(Ac)

<220>
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<222> (12)..(12)
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<400> 661
Xaa Gln Thr Trp Gln Cys Phe Xaa Leu Lys Asn Ala
1 5 10

<210> 662
<211> 12
<212> PRT
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<220>
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<220>
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<220>

<221> MOD_RES
<222> (7)..(7)
<223> Phe[4-(2-(acetyl-aminoethoxy)]]

<220>
<221> MOD_RES
<222> (8)..(8)
<223> 2-Nal

<220>
<221> MOD_RES
<222> (9)..(9)
<223> alpha-MeLys(Ac)

<400> 662
Xaa Gln Thr Trp Gln Cys Phe Xaa Lys Glu Asn Gln
1 5 10

<210> 663
<211> 12
<212> PRT
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<220>
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<222> (7)..(7)
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<220>
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<222> (8)..(8)
<223> 2-Nal

<220>
<221> MOD_RES
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<223> alpha-MeLys(Ac)

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Xaa Gln Thr Trp Gln Cys Phe Xaa Lys Glu Asn Asn
1 5 10

<210> 664
<211> 12
<212> PRT
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<220>
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<222> (7)..(7)
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<220>
<221> MOD_RES
<222> (8)..(8)
<223> 2-Nal

<220>
<221> MOD_RES
<222> (9)..(9)
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<400> 664
Xaa Gln Thr Trp Gln Cys Phe Xaa Leu Glu Asn Asn
1 5 10

<210> 665
<211> 12
<212> PRT
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<220>
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<220>
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<220>
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<222> (9)..(9)
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Xaa Gln Thr Trp Gln Cys Phe Xaa Leu Xaa Asn Asn
1 5 10

<210> 666
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<212> PRT
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<220>
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peptide

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<220>
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<223> Pen

<220>
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<222> (7)..(7)
<223> Phe(4-OMe)

<220>
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<222> (8)..(8)
<223> 2-Nal

<220>
<221> MOD_RES
<222> (9)..(9)
<223> alpha-MeLys

<220>
<221> MOD_RES
<222> (10)..(10)
<223> Lys(Ac)

<400> 666
Xaa Gln Thr Trp Gln Xaa Phe Xaa Lys Lys Asn Asn
1 5 10

<210> 667
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
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<220>
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<223> D-Lys

<220>
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<222> (2)..(2)
<223> Pen

<220>
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<222> (7)..(7)
<223> Pen

<220>
<221> MOD_RES
<222> (8)..(8)
<223> Phe(4-CONH2)

<220>
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<222> (9)..(9)
<223> 2-Nal

<220>
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<222> (10)..(10)
<223> alpha-MeVal

<220>
<221> MOD_RES
<222> (11)..(11)
<223> Lys(Ac)

<400> 667
Lys Xaa Gln Thr Trp Gln Xaa Phe Xaa Val Lys Asn Asn
1 5 10

<210> 668
<211> 12
<212> PRT
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<220>
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<223> Pen

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<221> MOD_RES
<222> (6)..(6)
<223> Pen

<220>
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<222> (7)..(7)
<223> Phe(4-CONH2)

<220>
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<223> 2-Nal

<220>
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<222> (9)..(9)
<223> alpha-MeLys

<220>
<221> MOD_RES
<222> (10)..(10)
<223> Lys(Ac)

<400> 668
Xaa Gln Thr Trp Gln Xaa Phe Xaa Lys Lys Asn Asn
1 5 10

<210> 669
<211> 12
<212> PRT

<213> Artificial Sequence

<220>
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<220>
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<222> (6)..(6)
<223> Pen

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<222> (7)..(7)
<223> Phe(4-CONH2)

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<223> 2-Nal

<220>
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<222> (9)..(9)
<223> alpha-MeVal

<220>
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<222> (10)..(10)
<223> Lys(Ac)

<400> 669
Xaa Gln Thr Trp Gln Xaa Phe Xaa Val Lys Asn Asn
1 5 10

<210> 670
<211> 12
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<220>
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<221> MOD_RES
<222> (6)..(6)
<223> Pen

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Phe(4-CONH2)

<220>

<221> MOD_RES
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<223> Phe(3,4-OMe2)

<220>
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<222> (9)..(9)
<223> alpha-MeVal

<220>
<221> MOD_RES
<222> (10)..(10)
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<400> 670
Xaa Gln Thr Trp Gln Xaa Phe Phe Val Lys Asn Asn
1 5 10

<210> 671
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
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<220>
<221> MOD_RES
<222> (2)..(2)
<223> Pen

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Pen

<220>
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<222> (8)..(8)
<223> Phe[4-(2-aminoethoxy)]

<220>
<221> MOD_RES
<222> (9)..(9)
<223> 2-Nal

<220>
<221> MOD_RES
<222> (10)..(10)
<223> Aib

<220>
<221> MOD_RES
<222> (11)..(11)
<223> Lys(Ac)

<400> 671
Phe Xaa Asn Thr Trp Gln Xaa Phe Xaa Xaa Lys Asn Asn
1 5 10

<210> 672
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

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<223> D-Phe

<220>
<221> MOD_RES
<222> (2)..(2)
<223> Pen

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Pen

<220>
<221> MOD_RES
<222> (8)..(8)
<223> Phe[4-(2-aminoethoxy)]

<220>
<221> MOD_RES
<222> (9)..(9)
<223> 2-Nal

<220>
<221> MOD_RES
<222> (10)..(10)
<223> 4-amino-4-carboxy-tetrahydropyran

<220>
<221> MOD_RES
<222> (11)..(11)
<223> Lys(Ac)

<400> 672
Phe Xaa Asn Thr Trp Gln Xaa Phe Xaa Xaa Lys Asn Asn
1 5 10

<210> 673
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

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<223> D-Phe

<220>
<221> MOD_RES

<222> (2)..(2)
<223> Pen

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Pen

<220>
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<222> (8)..(8)
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<220>
<221> MOD_RES
<222> (9)..(9)
<223> 2-Nal

<220>
<221> MOD_RES
<222> (10)..(10)
<223> Achc

<220>
<221> MOD_RES
<222> (11)..(11)
<223> Lys(Ac)

<400> 673
Phe Xaa Asn Thr Trp Gln Xaa Phe Xaa Xaa Lys Asn Asn
1 5 10

<210> 674
<211> 13
<212> PRT
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<220>
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<220>
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<220>
<221> MOD_RES
<222> (2)..(2)
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<220>
<221> MOD_RES
<222> (7)..(7)
<223> Pen

<220>
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<222> (8)..(8)
<223> Phe[4-(2-aminoethoxy)]

<220>
<221> MOD_RES
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<223> 2-Nal

<220>
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<222> (10)..(10)
<223> 4-amino-4-carboxy-tetrahydropyran

<220>
<221> MOD_RES
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<400> 674
Phe Xaa Asn Thr Trp Gln Xaa Phe Xaa Xaa Xaa Asn Asn
1 5 10

<210> 675
<211> 13
<212> PRT
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<220>
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<220>
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<220>
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<223> 2-Nal

<220>
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<222> (10)..(10)
<223> Achc

<220>
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<222> (11)..(11)
<223> Cit

<400> 675
Phe Xaa Asn Thr Trp Gln Xaa Phe Xaa Xaa Xaa Asn Asn
1 5 10

<210> 676
<211> 13
<212> PRT

<213> Artificial Sequence

<220>
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<220>
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<223> 2-Nal

<220>
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<222> (10)..(10)
<223> Aib

<220>
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<222> (11)..(11)
<223> Lys(Ac)

<220>
<221> MOD_RES
<222> (13)..(13)
<223> Beta-Ala

<400> 676
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1 5 10

<210> 677
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<220>
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<220>

<221> MOD_RES
<222> (2)..(2)
<223> Pen

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Pen

<220>
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<222> (8)..(8)
<223> Phe(4-OMe)

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<222> (9)..(9)
<223> 2-Nal

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<222> (10)..(10)
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<220>
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<222> (11)..(11)
<223> Lys(Ac)

<400> 677
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1 5 10

<210> 678
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<220>
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<220>
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<223> 2-Nal

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<220>
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<222> (11)..(11)
<223> Lys(Ac)

<400> 678
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1 5 10

<210> 679
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<222> (7)..(7)
<223> Pen

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<223> 2-Nal

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<223> 4-amino-4-carboxy-tetrahydropyran

<220>
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<400> 679
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<210> 680
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<212> PRT
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<223> Phe(4-OMe)

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<223> 2-Nal

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<222> (10)..(10)
<223> Achc

<220>
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<400> 680
Phe Xaa Asn Thr Trp Gln Xaa Phe Xaa Xaa Xaa Asn Asn
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<210> 681
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<212> PRT
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<220>
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<223> Pen

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<222> (7)..(7)
<223> Pen

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<222> (8)..(8)
<223> Phe(4-OMe)

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<223> 2-Nal

<220>
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<222> (10)..(10)
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<400> 681
Phe Xaa Asn Thr Trp Gln Xaa Phe Xaa Xaa Glu Asn Asn
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<210> 682
<211> 12
<212> PRT
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<220>
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<223> Pen

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<222> (7)..(7)
<223> Phe(4-CONH2)

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<222> (8)..(8)
<223> 2-Nal

<220>
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<222> (9)..(9)
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<400> 682
Xaa Asn Thr Trp Gln Xaa Phe Xaa Xaa Lys Asn Asn
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<210> 683
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<212> PRT
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<220>
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<222> (7)..(7)
<223> Phe(4-CONH2)

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<400> 683
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<210> 684
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<212> PRT
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<220>
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<222> (9)..(9)
<223> Achc

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<400> 684
Xaa Asn Thr Trp Gln Xaa Phe Xaa Xaa Lys Asn Asn
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<210> 685
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<220>
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<222> (6)..(6)
<223> Pen

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<223> Phe(4-CONH2)

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<223> 2-Nal

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Xaa Asn Thr Trp Gln Xaa Phe Xaa Xaa Lys Asn Asn
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<212> PRT
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<400> 686
Xaa Asn Thr Trp Gln Xaa Phe Xaa Leu Lys Asn Asn
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<210> 687
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<212> PRT
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<220>
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<223> Aib

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<400> 687
Xaa Asn Thr Trp Gln Xaa Phe Xaa Xaa Lys Asn Asn
1 5 10

<210> 688
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<220>
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<400> 688
Xaa Asn Thr Trp Gln Xaa Phe Xaa Xaa Lys Asn Asn
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<210> 689
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<220>
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<400> 689
Xaa Asn Thr Trp Gln Xaa Phe Xaa Xaa Lys Asn Asn
1 5 10

<210> 690
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<212> PRT
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<220>
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<220>
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<222> (13)..(13)
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<400> 690
Gln Asp Trp Gln Cys Tyr Trp Arg Glu Asn Gly Xaa Lys
1 5 10

<210> 691
<211> 14
<212> PRT
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<220>
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<223> (2-aminoethoxy)acetic acid

<220>
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<222> (14)..(14)
<223> D-Lys

<400> 691
Gln Asp Trp Gln Cys Cys Tyr Trp Arg Glu Asn Gly Xaa Lys
1 5 10

<210> 692
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
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<220>
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<220>
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<222> (14)..(14)
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<400> 692
Xaa Arg Thr Trp Gln Cys Tyr Trp Arg Lys Phe Gly Xaa Lys
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<400> 693
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1 5 10

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Xaa Gln Thr Trp Gln Cys Tyr Trp Arg Glu Asn Gly Xaa Lys
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Xaa Arg Thr Trp Gln Xaa Tyr Trp Arg Lys Phe Gly Xaa Lys
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Xaa Arg Thr Trp Gln Xaa Tyr Trp Arg Lys Phe Gly Xaa Lys
1 5 10

<210> 697
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<223> (2-aminoethoxy)acetic acid

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<223> D-Lys

<400> 697
Cys Arg Thr Trp Gln Xaa Tyr Trp Arg Lys Phe Gly Xaa Lys
1 5 10

<210> 698
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<223> Dap

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<223> (2-aminoethoxy)acetic acid

<220>
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<222> (14)..(14)
<223> D-Lys

<400> 698
Xaa Gln Thr Trp Gln Cys Tyr Trp Xaa Xaa Asn Gly Xaa Lys
1 5 10

<210> 699
<211> 12
<212> PRT
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<220>
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<222> (1)..(1)
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<220>
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<222> (9)..(9)
<223> hLeu

<400> 699
Xaa Gln Thr Trp Gln Cys Tyr Trp Leu Glu Asn Gly
1 5 10

<210> 700
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<212> PRT
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<220>
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<222> (6)..(6)
<223> D-Cys

<220>
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<222> (9)..(9)
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<400> 700
Xaa Gln Thr Trp Gln Cys Tyr Trp Leu Glu Asn Gly
1 5 10

<210> 701
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<212> PRT
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<220>
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<400> 701
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1 5 10

<210> 702
<211> 12
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<220>
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<220>
<221> MOD_RES
<222> (7)..(7)
<223> Phe(4-OMe)

<220>
<221> MOD_RES
<222> (8)..(8)
<223> 2-Nal

<220>
<221> MOD_RES
<222> (9)..(9)
<223> alpha-MeLys

<400> 702
Xaa Gln Thr Trp Gln Cys Phe Xaa Lys Glu Asn Gly
1 5 10

<210> 703
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<212> PRT
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<220>
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<223> alpha-MeLeu

<400> 703

Xaa Gln Thr Trp Gln Cys Tyr Trp Leu Glu Asn Gly
1 5 10

<210> 704
<211> 12
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<220>
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<222> (8)..(8)
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<220>
<221> MOD_RES
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<400> 704
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1 5 10

<210> 705
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<400> 705
Xaa Gln Thr Trp Gln Cys Phe Xaa Lys Glu Asn Gly
1 5 10

<210> 706
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<400> 706
Xaa Gln Thr Trp Gln Cys Phe Xaa Xaa Glu Asn Gly
1 5 10

<210> 707
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<400> 707
Xaa Gln Thr Trp Gln Cys Phe Trp Xaa Glu Asn Gly
1 5 10

<210> 708
<211> 12

<212> PRT
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<220>
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<222> (7)..(7)
<223> Phe(4-OMe)

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<222> (8)..(8)
<223> 2-Nal

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<400> 708
Xaa Gln Thr Trp Gln Cys Phe Xaa Lys Glu Asn Gly
1 5 10

<210> 709
<211> 12
<212> PRT
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<223> alpha-MeLys

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<400> 709
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1 5 10

<210> 710
<211> 12
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<220>
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<220>
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<222> (7)..(7)
<223> Phe(4-OMe)

<220>
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<223> alpha-MeLys

<400> 710
Xaa Gln Thr Trp Gln Cys Phe Trp Lys Glu Asn Gly
1 5 10

<210> 711
<211> 12
<212> PRT
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<220>
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<220>
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<222> (7)..(7)
<223> Phe(4-OMe)

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<223> 1-Nal

<220>
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<222> (9)..(9)
<223> alpha-MeLys

<220>
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<400> 711
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1 5 10

<210> 712
<211> 12
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<220>
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<220>
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<222> (7)..(7)
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<222> (8)..(8)
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<222> (9)..(9)
<223> alpha-MeLys

<220>
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<400> 712
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1 5 10

<210> 713
<211> 12
<212> PRT
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<220>
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<220>
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<220>
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<222> (9)..(9)
<223> alpha-MeOrn

<220>
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<223> Lys(Ac)

<400> 713

Xaa Gln Thr Trp Gln Cys Tyr Trp Xaa Lys Asn Gly
1 5 10

<210> 714
<211> 12
<212> PRT
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<220>
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<220>
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<222> (7)..(7)
<223> Phe(4-OMe)

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<222> (8)..(8)
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<222> (9)..(9)
<223> D-Asn

<220>
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<400> 714
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<210> 715
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<220>
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<220>
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<222> (7)..(7)
<223> Phe(4-Phenoxy)

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<222> (9)..(9)
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<400> 715
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1 5 10

<210> 716
<211> 12
<212> PRT
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<220>
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<220>
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<400> 716
Xaa Gln Thr Trp Gln Cys Phe Xaa Lys Lys Asn Gly
1 5 10

<210> 717
<211> 12
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<220>
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<400> 717
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1 5 10

<210> 718
<211> 12
<212> PRT
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<220>
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<220>
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<400> 718
Xaa Gln Thr Trp Gln Cys Phe Xaa Lys Lys Asn Gly
1 5 10

<210> 719
<211> 12
<212> PRT
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<220>
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<222> (7)..(7)
<223> Phe(3,4-Cl2)

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<223> 2-Nal

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<222> (9)..(9)
<223> alpha-MeLys

<220>
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<400> 719
Xaa Gln Thr Trp Gln Cys Phe Xaa Lys Lys Asn Gly
1 5 10

<210> 720
<211> 12
<212> PRT
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<220>
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<223> Pen

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<223> Phe(4-OMe)

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<221> MOD_RES
<222> (8)..(8)

<223> 2-Nal

<220>
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<222> (9)..(9)
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<400> 720
Xaa Gln Thr Trp Gln Xaa Phe Xaa Lys Glu Asn Gly
1 5 10

<210> 721
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
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<222> (6)..(6)
<223> Pen

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<223> Phe(4-OMe)

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<222> (9)..(9)
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<400> 721
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<210> 722
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<212> PRT
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<220>
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<222> (8)..(8)
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<223> alpha-MeLys

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<400> 722
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<220>
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<222> (7)..(7)
<223> Phe(4-OMe)

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<222> (8)..(8)
<223> Trp(2,5,7-tri-tert-Butyl)

<220>
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<222> (9)..(9)
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<400> 723
Xaa Gln Thr Trp Gln Cys Phe Trp Lys Glu Asn Gly
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<210> 724
<211> 12
<212> PRT
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<220>
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<223> Abu

<220>
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<222> (7)..(7)
<223> Phe(4-OMe)

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<223> Phe(4-Oallyl)

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1 5 10

<210> 725
<211> 12
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<220>
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<222> (7)..(7)
<223> Phe(4-OMe)

<220>
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<222> (8)..(8)
<223> Tyr(3-tBu)

<220>
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<222> (9)..(9)
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<400> 725
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1 5 10

<210> 726
<211> 12
<212> PRT
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<220>
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<222> (7)..(7)
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<222> (8)..(8)
<223> Phe(4-tBu)

<220>
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<222> (9)..(9)
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<400> 726
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1 5 10

<210> 727
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<212> PRT
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<220>
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<223> Abu

<220>
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<222> (7)..(7)
<223> Phe(4-OMe)

<220>
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<222> (8)..(8)
<223> Phe(4-guanidino)

<220>
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<400> 727
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<210> 728
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<212> PRT
<213> Artificial Sequence

<220>
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<223> Abu

<220>
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<222> (7)..(7)
<223> Phe(4-OMe)

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<222> (8)..(8)
<223> Phe(Bzl)

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<222> (9)..(9)
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Xaa Gln Thr Trp Gln Cys Phe Phe Lys Glu Asn Gly
1 5 10

<210> 729
<211> 12
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<220>
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<223> Abu

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Tyr(3-tBu)

<220>
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<222> (9)..(9)
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<400> 729
Xaa Gln Thr Trp Gln Cys Tyr Trp Lys Glu Asn Gly
1 5 10

<210> 730
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<212> PRT
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<220>
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<222> (8)..(8)
<223> 2-Nal

<220>
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<222> (9)..(9)
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<223> Lys(Ac)

<400> 730
Xaa Asn Thr Trp Gln Xaa Phe Xaa Xaa Lys Asn Asn
1 5 10

<210> 731
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<220>
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<222> (6)..(6)
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<221> MOD_RES
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<223> Phe(4-OMe)

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<222> (8)..(8)
<223> 2-Nal

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<220>
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<222> (10)..(10)
<223> Lys(Ac)

<400> 731
Xaa Asn Thr Trp Gln Xaa Phe Xaa Leu Lys Asn Asn
1 5 10

<210> 732
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<220>
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<220>
<221> MOD_RES
<222> (12)..(12)
<223> (2-aminoethoxy)acetic acid

<220>
<221> MOD_RES
<222> (13)..(13)
<223> D-Lys

<400> 732
Ala Asp Trp Val Cys Tyr Trp His Thr Phe Gly Xaa Lys
1 5 10

<210> 733
<211> 13
<212> PRT
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<220>
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<220>
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<222> (12)..(12)
<223> (2-aminoethoxy)acetic acid

<220>
<221> MOD_RES
<222> (13)..(13)
<223> D-Lys

<400> 733
Ala Asp Trp Val Xaa Tyr Trp His Thr Phe Gly Xaa Lys
1 5 10

<210> 734
<211> 13
<212> PRT
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<220>
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<222> (5)..(5)
<223> D-Pen

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<223> (2-aminoethoxy)acetic acid

<220>
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<223> D-Lys

<400> 734
Ala Asp Trp Val Xaa Tyr Trp His Thr Phe Gly Xaa Lys
1 5 10

<210> 735
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<220>
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<223> N-MeAla

<220>
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<220>
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<222> (12)..(12)
<223> (2-aminoethoxy)acetic acid

<220>
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<222> (13)..(13)
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<400> 735
Ala Asp Trp Val Cys Tyr Trp His Thr Phe Gly Xaa Lys
1 5 10

<210> 736
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<220>
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<223> (2-aminoethoxy)acetic acid

<220>
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<222> (13)..(13)
<223> D-Lys

<400> 736
Ala Asp Trp Val Cys Tyr Trp His Thr Phe Gly Xaa Lys
1 5 10

<210> 737
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<222> (12)..(12)
<223> (2-aminoethoxy)acetic acid

<220>
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<400> 737
Ala Asp Trp Val Xaa Tyr Trp His Thr Phe Gly Xaa Lys
1 5 10

<210> 738
<211> 13
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<220>
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<223> (2-aminoethoxy)acetic acid

<220>
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<400> 738
Ala Asp Trp Val Xaa Tyr Trp His Thr Phe Gly Xaa Lys
1 5 10

<210> 739
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<220>
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<223> (2-aminoethoxy)acetic acid

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<400> 739
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1 5 10

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<223> (2-aminoethoxy)acetic acid

<220>
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<222> (13)..(13)
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<400> 740
Gln Asp Trp Gln Cys Tyr Trp Arg Glu Asn Gly Xaa Lys
1 5 10

<210> 741
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<220>
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<223> (2-aminoethoxy)acetic acid

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<400> 741
Gln Asp Trp Gln Cys Tyr Trp Arg Glu Asn Gly Xaa Lys
1 5 10

<210> 742
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<400> 742
Gln Asp Trp Gln Cys Tyr Trp Arg Glu Asn Gly Xaa Lys
1 5 10

<210> 743
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<220>
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<220>
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<222> (13)..(13)
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<400> 743
Gln Asp Trp Gln Cys Tyr Trp Arg Glu Asn Gly Xaa Lys
1 5 10

<210> 744
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<220>
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<220>
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<222> (13)..(13)
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<400> 744
Gln Asp Trp Gln Cys Tyr Trp Arg Glu Asn Gly Xaa Lys
1 5 10

<210> 745
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<220>
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<220>
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<400> 745
Gln Asp Trp Gln Cys Tyr Trp Arg Glu Asn Gly Xaa Lys
1 5 10

<210> 746
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<220>
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<222> (12)..(12)
<223> (2-aminoethoxy)acetic acid

<220>
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<400> 746
Gln Asp Trp Gln Cys Tyr Trp Arg Glu Asn Gly Xaa Lys
1 5 10

<210> 747
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<220>
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<223> (2-aminoethoxy)acetic acid

<220>
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<400> 747
Gln Asp Trp Gln Cys Tyr Trp Arg Glu Asn Gly Xaa Lys
1 5 10

<210> 748
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<222> (12)..(12)
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<220>
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<223> D-Lys

<400> 748
Gln Asp Trp Gln Cys Tyr Trp Arg Glu Asn Gly Xaa Lys
1 5 10

<210> 749
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (5)..(5)
<223> hCys

<220>
<221> MOD_RES
<222> (12)..(12)
<223> (2-aminoethoxy)acetic acid

<220>
<221> MOD_RES
<222> (13)..(13)
<223> D-Lys

<400> 749
Gln Asp Trp Gln Cys Tyr Trp Arg Glu Asn Gly Xaa Lys
1 5 10

<210> 750

<400> 750
000

<210> 751

<400> 751
000

<210> 752
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Abu

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Phe[4-(2-aminoethoxy)]

<220>
<221> MOD_RES
<222> (8)..(8)
<223> 2-Nal

<220>
<221> MOD_RES
<222> (9)..(9)
<223> alpha-MeLeu

<220>
<221> MOD_RES
<222> (12)..(12)
<223> Beta-Ala

<400> 752
Xaa Gln Thr Trp Gln Cys Phe Xaa Leu Gln Asn Ala
1 5 10

<210> 753
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Abu

<220>

<221> MOD_RES
<222> (7)..(7)
<223> Phe[4-(2-aminoethoxy)]

<220>
<221> MOD_RES
<222> (8)..(8)
<223> 2-Nal

<220>
<221> MOD_RES
<222> (9)..(9)
<223> Acbc

<400> 753
Xaa Gln Thr Trp Gln Cys Phe Xaa Xaa Glu Asn Asn
1 5 10

<210> 754
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Abu

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Phe[4-(2-aminoethoxy)]

<220>
<221> MOD_RES
<222> (8)..(8)
<223> 2-Nal

<220>
<221> MOD_RES
<222> (9)..(9)
<223> Achc

<400> 754
Xaa Gln Thr Trp Gln Cys Phe Xaa Xaa Glu Asn Asn
1 5 10

<210> 755
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Abu

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Phe[4-(2-aminoethoxy)]]

<220>
<221> MOD_RES
<222> (8)..(8)
<223> 2-Nal

<220>
<221> MOD_RES
<222> (9)..(9)
<223> Acvc

<400> 755
Xaa Gln Thr Trp Gln Cys Phe Xaa Xaa Glu Asn Asn
1 5 10

<210> 756
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Pen

<220>
<221> MOD_RES
<222> (6)..(6)
<223> Pen

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Phe(4-OMe)

<220>
<221> MOD_RES
<222> (8)..(8)
<223> 2-Nal

<220>
<221> MOD_RES
<222> (9)..(9)
<223> alpha-MeVal

<220>
<221> MOD_RES
<222> (10)..(10)
<223> Lys(Ac)

<220>
<221> MOD_RES
<222> (13)..(13)
<223> D-Lys

<400> 756
Xaa Gln Thr Trp Gln Xaa Phe Xaa Val Lys Asn Asn Lys

1 5 10

<210> 757
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Pen

<220>
<221> MOD_RES
<222> (6)..(6)
<223> Pen

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Phe[4-(2-acetylaminoethoxy)]

<220>
<221> MOD_RES
<222> (8)..(8)
<223> 2-Nal

<220>
<221> MOD_RES
<222> (9)..(9)
<223> alpha-MeVal

<220>
<221> MOD_RES
<222> (10)..(10)
<223> Lys(Ac)

<220>
<221> MOD_RES
<222> (13)..(13)
<223> D-Lys

<400> 757
Xaa Gln Thr Trp Gln Xaa Phe Xaa Val Lys Asn Asn Lys
1 5 10

<210> 758
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Pen

<220>
<221> MOD_RES
<222> (6)..(6)
<223> Pen

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Phe[4-(2-acetylaminoethoxy)]]

<220>
<221> MOD_RES
<222> (8)..(8)
<223> 2-Nal

<220>
<221> MOD_RES
<222> (9)..(9)
<223> alpha-MeVal

<400> 758
Xaa Gln Thr Trp Gln Xaa Phe Xaa Val Lys Asn Asn
1 5 10

<210> 759
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Pen

<220>
<221> MOD_RES
<222> (6)..(6)
<223> Pen

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Phe[4-(2-acetylaminoethoxy)]]

<220>
<221> MOD_RES
<222> (8)..(8)
<223> 2-Nal

<220>
<221> MOD_RES
<222> (10)..(10)
<223> Lys(Ac)

<400> 759
Xaa Gln Thr Trp Gln Xaa Phe Xaa Lys Lys Asn Asn
1 5 10

<210> 760
<211> 629
<212> PRT

<213> Homo sapiens

<400> 760

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Met Asn Gln Val Thr Ile Gln Trp Asp Ala Val Ile Ala Leu Tyr Ile
1               5                  10                  15

Leu Phe Ser Trp Cys His Gly Gly Ile Thr Asn Ile Asn Cys Ser Gly
            20                  25                  30

His Ile Trp Val Glu Pro Ala Thr Ile Phe Lys Met Gly Met Asn Ile
        35                  40                  45

Ser Ile Tyr Cys Gln Ala Ala Ile Lys Asn Cys Gln Pro Arg Lys Leu
    50                  55                  60

His Phe Tyr Lys Asn Gly Ile Lys Glu Arg Phe Gln Ile Thr Arg Ile
65                  70                  75                  80

Asn Lys Thr Thr Ala Arg Leu Trp Tyr Lys Asn Phe Leu Glu Pro His
                85                  90                  95

Ala Ser Met Tyr Cys Thr Ala Glu Cys Pro Lys His Phe Gln Glu Thr
            100                 105                 110

Leu Ile Cys Gly Lys Asp Ile Ser Ser Gly Tyr Pro Pro Asp Ile Pro
        115                 120                 125

Asp Glu Val Thr Cys Val Ile Tyr Glu Tyr Ser Gly Asn Met Thr Cys
    130                 135                 140

Thr Trp Asn Ala Gly Lys Leu Thr Tyr Ile Asp Thr Lys Tyr Val Val
145                 150                 155                 160

His Val Lys Ser Leu Glu Thr Glu Glu Glu Gln Gln Tyr Leu Thr Ser
                165                 170                 175

Ser Tyr Ile Asn Ile Ser Thr Asp Ser Leu Gln Gly Gly Lys Lys Tyr
            180                 185                 190

Leu Val Trp Val Gln Ala Ala Asn Ala Leu Gly Met Glu Glu Ser Lys
        195                 200                 205

Gln Leu Gln Ile His Leu Asp Asp Ile Val Ile Pro Ser Ala Ala Val
    210                 215                 220

Ile Ser Arg Ala Glu Thr Ile Asn Ala Thr Val Pro Lys Thr Ile Ile
225                 230                 235                 240

Tyr Trp Lys Ser Gln Thr Thr Ile Glu Lys Val Ser Cys Glu Met Arg
                245                 250                 255

Tyr Lys Ala Thr Thr Asn Gln Thr Trp Asn Val Lys Glu Phe Asp Thr
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260 265 270

Asn Phe Thr Tyr Val Gln Gln Ser Glu Phe Tyr Leu Glu Pro Asn Ile
275 280 285

Lys Tyr Val Phe Gln Val Arg Cys Gln Glu Thr Gly Lys Arg Tyr Trp
290 295 300

Gln Pro Trp Ser Ser Leu Phe Phe His Lys Thr Pro Glu Thr Val Pro
305 310 315 320

Gln Val Thr Ser Lys Ala Phe Gln His Asp Thr Trp Asn Ser Gly Leu
325 330 335

Thr Val Ala Ser Ile Ser Thr Gly His Leu Thr Ser Asp Asn Arg Gly
340 345 350

Asp Ile Gly Leu Leu Leu Gly Met Ile Val Phe Ala Val Met Leu Ser
355 360 365

Ile Leu Ser Leu Ile Gly Ile Phe Asn Arg Ser Phe Arg Thr Gly Ile
370 375 380

Lys Arg Arg Ile Leu Leu Leu Ile Pro Lys Trp Leu Tyr Glu Asp Ile
385 390 395 400

Pro Asn Met Lys Asn Ser Asn Val Val Lys Met Leu Gln Glu Asn Ser
405 410 415

Glu Leu Met Asn Asn Asn Ser Ser Glu Gln Val Leu Tyr Val Asp Pro
420 425 430

Met Ile Thr Glu Ile Lys Glu Ile Phe Ile Pro Glu His Lys Pro Thr
435 440 445

Asp Tyr Lys Lys Glu Asn Thr Gly Pro Leu Glu Thr Arg Asp Tyr Pro
450 455 460

Gln Asn Ser Leu Phe Asp Asn Thr Thr Val Val Tyr Ile Pro Asp Leu
465 470 475 480

Asn Thr Gly Tyr Lys Pro Gln Ile Ser Asn Phe Leu Pro Glu Gly Ser
485 490 495

His Leu Ser Asn Asn Asn Glu Ile Thr Ser Leu Thr Leu Lys Pro Pro
500 505 510

Val Asp Ser Leu Asp Ser Gly Asn Asn Pro Arg Leu Gln Lys His Pro
515 520 525

Asn Phe Ala Phe Ser Val Ser Ser Val Asn Ser Leu Ser Asn Thr Ile

530 535 540

Phe Leu Gly Glu Leu Ser Leu Ile Leu Asn Gln Gly Glu Cys Ser Ser
545 550 555 560

Pro Asp Ile Gln Asn Ser Val Glu Glu Glu Thr Thr Met Leu Leu Glu
565 570 575

Asn Asp Ser Pro Ser Glu Thr Ile Pro Glu Gln Thr Leu Leu Pro Asp
580 585 590

Glu Phe Val Ser Cys Leu Gly Ile Val Asn Glu Glu Leu Pro Ser Ile
595 600 605

Asn Thr Tyr Phe Pro Gln Asn Ile Leu Glu Ser His Phe Asn Arg Ile
610 615 620

Ser Leu Leu Glu Lys
625

<210> 761
<211> 659
<212> PRT
<213> Mus musculus

<400> 761
Met Lys Arg Glu Arg Glu Met Arg Gly Phe Tyr Tyr Ile Trp Asp Met
1 5 10 15

Ser His Leu Thr Leu Gln Leu His Val Val Ile Ala Leu Tyr Val Leu
20 25 30

Phe Arg Trp Cys His Gly Gly Ile Thr Ser Ile Asn Cys Ser Gly Asp
35 40 45

Met Trp Val Glu Pro Gly Glu Ile Phe Gln Met Gly Met Asn Val Ser
50 55 60

Ile Tyr Cys Gln Glu Ala Leu Lys His Cys Arg Pro Arg Asn Leu Tyr
65 70 75 80

Phe Tyr Lys Asn Gly Phe Lys Glu Glu Phe Asp Ile Thr Arg Ile Asn
85 90 95

Arg Thr Thr Ala Arg Ile Trp Tyr Lys Gly Phe Ser Glu Pro His Ala
100 105 110

Tyr Met His Cys Thr Ala Glu Cys Pro Gly His Phe Gln Glu Thr Leu
115 120 125

Ile Cys Gly Lys Asp Ile Ser Ser Gly Tyr Pro Pro Asp Ala Pro Ser
130 135 140

Asn Leu Thr Cys Val Ile Tyr Glu Tyr Ser Gly Asn Met Thr Cys Thr
145 150 155 160

Trp Asn Thr Gly Lys Pro Thr Tyr Ile Asp Thr Lys Tyr Ile Val His
165 170 175

Val Lys Ser Leu Glu Thr Glu Glu Glu Gln Gln Tyr Leu Ala Ser Ser
180 185 190

Tyr Val Lys Ile Ser Thr Asp Ser Leu Gln Gly Gly Lys Lys Tyr Leu
195 200 205

Val Trp Val Gln Ala Val Asn Ser Leu Gly Met Glu Asn Ser Gln Gln
210 215 220

Leu His Val His Leu Asp Asp Ile Val Ile Pro Ser Ala Ser Ile Ile
225 230 235 240

Ser Arg Ala Glu Thr Thr Asn Asp Thr Val Pro Lys Thr Ile Ile Tyr
245 250 255

Trp Lys Ser Lys Thr Met Ile Glu Lys Val Phe Cys Glu Met Arg Tyr
260 265 270

Lys Thr Thr Thr Asn Gln Thr Trp Ser Val Lys Glu Phe Asp Ala Asn
275 280 285

Phe Thr Tyr Val Gln Gln Ser Glu Phe Tyr Leu Glu Pro Asp Ser Lys
290 295 300

Tyr Val Phe Gln Val Arg Cys Gln Glu Thr Gly Lys Arg Asn Trp Gln
305 310 315 320

Pro Trp Ser Ser Pro Phe Val His Gln Thr Ser Gln Glu Thr Gly Lys
325 330 335

Arg Asn Trp Gln Pro Trp Ser Ser Pro Phe Val His Gln Thr Ser Gln
340 345 350

Thr Val Ser Gln Val Thr Ala Lys Ser Ser His Glu Pro Gln Lys Met
355 360 365

Glu Met Leu Ser Ala Thr Ile Phe Arg Gly His Pro Ala Ser Gly Asn
370 375 380

His Gln Asp Ile Gly Leu Leu Ser Gly Met Val Phe Leu Ala Ile Met
385 390 395 400

Leu Pro Ile Phe Ser Leu Ile Gly Ile Phe Asn Arg Ser Leu Arg Ile
405 410 415

Gly Ile Lys Arg Lys Val Leu Leu Met Ile Pro Lys Trp Leu Tyr Glu
420 425 430

Asp Ile Pro Asn Met Glu Asn Ser Asn Val Ala Lys Leu Leu Gln Glu
435 440 445

Lys Ser Val Phe Glu Asn Asp Asn Ala Ser Glu Gln Ala Leu Tyr Val
450 455 460

Asp Pro Val Leu Thr Glu Ile Ser Glu Ile Ser Pro Leu Glu His Lys
465 470 475 480

Pro Thr Asp Tyr Lys Glu Glu Arg Leu Thr Gly Leu Leu Glu Thr Arg
485 490 495

Asp Cys Pro Leu Gly Met Leu Ser Thr Ser Ser Ser Val Val Tyr Ile
500 505 510

Pro Asp Leu Asn Thr Gly Tyr Lys Pro Gln Val Ser Asn Val Pro Pro
515 520 525

Gly Gly Asn Leu Phe Ile Asn Arg Asp Glu Arg Asp Pro Thr Ser Leu
530 535 540

Glu Thr Thr Asp Asp His Phe Ala Arg Leu Lys Thr Tyr Pro Asn Phe
545 550 555 560

Gln Phe Ser Ala Ser Ser Met Ala Leu Leu Asn Lys Thr Leu Ile Leu
565 570 575

Asp Glu Leu Cys Leu Val Leu Asn Gln Gly Glu Phe Asn Ser Leu Asp
580 585 590

Ile Lys Asn Ser Arg Gln Glu Glu Thr Ser Ile Val Leu Gln Ser Asp
595 600 605

Ser Pro Ser Glu Thr Ile Pro Ala Gln Thr Leu Leu Ser Asp Glu Phe
610 615 620

Val Ser Cys Leu Ala Ile Gly Asn Glu Asp Leu Pro Ser Ile Asn Ser
625 630 635 640

Tyr Phe Pro Gln Asn Val Leu Glu Ser His Phe Ser Arg Ile Ser Leu
645 650 655

Phe Gln Lys

<210> 762
<211> 639
<212> PRT

<213> Rattus norvegicus

<400> 762

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Met Arg Arg Glu Arg Glu Met Arg Gly Phe Tyr Tyr Ile Trp Asp Met
1               5                  10                  15

Ser His Val Ala Leu Gln Leu His Val Val Ile Ala Leu Tyr Ala Leu
            20                  25                  30

Phe Arg Trp Gly His Gly Gly Ile Ala Thr Ile Asn Cys Ser Gly Asn
        35                  40                  45

Met Trp Val Glu Pro Gly Glu Ile Phe Gln Met Gly Met Asn Val Ser
    50                  55                  60

Val Tyr Cys Gln Glu Ala Leu Lys Asn Cys Arg Pro Arg Asn Leu His
65                  70                  75                  80

Phe Tyr Lys Asn Gly Phe Lys Glu Arg Phe His Ile Thr Arg Ile Asn
                85                  90                  95

Arg Thr Thr Ala Arg Val Trp Thr Lys Gly Phe Ser Glu Pro His Ala
            100                 105                 110

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

Ile Cys Gly Lys Asp Ile Ser Ser Gly Tyr Pro Pro Asp Ala Pro Ser
    130                 135                 140

Asn Met Thr Cys Val Ile Tyr Glu Tyr Ser Gly Asn Met Thr Cys Thr
145                 150                 155                 160

Trp Asn Thr Gly Lys Pro Thr Tyr Ile Asp Thr Lys Tyr Thr Val His
                165                 170                 175

Val Lys Ser Leu Glu Thr Glu Glu Gln Gln Gln Tyr Leu Ala Ser Asn
            180                 185                 190

Tyr Val Asn Ile Ser Thr Asp Ser Leu Gln Gly Gly Lys Lys Tyr Leu
        195                 200                 205

Val Trp Val Gln Ala Val Asn Ala Leu Gly Met Glu Asn Ser Gln Gln
    210                 215                 220

Leu Gln Val His Leu Asp Asp Ile Val Ile Pro Ser Pro Ser Ile Ile
225                 230                 235                 240

Ser Arg Ala Glu Thr Thr Asn Ala Asn Val Pro Lys Thr Ile Ile Tyr
                245                 250                 255

Trp Lys Ser Lys Ile Met Thr Gly Lys Val Phe Cys Glu Met Arg Tyr
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260 265 270

Lys Ala Thr Thr Asn Gln Thr Trp Asn Val Lys Glu Phe Asp Thr Asn
275 280 285

Phe Thr Tyr Val Gln Gln Ser Glu Phe Tyr Leu Glu Pro Asn Ser Lys
290 295 300

Tyr Val Phe Gln Val Arg Cys Gln Gly Thr Gly Lys Arg Tyr Trp Gln
305 310 315 320

Pro Trp Ser Ser Pro Phe Val His Gln Thr Pro Gln Thr Ala Ser Gln
325 330 335

Val Thr Ser Lys Pro Pro His Glu Pro Gln Lys Ile Glu Met Leu Thr
340 345 350

Ala Thr Ile Phe Lys Gly His Ser Thr Ser Asp Asn Ser Gln Asp Ile
355 360 365

Gly Leu Leu Ser Gly Met Val Phe Leu Ala Ile Met Leu Pro Ile Phe
370 375 380

Ser Leu Ile Gly Ile Phe Asn Arg Ser Leu Arg Ile Gly Ile Lys Arg
385 390 395 400

Lys Val Leu Leu Met Ile Pro Lys Trp Leu Tyr Glu Asp Ile Pro Asn
405 410 415

Met Glu Asn Ser Asn Ile Ala Lys Leu Leu Gln Glu Lys Ser Val Phe
420 425 430

Glu Asn Glu Asn Ala Ser Glu Gln Ala Leu Tyr Val Asp Pro Ile Leu
435 440 445

Thr Glu Ile Ser Glu Ile Ser Pro Leu Glu His Lys Pro Thr Asp Tyr
450 455 460

Lys Lys Asp Arg Leu Thr Gly Phe Leu Glu Thr Arg Asp Cys Pro Leu
465 470 475 480

Thr Thr Leu Ser Thr Ser Ser Ser Val Val Tyr Ile Pro Asp Leu Asn
485 490 495

Thr Gly Tyr Lys Pro Gln Val Ser Asn Val Pro Pro Glu Glu Asn His
500 505 510

Phe Ile Asn Arg Asp Glu Arg Asp Pro Met Ser Leu Glu Ala Thr Gly
515 520 525

Asp His Phe Ala Arg Leu Lys Thr Tyr Pro Asn Phe Thr Phe Ser Ala

530 535 540

Ser Ser Met Thr Ser Leu Ser Lys Thr Leu Ile Leu Asp Glu Leu Ser
545 550 555 560

Leu Val Leu Asn Gln Gly Glu Phe Asn Ser Leu Asp Ile Gln Asn Ser
565 570 575

Arg Gln Glu Glu Thr Ser Met Ile Leu Gln Asn Asp Ser Pro Ser Glu
580 585 590

Thr Ile Pro Val Gln Thr Leu Leu Pro Asp Glu Phe Val Ser Cys Leu
595 600 605

Ala Ile Gly Ser Glu Asp Leu Pro Ser Ile Asn Ser Tyr Phe Pro Gln
610 615 620

Asn Val Leu Glu Ser His Phe Ser Gly Ile Pro Leu Leu Gln Lys
625 630 635

<210> 763
<211> 629
<212> PRT
<213> Pan sp.

<400> 763
Met Asn Gln Val Thr Ile Gln Trp Asp Ala Val Ile Ala Leu Tyr Ile
1 5 10 15

Leu Phe Ser Trp Cys His Gly Gly Ile Thr Asn Ile Asn Cys Ser Gly
20 25 30

His Ile Trp Val Glu Pro Ala Thr Ile Phe Lys Met Gly Met Asn Ile
35 40 45

Ser Ile Tyr Cys Gln Ala Ala Ile Lys Asn Cys Gln Pro Arg Lys Leu
50 55 60

His Phe Tyr Lys Asn Gly Ile Lys Glu Arg Phe Gln Ile Thr Arg Ile
65 70 75 80

Asn Lys Thr Thr Ala Arg Leu Trp Tyr Lys Asn Phe Leu Glu Pro His
85 90 95

Ala Ser Met Tyr Cys Thr Ala Glu Cys Pro Lys His Phe Gln Glu Thr
100 105 110

Leu Ile Cys Gly Lys Asp Ile Ser Ser Gly Tyr Pro Pro Asp Ile Pro
115 120 125

Asp Glu Val Thr Cys Val Ile Tyr Glu Tyr Ser Gly Asn Met Thr Cys
130 135 140

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Thr Trp Asn Ala Gly Lys Leu Thr Tyr Met Asp Thr Lys Tyr Val Val
145                 150                 155                 160

His Val Lys Ser Leu Glu Thr Glu Glu Glu Gln Gln Tyr Leu Thr Ser
                165                 170                 175

Ser Tyr Ile Asn Ile Ser Thr Asp Ser Leu Gln Gly Gly Lys Lys Tyr
            180                 185                 190

Leu Val Trp Val Gln Ala Ala Asn Ala Leu Gly Met Glu Glu Ser Lys
        195                 200                 205

Gln Leu Gln Ile Tyr Leu Asp Asp Ile Val Ile Pro Ser Ala Ser Val
    210                 215                 220

Ile Ser Arg Ala Glu Thr Ile Asn Ala Thr Val Pro Lys Thr Ile Ile
225                 230                 235                 240

Tyr Trp Asp Ser Gln Thr Thr Ile Glu Lys Val Ser Cys Glu Met Arg
                245                 250                 255

Tyr Lys Ala Thr Thr Asn Gln Thr Trp Asn Val Lys Glu Phe Asp Thr
            260                 265                 270

Asn Phe Thr Tyr Val Gln Gln Ser Glu Phe Tyr Leu Glu Pro Asn Ile
        275                 280                 285

Lys Tyr Val Phe Gln Val Arg Cys Gln Glu Thr Gly Lys Arg Tyr Trp
    290                 295                 300

Gln Pro Trp Ser Ser Pro Phe Phe His Lys Thr Pro Glu Thr Val Pro
305                 310                 315                 320

Gln Val Thr Ser Lys Ala Phe Gln His Asp Thr Trp Asn Ser Gly Leu
                325                 330                 335

Thr Val Ala Ser Ile Ser Thr Gly His Leu Thr Ser Asp Asn Arg Gly
            340                 345                 350

Asp Ile Gly Leu Leu Leu Gly Met Ile Val Phe Ala Val Met Leu Ser
        355                 360                 365

Ile Leu Ser Leu Ile Gly Ile Phe Asn Arg Ser Leu Arg Thr Gly Ile
    370                 375                 380

Lys Arg Arg Ile Leu Leu Leu Ile Pro Lys Trp Leu Tyr Glu Asp Ile
385                 390                 395                 400

Pro Asn Met Lys Asn Ser Asn Val Val Lys Met Leu Gln Glu Asn Ser
                405                 410                 415
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Glu Leu Met Asn Asn Asn Ser Ser Glu Gln Val Leu Tyr Val Asp Pro
420 425 430

Met Ile Thr Glu Ile Lys Glu Ile Phe Ile Pro Glu His Lys Pro Thr
435 440 445

Asp Tyr Lys Lys Leu Asn Thr Gly Pro Leu Glu Thr Arg Asp Thr Leu
450 455 460

Gln Asn Ser Leu Phe Asp Asn Thr Thr Val Val Tyr Ile Pro Asp Leu
465 470 475 480

Asn Thr Gly Tyr Lys Pro Gln Ile Ser Asn Phe Leu Pro Glu Gly Ser
485 490 495

His Leu Ser Asn Asn Asn Glu Ile Thr Ser Leu Thr Leu Lys Pro Pro
500 505 510

Val Asp Ser Leu Asp Ser Gly Asn Asn Pro Arg Leu Gln Lys His Pro
515 520 525

Asn Phe Ala Phe Ser Val Ser Ser Val Asn Ser Leu Ser Asn Thr Ile
530 535 540

Phe Leu Gly Glu Leu Ser Leu Ile Leu Asn Gln Gly Glu Cys Ser Ser
545 550 555 560

Pro Asp Ile Gln Asn Ser Val Glu Glu Glu Thr Thr Thr Leu Leu Glu
565 570 575

Asn Asp Ser Pro Ser Glu Thr Ile Pro Glu Gln Thr Leu Leu Pro Asp
580 585 590

Glu Phe Val Ser Cys Leu Gly Ile Val Asn Glu Glu Leu Pro Ser Ile
595 600 605

Asn Thr Tyr Phe Pro Gln Asn Ile Leu Glu Ser His Phe Asn Arg Ile
610 615 620

Ser Leu Leu Glu Lys
625

<210> 764
<211> 631
<212> PRT
<213> Canis familiaris

<400> 764
Met Asn Gln Ile Thr Ile Gln Trp Asp Val Val Ile Ala Leu Tyr Ile
1 5 10 15

Phe Phe Asn Trp Cys His Gly Gly Ile Thr Asn Ile Asn Cys Ser Gly

```
            20                  25                  30

His Ile Trp Val Glu Pro Ala Thr Ile Phe Lys Met Gly Met Asn Ile
        35                  40                  45

Ser Ile Tyr Cys Gln Ala Ala Ile Lys Asn Cys Gln Pro Arg Lys Leu
    50                  55                  60

Tyr Phe Tyr Lys Asn Gly Ile Lys Glu Arg Phe Gln Ile Thr Arg Ile
65                  70                  75                  80

Asn Lys Thr Thr Ala Arg Leu Trp Tyr Ser Asn Phe Leu Glu Pro His
                85                  90                  95

Ala Ser Met Tyr Cys Thr Ala Glu Cys Pro Gly Tyr Pro Gln Glu Thr
            100                 105                 110

Leu Ile Cys Gly Lys Asp Ile Ser Ser Gly Tyr Pro Pro Asp Val Pro
        115                 120                 125

Asp Lys Val Thr Cys Val Ile Tyr Glu Tyr Ser Gly Asn Met Thr Cys
    130                 135                 140

Thr Trp Asn Ser Gly Lys Pro Thr Tyr Ile Asp Thr Lys Tyr Val Val
145                 150                 155                 160

Tyr Val Lys Ser Leu Glu Lys Glu Glu Glu Gln Gln Tyr Leu Ser Ser
                165                 170                 175

Ser Tyr Ile Asn Ile Ser Thr Asp Ser Leu Gln Gly Gly Lys Lys Tyr
            180                 185                 190

Leu Val Trp Val Gln Ala Ala Asn Ala Leu Gly Met Glu Lys Ser Lys
        195                 200                 205

Gln Leu Gln Ile Asn Leu Asp Asp Ile Val Ile Pro Ser Ala Ala Ile
    210                 215                 220

Ile Ser Arg Ala Glu Asp Ile Asn Thr Thr Ile Pro Lys Thr Ile Ile
225                 230                 235                 240

His Trp Asn Ser Gln Thr Thr Ile Glu Asn Val Ser Cys Glu Met Arg
                245                 250                 255

His Lys Thr Thr Thr Asn Gln Thr Trp Lys Val Lys Glu Phe Asp Thr
            260                 265                 270

Asn Phe Pro Tyr Glu Gln Gln Ser Glu Phe Tyr Leu Glu Pro Asn Thr
        275                 280                 285

Lys Tyr Ile Phe Gln Val Arg Cys Gln Glu Thr Gly Lys Arg Tyr Trp
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290 295 300

Gln Pro Trp Ser Ser Pro Phe Phe His Lys Thr Ala Glu Thr Val Pro
305 310 315 320

Gln Val Thr Val Lys Ser Phe Gln His Asp Thr Gln Asn Ser Glu Leu
325 330 335

Leu Ile Ala Ser Ile Phe Lys Gly His Leu Thr Ser Asp Asn Arg Gln
340 345 350

Gln Asp Ile Gly Leu Leu Leu Gly Met Ile Phe Phe Ala Ala Met Leu
355 360 365

Ser Ile Leu Ser Leu Ile Gly Ile Phe Asn Arg Ser Ile Arg Thr Gly
370 375 380

Ile Lys Arg Arg Ile Leu Leu Leu Ile Pro Lys Trp Leu His Glu Asp
385 390 395 400

Ile Pro Asn Met Glu Asn Ser Lys Val Val Glu Met Leu Gln Lys Gln
405 410 415

Ser Glu Phe Met Asn Asn Asn Ser Ser Glu Gln Val Leu Tyr Ala Asp
420 425 430

Pro Val Ile Thr Glu Ile Glu Ile Phe Leu Pro Glu Glu His Lys Pro
435 440 445

Thr Asp Tyr Lys Ala Glu Lys Asn Thr Gly Ser Leu Glu Thr Arg Asp
450 455 460

Cys Leu Gln Asn Ser Leu Leu Thr Asn Thr Thr Val Val Tyr Ile Pro
465 470 475 480

Gly Leu Ser Thr Gly Tyr Lys Pro Gln Ile Ser Asn Phe Leu Thr Gly
485 490 495

Gly Asn His Leu Ser Lys Lys Asp Glu Thr Ser Ser Ser Thr Leu Lys
500 505 510

Pro Leu Ala Asp Ser Ser Asp Leu Gly Gly Asn Ala Arg Phe Lys Lys
515 520 525

Tyr Pro Asn Phe Ala Phe Ser Val Ser Ser Met Asn Ser Leu Ser Asn
530 535 540

Thr Leu Phe Leu Glu Glu Leu Ser Leu Ile Leu Asn Gln Gly Glu Arg
545 550 555 560

Ser Pro Leu Asp Met Gln Asn Ser Val Glu Gly Glu Thr Thr Met Leu

565 570 575

Leu Glu Asn Ala Ser Pro Asn Glu Thr Ile Pro Glu Gln Thr Leu Leu
580 585 590

Pro Asp Glu Phe Val Ser Cys Leu Gly Ile Met Asn Glu Glu Leu Pro
595 600 605

Ser Ile Asn Ser Tyr Phe Pro Gln Asn Ile Leu Glu Asn His Phe Asn
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Thr Ile Ser Leu Leu Glu Lys
625 630

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Phe Phe Ser Trp Cys His Gly Gly Ile Thr Asn Ile Asn Cys Ser Gly
20 25 30

His Ile Trp Val Glu Pro Ala Thr Ile Phe Lys Met Gly Met Asn Ile
35 40 45

Ser Ile Tyr Cys Gln Ala Ala Ile Lys Asn Cys Gln Pro Ser Lys Leu
50 55 60

Tyr Phe Tyr Lys Asn Gly Ile Lys Glu Arg Phe His Ile Thr Arg Ile
65 70 75 80

Asn Lys Thr Thr Ala Arg Leu Trp Tyr Asn Asn Phe Val Glu Pro Gln
85 90 95

Ala Phe Met Tyr Cys Thr Ala Glu Cys Ser Arg Tyr Phe Pro Glu Thr
100 105 110

Leu Ile Cys Gly Lys Asp Ile Ser Ser Gly Tyr Pro Pro Asp Val Pro
115 120 125

Asp Lys Val Ala Cys Val Ile Tyr Glu Tyr Ser Gly Asn Met Thr Cys
130 135 140

Thr Trp Asn Pro Gly Arg Pro Thr Tyr Ile Asp Thr Lys Tyr Val Val
145 150 155 160

Tyr Val Lys Ser Leu Glu Thr Glu Glu Glu Gln Glu Tyr Leu Thr Ser
165 170 175

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Ser Tyr Ile Asn Ile Ser Thr Asp Ser Leu Gln Lys Gly Lys Lys Tyr
            180                 185                 190

Leu Val Trp Val Gln Ala Ser Asn Val Leu Gly Met Glu Lys Ser Lys
        195                 200                 205

Gln Leu Gln Ile His Leu Asp Asp Ile Val Ile Pro Ser Ala Ser Ile
    210                 215                 220

Ile Ser Arg Ala Glu Asp Ile Asn Thr Thr Val Ser Lys Thr Val Ile
225                 230                 235                 240

His Trp Asp Ser Gln Thr Ser Ile Glu Lys Val Ser Cys Glu Met Arg
                245                 250                 255

Tyr Lys Ala Thr Thr Asn Gln Thr Trp Asn Val Lys Glu Phe Asp Thr
            260                 265                 270

Asn Phe Thr Tyr Glu Gln Gln Ser Glu Phe Tyr Leu Gln Pro Asn Ala
        275                 280                 285

Met Tyr Val Phe Gln Val Arg Cys Gln Glu Thr Gly Lys Lys Tyr Trp
    290                 295                 300

Gln Pro Trp Ser Ser Pro Phe Phe His Lys Thr Pro Glu Ile Val Pro
305                 310                 315                 320

Gln Val Thr Met Lys Ser Phe Gln His Asp Thr Gln Asn Ser Gly Leu
                325                 330                 335

Leu Ile Ala Ser Ile Phe Lys Lys His Leu Thr Ser Asp Asn Arg Lys
            340                 345                 350

Gln Asp Ile Gly Leu Leu Leu Gly Met Val Phe Phe Ala Val Met Leu
        355                 360                 365

Ser Val Leu Ser Leu Ile Gly Ile Phe Asn Arg Ser Leu Arg Thr Gly
    370                 375                 380

Ile Lys Arg Arg Ile Leu Leu Leu Ile Pro Lys Trp Leu Tyr Glu Asp
385                 390                 395                 400

Ile Pro Asn Met Glu Asn Ser Lys Val Val Lys Ile Leu Gln Glu Arg
                405                 410                 415

Asn Glu Phe Met Asn Asn Asn Ser Ser Glu Gln Val Leu Tyr Val Asp
            420                 425                 430

Pro Val Ile Thr Glu Ile Glu Ile Ile Leu Pro Glu Glu Lys Pro Met
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Gly Tyr Lys Lys Glu Asn Asn Thr Gly Cys Leu Glu Arg Lys Glu Ser
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Leu Glu Lys Ser Leu Leu Thr Asp Thr Thr Val Val Tyr Ile Pro Asp
465 470 475 480

Leu Asn Thr Gly Tyr Lys Pro Gln Ile Ser Ser Phe Leu Pro Gly Gly
485 490 495

Asn His Leu Ser Asn Asp Asp Glu Thr Ala Ser Ser Ile Leu Glu Pro
500 505 510

Pro Ala Asp Ser Leu Asn Leu Gly Asn Asn Ala Arg Phe Lys Lys Tyr
515 520 525

Pro Asp Phe Ala Phe Ser Val Ser Ser Thr Asn Ser Leu Ser Asn Thr
530 535 540

Leu Phe Leu Glu Glu Leu Asn Leu Ile Leu Asn Gln Gly Glu Cys Ser
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Pro Pro Asp Met Gln Asn Ser Ile Glu Gly Glu Thr Ala Met Leu Leu
565 570 575

Glu Asp Asp Leu Leu Asn Glu Thr Ile Pro Glu Gln Thr Leu Leu Pro
580 585 590

Asp Glu Phe Val Ser Cys Leu Gly Ser Met Asn Lys Glu Leu Pro Ser
595 600 605

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Ile Ser Leu Leu Glu Lys
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<223> 2-Nal

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<220>
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<220>
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<220>
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<223> alpha-MeLys

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1 5 10

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Xaa Ser Thr Trp Gln Cys Phe Xaa Lys Lys Asn Gly Glu
1 5 10

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Xaa Gln Thr Trp Gln Cys Phe Trp Lys Lys Asn Gly Glu
1 5 10

<210> 828
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<220>
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<400> 828
Xaa Gln Thr Trp Gln Cys Tyr Xaa Lys Lys Asn Gly Glu
1 5 10

<210> 829
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<220>
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<222> (7)..(7)
<223> Phe[4-(2-aminoethoxy)]

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<223> 2-Nal

<220>
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<222> (9)..(9)
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<400> 829
Xaa Gln Thr Trp Gln Cys Phe Xaa Lys Glu Asn Gly
1 5 10

<210> 830
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<212> PRT
<213> Artificial Sequence

<220>
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peptide

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<220>
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<222> (8)..(8)
<223> 2-Nal

<220>
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<222> (9)..(9)
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<400> 830
Xaa Gln Thr Gln Gln Cys Phe Xaa Lys Glu Asn Gly
1 5 10

<210> 831
<211> 12
<212> PRT
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<220>
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<220>
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<222> (7)..(7)
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<221> MOD_RES
<222> (8)..(8)
<223> 2-Nal

<220>
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<222> (9)..(9)
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<400> 831
Xaa Gln Thr His Gln Cys Phe Xaa Lys Glu Asn Gly
1 5 10

<210> 832
<211> 12
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<220>
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<220>
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<222> (9)..(9)
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<400> 832
Xaa Gln Thr Phe Gln Cys Phe Xaa Lys Glu Asn Gly
1 5 10

<210> 833
<211> 12
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<223> Phe[4-(2-aminoethoxy)]

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<221> MOD_RES
<222> (8)..(8)
<223> 2-Nal

<220>
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<223> alpha-MeLys

<400> 833
Xaa Gln Thr Glu Gln Cys Phe Xaa Lys Glu Asn Gly
1 5 10

<210> 834
<211> 12
<212> PRT
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<220>
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<222> (7)..(7)
<223> Phe[4-(2-aminoethoxy)]

<220>
<221> MOD_RES
<222> (8)..(8)
<223> 2-Nal

<220>
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<400> 834
Xaa Gln Thr Xaa Gln Cys Phe Xaa Lys Glu Asn Gly
1 5 10

<210> 835
<211> 12
<212> PRT
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<220>
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<222> (9)..(9)
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<400> 835
Xaa Gln Thr Xaa Gln Cys Phe Xaa Lys Glu Asn Gly
1 5 10

<210> 836
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<212> PRT
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<220>
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<222> (4)..(4)
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<220>
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<223> Phe[4-(2-aminoethoxy)]

<220>
<221> MOD_RES
<222> (8)..(8)
<223> 2-Nal

<220>
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<400> 836
Xaa Gln Thr Phe Gln Cys Phe Xaa Lys Glu Asn Gly
1 5 10

<210> 837
<211> 12
<212> PRT
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<220>
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<222> (7)..(7)
<223> Phe[4-(2-aminoethoxy)]

<220>
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<220>
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<400> 837
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1 5 10

<210> 838
<211> 12
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<220>
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<221> MOD_RES
<222> (4)..(4)
<223> Phe(4-OMe)

<220>
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<222> (7)..(7)
<223> Phe[4-(2-aminoethoxy)]

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<220>
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<400> 838
Xaa Gln Thr Phe Gln Cys Phe Xaa Lys Glu Asn Gly

1 5 10

<210> 839
<211> 12
<212> PRT
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<220>
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<222> (4)..(4)
<223> Orn(Benzyl)

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<222> (7)..(7)
<223> Phe[4-(2-aminoethoxy)]

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<221> MOD_RES
<222> (8)..(8)
<223> 2-Nal

<220>
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<400> 839
Xaa Gln Thr Xaa Gln Cys Phe Xaa Lys Glu Asn Gly
1 5 10

<210> 840
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
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<223> Abu

<220>
<221> MOD_RES
<222> (4)..(4)
<223> Orn(Benzaldehyde)

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Phe[4-(2-aminoethoxy)]

<220>
<221> MOD_RES
<222> (8)..(8)
<223> 2-Nal

<220>
<221> MOD_RES
<222> (9)..(9)
<223> alpha-MeLys

<400> 840
Xaa Gln Thr Xaa Gln Cys Phe Xaa Lys Glu Asn Gly
1 5 10

<210> 841
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
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<222> (1)..(1)
<223> Abu

<220>
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<222> (7)..(7)
<223> Phe-OCH2CH2NHAc

<220>
<221> MOD_RES
<222> (8)..(8)
<223> 2-Nal

<220>
<221> MOD_RES
<222> (9)..(9)
<223> alpha-MeLys

<400> 841
Xaa Gln Thr Trp Gln Cys Phe Xaa Lys Glu Asn Gly
1 5 10

<210> 842
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
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<220>
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<223> Abu

<220>
<221> MOD_RES
<222> (7)..(7)

<223> Phe[4-(2-aminoethoxy)]

<220>
<221> MOD_RES
<222> (8)..(8)
<223> 2-Nal

<220>
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<222> (9)..(9)
<223> alpha-MeLeu

<400> 842
Xaa Gln Thr Trp Gln Cys Phe Xaa Leu Glu Asn Gly
1 5 10

<210> 843
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
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<220>
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<220>
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<222> (4)..(4)
<223> 5-hydroxyTrp

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Phe[4-(2-aminoethoxy)]

<220>
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<222> (8)..(8)
<223> 2-Nal

<220>
<221> MOD_RES
<222> (9)..(9)
<223> alpha-MeLys

<400> 843
Xaa Gln Thr Trp Gln Cys Phe Xaa Lys Glu Asn Gly
1 5 10

<210> 844
<211> 12
<212> PRT
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<220>
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<220>

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<223> Abu

<220>
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<222> (4)..(4)
<223> 6-chloroTrp

<220>
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<222> (7)..(7)
<223> Phe[4-(2-aminoethoxy)]

<220>
<221> MOD_RES
<222> (8)..(8)
<223> 2-Nal

<220>
<221> MOD_RES
<222> (9)..(9)
<223> alpha-MeLys

<400> 844
Xaa Gln Thr Trp Gln Cys Phe Xaa Lys Glu Asn Gly
1 5 10

<210> 845
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Abu

<220>
<221> MOD_RES
<222> (4)..(4)
<223> N-MeTrp

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Phe[4-(2-aminoethoxy)]

<220>
<221> MOD_RES
<222> (8)..(8)
<223> 2-Nal

<220>
<221> MOD_RES
<222> (9)..(9)
<223> alpha-MeLys

<400> 845
Xaa Gln Thr Trp Gln Cys Phe Xaa Lys Glu Asn Gly
1 5 10

<210> 846
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
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<220>
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<222> (1)..(1)
<223> Abu

<220>
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<222> (4)..(4)
<223> 1,2,3,4-tetrahydro-norharman

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Phe[4-(2-aminoethoxy)]

<220>
<221> MOD_RES
<222> (8)..(8)
<223> 2-Nal

<220>
<221> MOD_RES
<222> (9)..(9)
<223> alpha-MeLys

<400> 846
Xaa Gln Thr Xaa Gln Cys Phe Xaa Lys Glu Asn Gly
1 5 10

<210> 847
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
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<220>
<221> MOD_RES
<222> (1)..(1)
<223> Abu

<220>
<221> MOD_RES
<222> (4)..(4)
<223> Phe(4-CO2H)

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Phe[4-(2-aminoethoxy)]

<220>
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<222> (8)..(8)
<223> 2-Nal

<220>
<221> MOD_RES
<222> (9)..(9)
<223> alpha-MeLys]

<400> 847
Xaa Gln Thr Phe Gln Cys Phe Xaa Lys Glu Asn Gly
1 5 10

<210> 848
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Abu

<220>
<221> MOD_RES
<222> (4)..(4)
<223> Phe(4-CONH2)

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Phe[4-(2-aminoethoxy)]

<220>
<221> MOD_RES
<222> (8)..(8)
<223> 2-Nal

<220>
<221> MOD_RES
<222> (9)..(9)
<223> alpha-MeLys

<400> 848
Xaa Gln Thr Phe Gln Cys Phe Xaa Lys Glu Asn Gly
1 5 10

<210> 849
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Abu

<220>
<221> MOD_RES
<222> (4)..(4)
<223> Phe(4-CONH2)

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Phe[4-(2-aminoethoxy)]

<220>
<221> MOD_RES
<222> (8)..(8)
<223> 2-Nal

<220>
<221> MOD_RES
<222> (9)..(9)
<223> alpha-MeLys

<400> 849
Xaa Gln Thr Phe Gln Cys Phe Xaa Lys Glu Asn Gly
1 5 10

<210> 850
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Abu

<220>
<221> MOD_RES
<222> (4)..(4)
<223> Phe(3,4-OMe)

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Phe[4-(2-aminoethoxy)]

<220>
<221> MOD_RES
<222> (8)..(8)
<223> 2-Nal

<220>
<221> MOD_RES
<222> (9)..(9)
<223> alpha-MeLys

<400> 850
Xaa Gln Thr Phe Gln Cys Phe Xaa Lys Glu Asn Gly
1 5 10

<210> 851
<211> 12
<212> PRT

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Abu

<220>
<221> MOD_RES
<222> (4)..(4)
<223> alpha-MePhe

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Phe[4-(2-aminoethoxy)]

<220>
<221> MOD_RES
<222> (8)..(8)
<223> 2-Nal

<220>
<221> MOD_RES
<222> (9)..(9)
<223> alpha-MeLys

<400> 851
Xaa Gln Thr Phe Gln Cys Phe Xaa Lys Glu Asn Gly
1 5 10

<210> 852
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Abu

<220>
<221> MOD_RES
<222> (4)..(4)
<223> Phe(4-CF3)

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Phe[4-(2-aminoethoxy)]

<220>
<221> MOD_RES
<222> (8)..(8)
<223> 2-Nal

<220>

<221> MOD_RES
<222> (9)..(9)
<223> alpha-MeLys

<400> 852
Xaa Gln Thr Phe Gln Cys Phe Xaa Lys Glu Asn Gly
1 5 10

<210> 853
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Abu

<220>
<221> MOD_RES
<222> (4)..(4)
<223> Phe(4-tBu)

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Phe[4-(2-aminoethoxy)]

<220>
<221> MOD_RES
<222> (8)..(8)
<223> 2-Nal

<220>
<221> MOD_RES
<222> (9)..(9)
<223> alpha-MeLys]

<400> 853
Xaa Gln Thr Phe Gln Cys Phe Xaa Lys Glu Asn Gly
1 5 10

<210> 854
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Abu

<220>
<221> MOD_RES
<222> (4)..(4)
<223> Phe(2,4-Me2)

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Phe[4-(2-aminoethoxy)]

<220>
<221> MOD_RES
<222> (8)..(8)
<223> 2-Nal

<220>
<221> MOD_RES
<222> (9)..(9)
<223> alpha-MeLys

<400> 854
Xaa Gln Thr Phe Gln Cys Phe Xaa Lys Glu Asn Gly
1 5 10

<210> 855
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Abu

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Phe[4-(2-aminoethoxy)]

<220>
<221> MOD_RES
<222> (8)..(8)
<223> 2-Nal

<220>
<221> MOD_RES
<222> (9)..(9)
<223> alpha-MeLys

<400> 855
Xaa Gln Thr Trp Gln Cys Phe Xaa Lys Asp Asn Gly
1 5 10

<210> 856
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES

<222> (1)..(1)
<223> Abu

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Phe[4-(2-aminoethoxy)]

<220>
<221> MOD_RES
<222> (8)..(8)
<223> 2-Nal

<220>
<221> MOD_RES
<222> (9)..(9)
<223> alpha-MeLys

<400> 856
Xaa Gln Thr Trp Gln Cys Phe Xaa Lys Gln Asn Gly
1 5 10

<210> 857
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Abu

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Phe[4-(2-aminoethoxy)]

<220>
<221> MOD_RES
<222> (8)..(8)
<223> 2-Nal

<220>
<221> MOD_RES
<222> (9)..(9)
<223> alpha-MeLys

<220>
<221> MOD_RES
<222> (10)..(10)
<223> Lys(Benzoic acid)

<400> 857
Xaa Gln Thr Trp Gln Cys Phe Xaa Lys Lys Asn Gly
1 5 10

<210> 858
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Abu

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Phe[4-(2-aminoethoxy)]

<220>
<221> MOD_RES
<222> (8)..(8)
<223> 2-Nal

<220>
<221> MOD_RES
<222> (9)..(9)
<223> alpha-MeLys

<220>
<221> MOD_RES
<222> (10)..(10)
<223> Lys(succinic acid)

<400> 858
Xaa Gln Thr Trp Gln Cys Phe Xaa Lys Lys Asn Gly
1 5 10

<210> 859
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Abu

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Phe[4-(2-aminoethoxy)]

<220>
<221> MOD_RES
<222> (8)..(8)
<223> 2-Nal

<220>
<221> MOD_RES
<222> (9)..(9)
<223> alpha-MeLys

<220>
<221> MOD_RES
<222> (10)..(10)

<223> Lys(glutaric acid)

<400> 859
Xaa Gln Thr Trp Gln Cys Phe Xaa Lys Lys Asn Gly
1 5 10

<210> 860
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Abu

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Phe[4-(2-aminoethoxy)]

<220>
<221> MOD_RES
<222> (8)..(8)
<223> 2-Nal

<220>
<221> MOD_RES
<222> (9)..(9)
<223> alpha-MeLys

<220>
<221> MOD_RES
<222> (10)..(10)
<223> Lys(pyroglutamic acid) conjugated through side chain

<400> 860
Xaa Gln Thr Trp Gln Cys Phe Xaa Lys Lys Asn Gly
1 5 10

<210> 861
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Abu

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Phe[4-(2-aminoethoxy)]

<220>

<221> MOD_RES
<222> (8)..(8)
<223> 2-Nal

<220>
<221> MOD_RES
<222> (9)..(9)
<223> alpha-MeLys

<220>
<221> MOD_RES
<222> (10)..(10)
<223> Lys(isovaleric acid)

<400> 861
Xaa Gln Thr Trp Gln Cys Phe Xaa Lys Lys Asn Gly
1 5 10

<210> 862
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Abu

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Phe[4-(2-aminoethoxy)]

<220>
<221> MOD_RES
<222> (8)..(8)
<223> 2-Nal

<220>
<221> MOD_RES
<222> (9)..(9)
<223> alpha-MeLys

<220>
<221> MOD_RES
<222> (10)..(10)
<223> Lys(Palm)

<400> 862
Xaa Gln Thr Trp Gln Cys Phe Xaa Lys Lys Asn Gly
1 5 10

<210> 863
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Abu

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Phe[4-(2-aminoethoxy)]

<220>
<221> MOD_RES
<222> (8)..(8)
<223> 2-Nal

<220>
<221> MOD_RES
<222> (9)..(9)
<223> alpha-MeLys

<220>
<221> MOD_RES
<222> (10)..(10)
<223> Lys(PEG1)

<400> 863
Xaa Gln Thr Trp Gln Cys Phe Xaa Lys Lys Asn Gly
1 5 10

<210> 864
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Abu

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Phe[4-(2-aminoethoxy)]

<220>
<221> MOD_RES
<222> (8)..(8)
<223> 2-Nal

<220>
<221> MOD_RES
<222> (9)..(9)
<223> alpha-MeLys

<220>
<221> MOD_RES
<222> (10)..(10)
<223> Lys(PEG2)

<400> 864
Xaa Gln Thr Trp Gln Cys Phe Xaa Lys Lys Asn Gly

1 5 10

<210> 865
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Abu

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Phe[4-(2-aminoethoxy)]

<220>
<221> MOD_RES
<222> (8)..(8)
<223> 2-Nal

<220>
<221> MOD_RES
<222> (9)..(9)
<223> alpha-MeLys

<220>
<221> MOD_RES
<222> (10)..(10)
<223> Dap(Benzoic acid)

<400> 865
Xaa Gln Thr Trp Gln Cys Phe Xaa Lys Xaa Asn Gly
1 5 10

<210> 866
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Abu

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Phe[4-(2-aminoethoxy)]

<220>
<221> MOD_RES
<222> (8)..(8)
<223> 2-Nal

<220>
<221> MOD_RES
<222> (9)..(9)
<223> alpha-MeLys

<220>
<221> MOD_RES
<222> (10)..(10)
<223> Dap(succinic acid)

<400> 866
Xaa Gln Thr Trp Gln Cys Phe Xaa Lys Xaa Asn Gly
1 5 10

<210> 867
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Abu

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Phe[4-(2-aminoethoxy)]

<220>
<221> MOD_RES
<222> (8)..(8)
<223> 2-Nal

<220>
<221> MOD_RES
<222> (9)..(9)
<223> alpha-MeLys

<220>
<221> MOD_RES
<222> (10)..(10)
<223> Dap(glutaric acid)

<400> 867
Xaa Gln Thr Trp Gln Cys Phe Xaa Lys Xaa Asn Gly
1 5 10

<210> 868
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (1)..(1)

<223> Abu

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Phe[4-(2-aminoethoxy)]

<220>
<221> MOD_RES
<222> (8)..(8)
<223> 2-Nal

<220>
<221> MOD_RES
<222> (9)..(9)
<223> alpha-MeLys

<220>
<221> MOD_RES
<222> (10)..(10)
<223> Dap(pyroglutamic acid) conjugated through side chain

<400> 868
Xaa Gln Thr Trp Gln Cys Phe Xaa Lys Xaa Asn Gly
1 5 10

<210> 869
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Abu

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Phe[4-(2-aminoethoxy)]

<220>
<221> MOD_RES
<222> (8)..(8)
<223> 2-Nal

<220>
<221> MOD_RES
<222> (9)..(9)
<223> alpha-MeLys

<220>
<221> MOD_RES
<222> (10)..(10)
<223> Dap(IVA)

<400> 869
Xaa Gln Thr Trp Gln Cys Phe Xaa Lys Xaa Asn Gly
1 5 10

<210> 870

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

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Abu

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Phe[4-(2-aminoethoxy)]

<220>
<221> MOD_RES
<222> (8)..(8)
<223> 2-Nal

<220>
<221> MOD_RES
<222> (9)..(9)
<223> alpha-MeLys

<220>
<221> MOD_RES
<222> (10)..(10)
<223> Dap(PEG1)

<400> 870
Xaa Gln Thr Trp Gln Cys Phe Xaa Lys Xaa Asn Gly
1 5 10

<210> 871
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Abu

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Phe[4-(2-aminoethoxy)]

<220>
<221> MOD_RES
<222> (8)..(8)
<223> 2-Nal

<220>
<221> MOD_RES
<222> (9)..(9)
<223> alpha-MeLys

<220>
<221> MOD_RES
<222> (10)..(10)
<223> Dap(PEG2)

<400> 871
Xaa Gln Thr Trp Gln Cys Phe Xaa Lys Xaa Asn Gly
1 5 10

<210> 872
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Abu

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Phe[4-(2-aminoethoxy)]

<220>
<221> MOD_RES
<222> (8)..(8)
<223> 2-Nal

<220>
<221> MOD_RES
<222> (9)..(9)
<223> alpha-MeLys

<220>
<221> MOD_RES
<222> (10)..(10)
<223> Dap(PEG2-Ac)

<400> 872
Xaa Gln Thr Trp Gln Cys Phe Xaa Lys Xaa Asn Gly
1 5 10

<210> 873
<211> 14
<212> PRT
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<220>
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<220>
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<222> (7)..(7)
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<220>
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<220>
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<220>
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<222> (10)..(10)
<223> Lys(Ac)

<220>
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<222> (13)..(13)
<223> (2-aminoethoxy)acetic acid

<220>
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<222> (14)..(14)
<223> D-Lys

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<210> 874
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<220>
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<222> (7)..(7)
<223> Phe[4-(2-aminoethoxy)]

<220>
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<223> 2-Nal

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<223> Lys(Ac)

<220>
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<222> (13)..(13)
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<210> 875
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<220>
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<223> 2-Nal

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<220>
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1 5 10

<210> 876
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<223> Phe[4-(2-aminoethoxy)]

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<220>
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<222> (7)..(7)
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<210> 880
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<222> (7)..(7)
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<222> (7)..(7)
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<223> 2-Nal

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<223> alpha-MeLys

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<223> alpha-MeLys

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<220>
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<220>
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<220>
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1 5 10

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Xaa Gln Thr Trp Gln Cys Phe Xaa Lys Lys Asn Gly
1 5 10

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1 5 10

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<220>
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1 5 10

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<220>
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<400> 895

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Xaa Gln Thr Trp Gln Cys Phe Trp Xaa Xaa Asn Gly
1 5 10

<210> 896
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<212> PRT
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<220>
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<222> (7)..(7)
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<223> Orn

<220>
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<210> 897
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<220>
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<223> Orn

<220>
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1 5 10

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<223> Orn

<220>
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Xaa Gln Thr Trp Gln Cys Phe Xaa Xaa Xaa Asn Gly
1 5 10

<210> 899
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<222> (7)..(7)
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<220>
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<400> 899
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<210> 900
<211> 12
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<220>
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<223> alpha-MeLys(Ac)

<220>
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<220>
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<222> (8)..(8)
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<220>
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<222> (9)..(9)
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1 5 10

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<400> 903
Xaa Gln Thr Trp Gln Cys Phe Trp Lys Lys Xaa Gly
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<220>
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<210> 906
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1 5 10

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<220>
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<220>
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<210> 926
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<223> alpha-MeLys

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1 5 10

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<223> Lys(Ac)

<220>
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1 5 10

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<223> 2-Nal

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1 5 10

<210> 932
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<223> 2-Nal

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Xaa Xaa Thr Trp Gln Cys Phe Xaa Lys Glu Asn Gly
1 5 10

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<223> 2-Nal

<220>
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<220>
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<222> (8)..(8)
<223> 2-Nal

<220>
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Xaa Ser Thr Trp Gln Cys Phe Xaa Lys Lys Asn Gly Gly Glu

1 5 10

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<222> (7)..(7)
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<220>
<221> MOD_RES
<222> (8)..(8)
<223> 2-Nal

<220>
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<222> (9)..(9)
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Xaa Gln Thr Trp Gln Cys Phe Xaa Lys Glu Asn Gln
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<210> 936
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<222> (7)..(7)
<223> Phe[4-(2-(acetyl-aminoethoxy)]

<220>
<221> MOD_RES
<222> (8)..(8)
<223> 2-Nal

<220>
<221> MOD_RES
<222> (9)..(9)
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1 5 10

<210> 937
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<222> (7)..(7)
<223> 2-Nal

<220>
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<222> (8)..(8)
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<400> 937
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1 5 10

<210> 938
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<220>
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<220>
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<223> alpha-MeLys

<220>
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<210> 939
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<220>
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1 5 10

<210> 940
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1 5 10

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<220>
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<223> Abu

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<220>
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<222> (8)..(8)
<223> alpha-MeTrp

<220>
<221> MOD_RES
<222> (9)..(9)
<223> alpha-MeLys

<220>
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<222> (10)..(10)
<223> Lys(Ac)

<400> 941
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1 5 10

<210> 942
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<220>
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<220>
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<223> Abu

<220>
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<223> alpha-MeSer

<220>
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<222> (7)..(7)
<223> Phe[4-(2-aminoethoxy)]

<220>
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<222> (8)..(8)
<223> 2-Nal

<220>
<221> MOD_RES
<222> (9)..(9)
<223> alpha-MeLys

<220>
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<223> Lys(Ac)

<400> 942
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1 5 10

<210> 943
<211> 12
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<220>
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<223> alpha-MeSer

<220>
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<223> Phe[4-(2-aminoethoxy)]

<220>
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<222> (8)..(8)
<223> 2-Nal

<220>
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<222> (9)..(9)
<223> alpha-MeLys

<220>
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<223> Lys(Ac)

<400> 943
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1 5 10

<210> 944
<211> 12
<212> PRT
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<220>
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<220>
<221> MOD_RES
<222> (7)..(7)
<223> Phe[4-(2-aminoethoxy)]

<220>
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<222> (8)..(8)
<223> alpha-MePhe

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<222> (9)..(9)
<223> alpha-MeLys

<220>
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<400> 944
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1 5 10

<210> 945
<211> 12
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<220>
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<220>
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<220>
<221> MOD_RES
<222> (7)..(7)
<223> Phe[4-(2-aminoethoxy)]

<220>
<221> MOD_RES
<222> (9)..(9)
<223> Aib

<400> 945
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1 5 10

<210> 946
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<220>
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<222> (7)..(7)
<223> Phe[4-(2-aminoethoxy)]

<220>
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<223> 2-Nal

<220>
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<223> Aib

<220>
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<400> 946
Xaa Gln Thr Trp Gln Cys Phe Xaa Xaa Lys Asn Gly
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<210> 947
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<220>
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<223> Abu

<220>
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<222> (7)..(7)
<223> Phe[4-(2-aminoethoxy)]

<220>
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<222> (8)..(8)
<223> 2-Nal

<220>
<221> MOD_RES
<222> (9)..(9)
<223> Aib

<220>
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<222> (11)..(11)
<223> Dap(Ac)

<400> 947
Xaa Gln Thr Trp Gln Cys Phe Xaa Xaa Glu Xaa Gly
1 5 10

<210> 948
<211> 12
<212> PRT
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<220>
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<220>
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<222> (7)..(7)
<223> Phe[4-(2-aminoethoxy)]

<220>
<221> MOD_RES
<222> (8)..(8)
<223> 2-Nal

<220>
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<222> (9)..(9)
<223> Aib

<220>
<221> MOD_RES
<222> (11)..(11)
<223> Dab(Ac)

<400> 948

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Xaa Gln Thr Trp Gln Cys Phe Xaa Xaa Glu Xaa Gly
1 5 10

<210> 949
<211> 12
<212> PRT
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<220>
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<220>
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<222> (7)..(7)
<223> Phe[4-(2-aminoethoxy)]

<220>
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<222> (8)..(8)
<223> 2-Nal

<220>
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<222> (9)..(9)
<223> Aib

<220>
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<222> (11)..(11)
<223> Lys(Ac)

<400> 949
Xaa Gln Thr Trp Gln Cys Phe Xaa Xaa Glu Lys Gly
1 5 10

<210> 950
<211> 12
<212> PRT
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<220>
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<220>
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<222> (7)..(7)
<223> Phe[4-(2-aminoethoxy)]

<220>
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<222> (9)..(9)
<223> Aib

<400> 950
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<210> 951
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<212> PRT
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<220>
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<220>
<221> MOD_RES
<222> (7)..(7)
<223> Phe[4-(2-aminoethoxy)]

<220>
<221> MOD_RES
<222> (8)..(8)
<223> 2-Nal

<220>
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<222> (9)..(9)
<223> alpha-MeLeu

<400> 951
Xaa Gln Thr Trp Gln Cys Phe Xaa Leu Glu Asn Asn
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<210> 952
<211> 12
<212> PRT
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<220>
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<220>
<221> MOD_RES
<222> (7)..(7)
<223> Phe[4-(2-aminoethoxy)]

<220>
<221> MOD_RES
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<223> Phe(3,4-OMe2)

<220>
<221> MOD_RES

<222> (9)..(9)
<223> Aib

<400> 952
Xaa Gln Thr Trp Gln Cys Phe Phe Xaa Glu Asn Gly
1 5 10

<210> 953
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<212> PRT
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<220>
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<220>
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<222> (7)..(7)
<223> Phe[4-(2-aminoethoxy)]

<220>
<221> MOD_RES
<222> (8)..(8)
<223> Phe(3,4-Cl2)

<220>
<221> MOD_RES
<222> (9)..(9)
<223> Aib

<400> 953
Xaa Gln Thr Trp Gln Cys Phe Phe Xaa Glu Asn Asn
1 5 10

<210> 954
<211> 12
<212> PRT
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<220>
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<220>
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<222> (7)..(7)
<223> Phe[4-(2-aminoethoxy)]

<220>
<221> MOD_RES
<222> (8)..(8)
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<220>
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<222> (9)..(9)
<223> alpha-MeLeu

<220>
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1 5 10

<210> 955
<211> 12
<212> PRT
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<220>
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<223> Abu

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<222> (7)..(7)
<223> Phe[4-(2-aminoethoxy)]

<220>
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<222> (8)..(8)
<223> 2-Nal

<220>
<221> MOD_RES
<222> (9)..(9)
<223> alpha-MeLeu

<220>
<221> MOD_RES
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<223> Lys(Ac)

<400> 955
Xaa Gln Thr Trp Gln Cys Phe Xaa Leu Lys Asn Asn
1 5 10

<210> 956
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
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<223> Abu

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Phe(4-Me)

<220>
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<222> (8)..(8)
<223> 2-Nal

<220>
<221> MOD_RES
<222> (9)..(9)
<223> Aib

<400> 956
Xaa Gln Thr Trp Gln Cys Phe Xaa Xaa Glu Asn Gly
1 5 10

<210> 957
<211> 12
<212> PRT
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<220>
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<222> (7)..(7)
<223> Phe(3,4-F2)

<220>
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<222> (8)..(8)
<223> 2-Nal

<220>
<221> MOD_RES
<222> (9)..(9)
<223> Aib

<400> 957
Xaa Gln Thr Trp Gln Cys Phe Xaa Xaa Glu Asn Gly
1 5 10

<210> 958
<211> 12
<212> PRT
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<220>
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<220>

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<223> Abu

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<222> (7)..(7)
<223> Phe(3-CONH2)

<220>
<221> MOD_RES
<222> (8)..(8)
<223> 2-Nal

<220>
<221> MOD_RES
<222> (9)..(9)
<223> Aib

<400> 958
Xaa Gln Thr Trp Gln Cys Phe Xaa Xaa Glu Asn Gly
1 5 10

<210> 959
<211> 12
<212> PRT
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<220>
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<223> Abu

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<222> (7)..(7)
<223> Phe(2,4-Cl2)

<220>
<221> MOD_RES
<222> (8)..(8)
<223> 2-Nal

<220>
<221> MOD_RES
<222> (9)..(9)
<223> Aib

<400> 959
Xaa Gln Thr Trp Gln Cys Phe Xaa Xaa Glu Asn Gly
1 5 10

<210> 960
<211> 12
<212> PRT
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<220>
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<223> Abu

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Phe(3-Me)

<220>
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<222> (8)..(8)
<223> 2-Nal

<220>
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<222> (9)..(9)
<223> Aib

<400> 960
Xaa Gln Thr Trp Gln Cys Phe Xaa Xaa Glu Asn Gly
1 5 10

<210> 961
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<212> PRT
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<220>
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<220>
<221> MOD_RES
<222> (7)..(7)
<223> Phe(4-Cl)

<220>
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<222> (8)..(8)
<223> 2-Nal

<220>
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<222> (9)..(9)
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<400> 961
Xaa Gln Thr Trp Gln Cys Phe Xaa Xaa Glu Asn Gly
1 5 10

<210> 962
<211> 12
<212> PRT
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<220>
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peptide

<220>
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<223> Abu

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Phe(4-F)

<220>
<221> MOD_RES
<222> (8)..(8)
<223> 2-Nal

<220>
<221> MOD_RES
<222> (9)..(9)
<223> Aib

<400> 962
Xaa Gln Thr Trp Gln Cys Phe Xaa Xaa Glu Asn Gly
1 5 10

<210> 963
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
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<220>
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<223> Abu

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Phe(2,4-Cl2, 4-OBz)

<220>
<221> MOD_RES
<222> (8)..(8)
<223> 2-Nal

<220>
<221> MOD_RES
<222> (9)..(9)
<223> Aib

<400> 963
Xaa Gln Thr Trp Gln Cys Phe Xaa Xaa Glu Asn Gly
1 5 10

<210> 964
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
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<220>
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<223> Abu

<220>
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<222> (7)..(7)
<223> Phe(4-OMe)

<220>
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<222> (8)..(8)
<223> 2-Nal

<220>
<221> MOD_RES
<222> (9)..(9)
<223> alpha-MeLeu

<220>
<221> MOD_RES
<222> (13)..(13)
<223> D-Lys

<400> 964
Xaa Gln Thr Trp Gln Cys Phe Xaa Leu Glu Asn Gly Lys
1 5 10

<210> 965
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
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<220>
<221> MOD_RES
<222> (2)..(2)
<223> Abu

<220>
<221> MOD_RES
<222> (8)..(8)
<223> Phe[4-(2-aminoethoxy)]

<220>
<221> MOD_RES
<222> (9)..(9)
<223> 2-Nal

<220>
<221> MOD_RES
<222> (10)..(10)
<223> alpha-MeLys

<400> 965
Glu Xaa Gln Thr Trp Gln Cys Phe Xaa Lys Glu Asn Asn
1 5 10

<210> 966
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
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<220>
<221> MOD_RES
<222> (1)..(1)
<223> D-Glu

<220>
<221> MOD_RES
<222> (2)..(2)
<223> Abu

<220>
<221> MOD_RES
<222> (8)..(8)
<223> Phe[4-(2-aminoethoxy)]

<220>
<221> MOD_RES
<222> (9)..(9)
<223> 2-Nal

<220>
<221> MOD_RES
<222> (10)..(10)
<223> alpha-MeLys

<400> 966
Glu Xaa Gln Thr Trp Gln Cys Phe Xaa Lys Glu Asn Asn
1 5 10

<210> 967
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
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<220>
<221> MOD_RES
<222> (2)..(2)
<223> Abu

<220>
<221> MOD_RES
<222> (8)..(8)
<223> Phe[4-(2-aminoethoxy)]

<220>
<221> MOD_RES
<222> (9)..(9)
<223> 2-Nal

<220>

<221> MOD_RES
<222> (10)..(10)
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<400> 967
Arg Xaa Gln Thr Trp Gln Cys Phe Xaa Lys Glu Asn Asn
1 5 10

<210> 968
<211> 13
<212> PRT
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<220>
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<220>
<221> MOD_RES
<222> (2)..(2)
<223> Abu

<220>
<221> MOD_RES
<222> (8)..(8)
<223> Phe[4-(2-aminoethoxy)]

<220>
<221> MOD_RES
<222> (9)..(9)
<223> 2-Nal

<220>
<221> MOD_RES
<222> (10)..(10)
<223> alpha-MeLys

<400> 968
Arg Xaa Gln Thr Trp Gln Cys Phe Xaa Lys Glu Asn Asn
1 5 10

<210> 969
<211> 13
<212> PRT
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<220>
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<220>
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<222> (2)..(2)
<223> Abu

<220>
<221> MOD_RES
<222> (8)..(8)
<223> Phe[4-(2-aminoethoxy)]

<220>
<221> MOD_RES
<222> (9)..(9)
<223> 2-Nal

<220>
<221> MOD_RES
<222> (10)..(10)
<223> alpha-MeLys

<400> 969
Phe Xaa Gln Thr Trp Gln Cys Phe Xaa Lys Glu Asn Asn
1 5 10

<210> 970
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
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<223> D-Phe

<220>
<221> MOD_RES
<222> (2)..(2)
<223> Abu

<220>
<221> MOD_RES
<222> (8)..(8)
<223> Phe[4-(2-aminoethoxy)]

<220>
<221> MOD_RES
<222> (9)..(9)
<223> 2-Nal

<220>
<221> MOD_RES
<222> (10)..(10)
<223> alpha-MeLys

<400> 970
Phe Xaa Gln Thr Trp Gln Cys Phe Xaa Lys Glu Asn Asn
1 5 10

<210> 971
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
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<220>
<221> MOD_RES

<222> (1)..(1)
<223> 2-Nal

<220>
<221> MOD_RES
<222> (2)..(2)
<223> Abu

<220>
<221> MOD_RES
<222> (8)..(8)
<223> Phe[4-(2-aminoethoxy)]

<220>
<221> MOD_RES
<222> (9)..(9)
<223> 2-Nal

<220>
<221> MOD_RES
<222> (10)..(10)
<223> alpha-MeLys

<400> 971
Xaa Xaa Gln Thr Trp Gln Cys Phe Xaa Lys Glu Asn Asn
1 5 10

<210> 972
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
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<220>
<221> MOD_RES
<222> (2)..(2)
<223> Abu

<220>
<221> MOD_RES
<222> (8)..(8)
<223> Phe[4-(2-aminoethoxy)]

<220>
<221> MOD_RES
<222> (9)..(9)
<223> 2-Nal

<220>
<221> MOD_RES
<222> (10)..(10)
<223> alpha-MeLys

<400> 972
Thr Xaa Gln Thr Trp Gln Cys Phe Xaa Lys Glu Asn Asn
1 5 10

<210> 973
<211> 13
<212> PRT
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<220>
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<220>
<221> MOD_RES
<222> (2)..(2)
<223> Abu

<220>
<221> MOD_RES
<222> (8)..(8)
<223> Phe[4-(2-aminoethoxy)]

<220>
<221> MOD_RES
<222> (9)..(9)
<223> 2-Nal

<220>
<221> MOD_RES
<222> (10)..(10)
<223> alpha-MeLys

<400> 973
Leu Xaa Gln Thr Trp Gln Cys Phe Xaa Lys Glu Asn Asn
1 5 10

<210> 974
<211> 13
<212> PRT
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<220>
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<223> D-Gln

<220>
<221> MOD_RES
<222> (2)..(2)
<223> Abu

<220>
<221> MOD_RES
<222> (8)..(8)
<223> Phe[4-(2-aminoethoxy)]

<220>
<221> MOD_RES
<222> (9)..(9)
<223> 2-Nal

<220>
<221> MOD_RES
<222> (10)..(10)
<223> alpha-MeLys

<400> 974
Gln Xaa Gln Thr Trp Gln Cys Phe Xaa Lys Glu Asn Asn
1 5 10

<210> 975
<211> 12
<212> PRT
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<220>
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<220>
<221> MOD_RES
<222> (7)..(7)
<223> Phe[4-(2-aminoethoxy)]

<220>
<221> MOD_RES
<222> (8)..(8)
<223> 2-Nal

<220>
<221> MOD_RES
<222> (9)..(9)
<223> Acpc

<400> 975
Xaa Gln Thr Trp Gln Cys Phe Xaa Xaa Glu Asn Asn
1 5 10

<210> 976
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
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<220>
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<220>
<221> MOD_RES
<222> (7)..(7)
<223> Phe[4-(2-aminoethoxy)]

<220>
<221> MOD_RES
<222> (8)..(8)
<223> 2-Nal

<220>
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<223> Acbc

<400> 976

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1 5 10

<210> 977
<211> 12
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<220>
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<220>
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<220>
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<222> (7)..(7)
<223> Phe[4-(2-aminoethoxy)]

<220>
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<222> (8)..(8)
<223> 2-Nal

<220>
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<222> (9)..(9)
<223> Achc

<400> 977
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1 5 10

<210> 978
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
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<220>
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<222> (1)..(1)
<223> Abu

<220>
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<222> (7)..(7)
<223> Phe[4-(2-aminoethoxy)]

<220>
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<222> (8)..(8)
<223> 2-Nal

<220>
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<222> (9)..(9)
<223> Acvc

<400> 978
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1 5 10

<210> 979
<211> 12
<212> PRT
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<220>
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<220>
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<223> Abu

<220>
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<222> (7)..(7)
<223> Phe[4-(2-aminoethoxy)]

<220>
<221> MOD_RES
<222> (8)..(8)
<223> 2-Nal

<220>
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<223> 4-amino-4-carboxy-piperidine

<400> 979
Xaa Gln Thr Trp Gln Cys Phe Xaa Xaa Glu Asn Asn
1 5 10

<210> 980
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<220>
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<223> Abu

<220>
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<222> (7)..(7)
<223> Phe[4-(2-aminoethoxy)]

<220>
<221> MOD_RES
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<223> 2-Nal

<220>
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<222> (9)..(9)
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1 5 10

<210> 981
<211> 12
<212> PRT
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<220>
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<223> Abu

<220>
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<223> Phe[4-(2-aminoethoxy)]

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<223> 2-Nal

<220>
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<222> (9)..(9)
<223> alpha-MeLeu

<220>
<221> MOD_RES
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<223> Lys(Ac)

<400> 981
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1 5 10

<210> 982
<211> 12
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<220>
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<220>
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<220>
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<222> (7)..(7)
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<220>
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<222> (8)..(8)
<223> 2-Nal

<220>
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<222> (9)..(9)
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<210> 983
<211> 12
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<220>
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<220>
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<222> (7)..(7)
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<222> (8)..(8)
<223> 2-Nal

<220>
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<222> (9)..(9)
<223> alpha-MeLeu

<400> 983
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<210> 984
<211> 12
<212> PRT
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<220>
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<220>
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<222> (7)..(7)

<223> Phe[4-(2-aminoethoxy)]

<220>
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<223> 2-Nal

<220>
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<222> (9)..(9)
<223> alpha-MeLeu

<220>
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<222> (12)..(12)
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<400> 984
Xaa Gln Thr Trp Gln Cys Phe Xaa Leu Gln Asn Ala
1 5 10

<210> 985
<211> 12
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<220>
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<223> Abu

<220>
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<222> (7)..(7)
<223> Phe[4-(2-aminoethoxy)]

<220>
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<222> (8)..(8)
<223> 2-Nal

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1 5 10

<210> 986
<211> 12
<212> PRT
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<220>
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<223> Abu

<220>
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<222> (7)..(7)
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<220>
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<223> 2-Nal

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Xaa Gln Thr Trp Gln Cys Phe Xaa Leu Gln Asp Gly
1 5 10

<210> 987
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<220>
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<222> (7)..(7)
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<222> (8)..(8)
<223> 2-Nal

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<222> (9)..(9)
<223> Aib

<220>
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<223> Beta-Ala

<400> 987
Xaa Gln Thr Trp Gln Cys Phe Xaa Xaa Gln Asn Ala
1 5 10

<210> 988
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
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<222> (7)..(7)
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<220>
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<223> 1,2,3,4-tetrahydro-norharman

<220>
<221> MOD_RES
<222> (9)..(9)
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<400> 988
Xaa Gln Thr Trp Gln Cys Phe Xaa Xaa Gln Asn Gly
1 5 10

<210> 989
<211> 12
<212> PRT
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<220>
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<220>
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<220>
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<222> (7)..(7)
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<220>
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<222> (8)..(8)
<223> 5-hydroxyTrp

<220>
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<222> (9)..(9)
<223> Aib

<400> 989
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<210> 990
<211> 13

<212> PRT
<213> Artificial Sequence

<220>
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<222> (7)..(7)
<223> Phe[4-(2-aminoethoxy)]

<220>
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<222> (8)..(8)
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<220>
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<222> (9)..(9)
<223> alpha-MeLys

<220>
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<222> (10)..(10)
<223> Lys(Ac)

<220>
<221> MOD_RES
<222> (11)..(11)
<223> Asn(isobutyl)

<400> 990
Xaa Gln Thr Trp Gln Cys Phe Xaa Lys Lys Asn Gly Asn
1 5 10

<210> 991
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
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<220>
<221> MOD_RES
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<223> Abu

<220>
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<222> (7)..(7)
<223> Phe[4-(2-aminoethoxy)]

<220>
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<222> (8)..(8)
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<222> (9)..(9)
<223> alpha-MeLys

<220>
<221> MOD_RES
<222> (10)..(10)
<223> Lys(Ac)

<220>
<221> MOD_RES
<222> (11)..(11)
<223> Asp(1,4-diaminoethane)

<400> 991
Xaa Gln Thr Trp Gln Cys Phe Xaa Lys Lys Asp Gly
1 5 10

<210> 992
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
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<223> D-Phe

<220>
<221> MOD_RES
<222> (2)..(2)
<223> Abu

<220>
<221> MOD_RES
<222> (8)..(8)
<223> Phe[4-(2-aminoethoxy)]

<220>
<221> MOD_RES
<222> (9)..(9)
<223> 2-Nal

<220>
<221> MOD_RES
<222> (10)..(10)
<223> 4-amino-4-carboxy-tetrahydropyran

<400> 992
Phe Xaa Gln Thr Trp Gln Cys Phe Xaa Xaa Glu Asn Asn
1 5 10

<210> 993
<211> 13
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<220>
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<220>
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<223> D-Arg

<220>
<221> MOD_RES
<222> (2)..(2)
<223> Abu

<220>
<221> MOD_RES
<222> (8)..(8)
<223> Phe[4-(2-aminoethoxy)]

<220>
<221> MOD_RES
<222> (9)..(9)
<223> 2-Nal

<220>
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<222> (10)..(10)
<223> 4-amino-4-carboxy-tetrahydropyran

<400> 993
Arg Xaa Gln Thr Trp Gln Cys Phe Xaa Xaa Glu Asn Asn
1 5 10

<210> 994
<211> 13
<212> PRT
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<220>
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<220>
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<222> (2)..(2)
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<222> (8)..(8)
<223> Phe(4-OMe)

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<222> (9)..(9)
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<220>
<221> MOD_RES
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<400> 994

Lys Xaa Gln Thr Trp Gln Cys Phe Xaa Leu Glu Asn Gly
1 5 10

<210> 995
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<220>
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<222> (7)..(7)
<223> Phe[4-(2-aminoethoxy)]

<220>
<221> MOD_RES
<222> (8)..(8)
<223> 2-Nal

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<222> (9)..(9)
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<400> 995
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1 5 10

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<210> 997
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<222> (8)..(8)
<223> Phe(4-OMe)

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1 5 10

<210> 998
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<220>
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<220>
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<220>
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<222> (7)..(7)
<223> Phe(4-OBzl)

<220>
<221> MOD_RES

<222> (9)..(9)
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<400> 998
Xaa Gln Thr Trp Gln Cys Phe Trp Lys Glu Asn Gly
1 5 10

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<220>
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<220>
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<223> Abu

<220>
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<222> (7)..(7)
<223> Tyr(Bzl)

<220>
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<222> (9)..(9)
<223> alpha-MeLys

<400> 999
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1 5 10

<210> 1000
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<220>
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<220>
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<222> (6)..(6)
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<400> 1000
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1 5 10

<210> 1001
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<220>
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<220>
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<223> allylGly

<220>
<221> MOD_RES
<222> (6)..(6)
<223> allylGly

<400> 1001
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1 5 10

<210> 1002
<211> 14
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<220>
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<220>
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<223> 2-(3'-butenyl)Gly

<220>
<221> MOD_RES
<222> (6)..(6)
<223> 2-(4'-pentenyl)Gly

<220>
<221> MOD_RES
<222> (13)..(13)
<223> (2-aminoethoxy)acetic acid

<220>
<221> MOD_RES
<222> (14)..(14)
<223> D-Lys

<400> 1002
Gly Arg Thr Trp Gln Gly Tyr Trp Arg Lys Phe Gly Xaa Lys
1 5 10

<210> 1003
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
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<221> MOD_RES
<222> (1)..(1)

<223> 2-(4'-pentenyl)Gly

<220>
<221> MOD_RES
<222> (6)..(6)
<223> 2-(3'-butenyl)Gly

<220>
<221> MOD_RES
<222> (13)..(13)
<223> (2-aminoethoxy)acetic acid

<220>
<221> MOD_RES
<222> (14)..(14)
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<400> 1003
Gly Arg Thr Trp Gln Gly Tyr Trp Arg Lys Phe Gly Xaa Lys
1 5 10

<210> 1004
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
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<222> (1)..(1)
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<220>
<221> MOD_RES
<222> (6)..(6)
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<220>
<221> MOD_RES
<222> (13)..(13)
<223> (2-aminoethoxy)acetic acid

<220>
<221> MOD_RES
<222> (14)..(14)
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<400> 1004
Gly Arg Thr Trp Gln Gly Tyr Trp Arg Lys Phe Gly Xaa Lys
1 5 10

<210> 1005
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
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<220>
<221> MOD_RES

<222> (1)..(1)
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<220>
<221> MOD_RES
<222> (6)..(6)
<223> allylGly

<220>
<221> MOD_RES
<222> (13)..(13)
<223> (2-aminoethoxy)acetic acid

<220>
<221> MOD_RES
<222> (14)..(14)
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<400> 1005
Gly Arg Thr Trp Gln Gly Tyr Trp Arg Lys Phe Gly Xaa Lys
1 5 10

<210> 1006
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
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<220>
<221> MOD_RES
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<220>
<221> MOD_RES
<222> (13)..(13)
<223> (2-aminoethoxy)acetic acid

<220>
<221> MOD_RES
<222> (14)..(14)
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<400> 1006
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1 5 10

<210> 1007
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<212> PRT
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<220>
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<222> (6)..(6)
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<220>
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Gly Arg Thr Trp Gln Gly Tyr Trp Arg Lys Phe Gly Xaa Lys
1 5 10

<210> 1008
<211> 14
<212> PRT
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<220>
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<220>
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<220>
<221> MOD_RES
<222> (6)..(6)
<223> 2-(3'-butenyl)Gly

<220>
<221> MOD_RES
<222> (13)..(13)
<223> (2-aminoethoxy)acetic acid

<220>
<221> MOD_RES
<222> (14)..(14)
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<400> 1008
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1 5 10

<210> 1009
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<220>
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<220>
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<221> MOD_RES
<222> (13)..(13)
<223> (2-aminoethoxy)acetic acid

<220>
<221> MOD_RES
<222> (14)..(14)
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<400> 1009
Xaa Gln Thr Trp Gln Glu Tyr Trp Arg Glu Asn Gly Xaa Lys
1 5 10

<210> 1010
<211> 14
<212> PRT
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<220>
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<220>
<221> MOD_RES
<222> (6)..(6)
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<220>
<221> MOD_RES
<222> (13)..(13)
<223> (2-aminoethoxy)acetic acid

<220>
<221> MOD_RES
<222> (14)..(14)
<223> D-Lys

<400> 1010
Glu Gln Thr Trp Gln Xaa Tyr Trp Arg Glu Asn Gly Xaa Lys
1 5 10

<210> 1011
<211> 14
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<220>
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<222> (6)..(6)
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<220>

<221> MOD_RES
<222> (13)..(13)
<223> (2-aminoethoxy)acetic acid

<220>
<221> MOD_RES
<222> (14)..(14)
<223> D-Lys

<400> 1011
Glu Gln Thr Trp Gln Xaa Tyr Trp Arg Glu Asn Gly Xaa Lys
1 5 10

<210> 1012
<211> 14
<212> PRT
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<220>
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<220>
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<222> (13)..(13)
<223> (2-aminoethoxy)acetic acid

<220>
<221> MOD_RES
<222> (14)..(14)
<223> D-Lys

<400> 1012
Xaa Gln Thr Trp Gln Glu Tyr Trp Arg Glu Asn Gly Xaa Lys
1 5 10

<210> 1013
<211> 14
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<220>
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<222> (6)..(6)
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<220>
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<222> (13)..(13)
<223> (2-aminoethoxy)acetic acid

<220>
<221> MOD_RES
<222> (14)..(14)
<223> D-Lys

<400> 1013
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1 5 10

<210> 1014
<211> 14
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<220>
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<220>
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<223> Dap

<220>
<221> MOD_RES
<222> (13)..(13)
<223> (2-aminoethoxy)acetic acid

<220>
<221> MOD_RES
<222> (14)..(14)
<223> D-Lys

<400> 1014
Xaa Gln Thr Trp Gln Asp Tyr Trp Arg Glu Asn Gly Xaa Lys
1 5 10

<210> 1015
<211> 14
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<220>
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<220>
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<223> Dab

<220>
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<222> (13)..(13)
<223> (2-aminoethoxy)acetic acid

<220>
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<223> D-Lys

<400> 1015
Asp Gln Thr Trp Gln Xaa Tyr Trp Arg Glu Asn Gly Xaa Lys

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1 5 10

<210> 1016
<211> 14
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<220>
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<220>
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<223> Dab

<220>
<221> MOD_RES
<222> (13)..(13)
<223> (2-aminoethoxy)acetic acid

<220>
<221> MOD_RES
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<400> 1016
Xaa Gln Thr Trp Gln Asp Tyr Trp Arg Glu Asn Gly Xaa Lys
1 5 10

<210> 1017
<211> 14
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<220>
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<220>
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<222> (13)..(13)
<223> (2-aminoethoxy)acetic acid

<220>
<221> MOD_RES
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<223> D-Lys

<400> 1017
Xaa Gln Thr Trp Gln Asp Tyr Trp Arg Glu Asn Gly Xaa Lys
1 5 10

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<220>
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<223> (2-aminoethoxy)acetic acid

<220>
<221> MOD_RES
<222> (14)..(14)
<223> D-Lys

<400> 1018
Asp Gln Thr Trp Gln Xaa Tyr Trp Arg Glu Asn Gly Xaa Lys
1 5 10

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<220>
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<223> (2-aminoethoxy)acetic acid

<220>
<221> MOD_RES
<222> (14)..(14)
<223> D-Lys

<400> 1019
Asp Gln Thr Trp Gln Xaa Tyr Trp Arg Glu Asn Gly Xaa Lys
1 5 10

<210> 1020
<211> 12
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<220>
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<210> 1021
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<220>
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<220>
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<400> 1021
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1 5 10

<210> 1022
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<223> D-Pen

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<222> (13)..(13)
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<220>
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<400> 1022

Xaa Ala Asp Trp Val Cys Tyr Trp His Thr Phe Gly Xaa Lys
1 5 10

<210> 1023
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<220>
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<222> (6)..(6)
<223> D-Pen

<220>
<221> MOD_RES
<222> (13)..(13)
<223> (2-aminoethoxy)acetic acid

<220>
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<222> (14)..(14)
<223> D-Lys

<400> 1023
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1 5 10

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

<220>
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<221> MOD_RES
<222> (13)..(13)
<223> (2-aminoethoxy)acetic acid

<220>
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<222> (14)..(14)
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<400> 1024
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1 5 10

<210> 1025
<211> 14
<212> PRT
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<220>
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<220>
<221> MOD_RES
<222> (13)..(13)
<223> (2-aminoethoxy)acetic acid

<220>
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<222> (14)..(14)
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<400> 1025
Ala Cys Asp Trp Val Xaa Tyr Trp Arg Lys Phe Gly Xaa Lys
1 5 10

<210> 1026
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<220>
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<222> (13)..(13)
<223> (2-aminoethoxy)acetic acid

<220>
<221> MOD_RES
<222> (14)..(14)
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<400> 1026
Ala Xaa Asp Trp Val Cys Tyr Trp Arg Lys Phe Gly Xaa Lys
1 5 10

<210> 1027
<211> 14
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<222> (2)..(2)
<223> hCys

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<222> (13)..(13)
<223> (2-aminoethoxy)acetic acid

<220>
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<222> (14)..(14)
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<400> 1027
Ala Cys Asp Trp Val Xaa Tyr Trp Arg Lys Phe Gly Xaa Lys
1 5 10

<210> 1028
<211> 12
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<220>
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<222> (6)..(6)
<223> Pen

<220>
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<222> (9)..(9)
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<400> 1028
Cys Gln Thr Trp Gln Xaa Tyr Trp Leu Glu Asn Gly
1 5 10

<210> 1029
<211> 12
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<220>
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<220>
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<222> (6)..(6)
<223> Pen

<220>
<221> MOD_RES
<222> (9)..(9)
<223> D-Asn

<400> 1029
Cys Gln Thr Trp Gln Xaa Tyr Trp Asn Glu Asn Gly
1 5 10

<210> 1030
<211> 12
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<220>
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<223> Pen

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<222> (9)..(9)
<223> N-Me-Arg

<400> 1030
Xaa Gln Thr Trp Gln Xaa Tyr Trp Arg Glu Asn Gly
1 5 10

<210> 1031
<211> 12
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<220>
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<222> (6)..(6)
<223> Pen

<220>
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<222> (7)..(7)
<223> [Phe(4-OMe)](OMe)

<220>
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<222> (8)..(8)
<223> 2-Nal

<220>
<221> MOD_RES
<222> (9)..(9)

<223> alpha-MeOrn

<220>
<221> MOD_RES
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<223> Lys(Ac)

<400> 1031
Xaa Gln Thr Trp Gln Xaa Phe Xaa Xaa Lys Asn Gly
1 5 10

<210> 1032
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<212> PRT
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<220>
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<220>
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<223> Phe(4-OMe)

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<222> (9)..(9)
<223> alpha-MeLys

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<400> 1032
Xaa Gln Thr Trp Gln Xaa Phe Trp Lys Lys Asn Gly
1 5 10

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<211> 12
<212> PRT
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<220>
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<222> (7)..(7)
<223> Phe(4-OMe)

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<222> (9)..(9)
<223> alpha-MeLys

<220>
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<400> 1033
Xaa Gln Thr Trp Gln Xaa Phe Xaa Lys Lys Asn Gly
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<210> 1034
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<220>
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<222> (6)..(6)
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<220>
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<222> (7)..(7)
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<220>
<221> MOD_RES
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<220>
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<222> (9)..(9)
<223> alpha-MeLys

<220>
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<400> 1034
Xaa Gln Thr Trp Gln Xaa Phe Xaa Lys Lys Asn Asn
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<210> 1035
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<212> PRT
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<220>
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<220>
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<222> (2)..(2)
<223> Pen

<220>
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<222> (7)..(7)
<223> Pen

<220>
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<222> (8)..(8)
<223> Phe[4-(2-aminoethoxy)]

<220>
<221> MOD_RES
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<223> 2-Nal

<220>
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<222> (10)..(10)
<223> Aib

<220>
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<222> (11)..(11)
<223> Lys(Ac)

<400> 1035
Phe Xaa Asn Thr Trp Gln Xaa Phe Xaa Xaa Lys Asn Asn
1 5 10

<210> 1036
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
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<222> (7)..(7)
<223> Phe(4-CONH2)

<220>
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<222> (8)..(8)
<223> 2-Nal

<220>
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<222> (9)..(9)
<223> Acvc

<220>
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<222> (10)..(10)
<223> Lys(Ac)

<400> 1036
Xaa Asn Thr Trp Gln Xaa Phe Xaa Xaa Lys Asn Asn
1 5 10

<210> 1037
<211> 12
<212> PRT
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<220>
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<223> Phe(4-OMe)

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<400> 1037
Xaa Asn Thr Trp Gln Xaa Phe Xaa Xaa Lys Asn Asn
1 5 10

<210> 1038
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
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<220>
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<223> Phe(4-OMe)

<220>
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<222> (9)..(9)
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<400> 1038
Xaa Gln Thr Trp Gln Cys Phe Xaa Lys Glu Asn Gly
1 5 10

<210> 1039
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

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<223> D-Lys

<220>
<221> MOD_RES
<222> (2)..(2)
<223> Abu

<220>
<221> MOD_RES
<222> (8)..(8)

<223> Phe(4-OMe)

<220>
<221> MOD_RES
<222> (9)..(9)
<223> 2-Nal

<220>
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<222> (10)..(10)
<223> alpha-MeLeu

<400> 1039
Lys Xaa Gln Thr Trp Gln Cys Phe Xaa Leu Glu Asn Gly
1 5 10

<210> 1040
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

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<223> Abu

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Tyr(Bzl)

<220>
<221> MOD_RES
<222> (9)..(9)
<223> alpha-MeLys

<400> 1040
Xaa Gln Thr Trp Gln Cys Tyr Trp Lys Glu Asn Gly
1 5 10

<210> 1041
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
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<223> D-Arg

<220>
<221> MOD_RES
<222> (2)..(2)
<223> Abu

<220>

<221> MOD_RES
<222> (8)..(8)
<223> Phe[4-(2-aminoethoxy)]

<220>
<221> MOD_RES
<222> (9)..(9)
<223> 2-Nal

<220>
<221> MOD_RES
<222> (10)..(10)
<223> alpha-MeLys

<400> 1041
Arg Xaa Gln Thr Trp Gln Cys Phe Xaa Lys Glu Asn Asn
1 5 10

<210> 1042
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
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<222> (1)..(1)
<223> D-Gln

<220>
<221> MOD_RES
<222> (2)..(2)
<223> Abu

<220>
<221> MOD_RES
<222> (8)..(8)
<223> Phe[4-(2-aminoethoxy)]

<220>
<221> MOD_RES
<222> (9)..(9)
<223> 2-Nal

<220>
<221> MOD_RES
<222> (10)..(10)
<223> alpha-MeLys

<400> 1042
Gln Xaa Gln Thr Trp Gln Cys Phe Xaa Lys Glu Asn Asn
1 5 10

<210> 1043
<211> 12
<212> PRT
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<220>
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<220>
<221> MOD_RES
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<223> Abu

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Phe[4-(2-aminoethoxy)]

<220>
<221> MOD_RES
<222> (8)..(8)
<223> 2-Nal

<220>
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<222> (9)..(9)
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<400> 1043
Xaa Gln Thr Trp Gln Cys Phe Xaa Xaa Glu Asn Asn
1 5 10

<210> 1044
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (9)..(9)
<223> hLeu

<400> 1044
Cys Gln Thr Trp Gln Cys Tyr Trp Leu Glu Asn Gly
1 5 10

<210> 1045
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
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<220>
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<222> (15)..(15)
<223> Azt

<220>
<221> MOD_RES
<222> (16)..(16)
<223> D-Lys

<400> 1045
Cys Ala Asp Trp Val Trp Cys Tyr Trp His Thr Phe Gly Ala Xaa Lys

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<210> 1046
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
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<220>
<221> MOD_RES
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<223> Abu

<220>
<221> MOD_RES
<222> (13)..(13)
<223> (2-aminoethoxy)acetic acid

<220>
<221> MOD_RES
<222> (14)..(14)
<223> D-Lys

<400> 1046
Xaa Arg Thr Trp Gln Cys Tyr Trp Arg Lys Phe Gly Xaa Lys
1 5 10

<210> 1047
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Abu

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Phe[4-(2-aminoethoxy)]

<220>
<221> MOD_RES
<222> (8)..(8)
<223> 2-Nal

<220>
<221> MOD_RES
<222> (9)..(9)
<223> Achc

<400> 1047
Xaa Gln Thr Trp Gln Cys Phe Xaa Xaa Glu Asn Asn
1 5 10

<210> 1048
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (1)..(1)
<223> D-Phe

<220>
<221> MOD_RES
<222> (2)..(2)
<223> Pen

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Pen

<220>
<221> MOD_RES
<222> (8)..(8)
<223> Phe(4-OMe)

<220>
<221> MOD_RES
<222> (9)..(9)
<223> 2-Nal

<220>
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<222> (10)..(10)
<223> 4-amino-4-carboxy-tetrahydropyran

<220>
<221> MOD_RES
<222> (11)..(11)
<223> Cit

<400> 1048
Phe Xaa Asn Thr Trp Gln Xaa Phe Xaa Xaa Xaa Asn Asn
1 5 10

<210> 1049
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (1)..(1)
<223> D-Phe

<220>
<221> MOD_RES
<222> (2)..(2)

<223> Pen

<220>
<221> MOD_RES
<222> (7)..(7)
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<220>
<221> MOD_RES
<222> (8)..(8)
<223> Phe(4-OMe)

<220>
<221> MOD_RES
<222> (9)..(9)
<223> 2-Nal

<220>
<221> MOD_RES
<222> (10)..(10)
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<400> 1049
Phe Xaa Asn Thr Trp Gln Xaa Phe Xaa Xaa Glu Asn Asn
1 5 10

<210> 1050
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
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<222> (1)..(1)
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<220>
<221> MOD_RES
<222> (6)..(6)
<223> Pen

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Phe(CONH2)

<220>
<221> MOD_RES
<222> (8)..(8)
<223> 2-Nal

<220>
<221> MOD_RES
<222> (9)..(9)
<223> Aib

<220>
<221> MOD_RES
<222> (10)..(10)
<223> Lys(Ac)

<400> 1050

Xaa Asn Thr Trp Gln Xaa Phe Xaa Xaa Lys Asn Asn
1 5 10

<210> 1051
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1051
Cys Arg Ser Trp Gln Cys Tyr Trp Asn Lys Phe Gly Ala Asp Asp
1 5 10 15

<210> 1052
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1052
Cys His Thr Trp Gln Cys Tyr Trp Leu Asn Phe Gly Asp Glu Glu
1 5 10 15

<210> 1053
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1053
Cys Arg Thr Trp Gln Cys Tyr Trp Leu Asn Phe Gly Asn Glu Gln
1 5 10 15

<210> 1054
<211> 15
<212> PRT
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<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1054
Cys Arg Thr Trp Gln Cys Tyr Trp Ser Glu Phe Gly Thr Gly Glu
1 5 10 15

<210> 1055
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1055
Cys Arg Thr Trp Gln Cys Tyr Trp Leu Arg Leu Gly Asp Glu Gly
1 5 10 15

<210> 1056
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1056
Cys His Thr Trp Gln Cys Tyr Trp Ser Thr Leu Gly Pro Glu Ala
1 5 10 15

<210> 1057
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1057
Cys Ser Thr Trp Gln Cys Tyr Trp Ser Lys Gln Ser Gly Gly Ser
1 5 10 15

<210> 1058
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1058
Cys His Thr Trp Gln Cys Tyr Trp Leu Asn Asn Gly Thr Ser Gln
1 5 10 15

<210> 1059
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1059
Cys His Thr Trp Gln Cys Tyr Trp Arg Ala Asn Asp Gly Arg Asp
1 5 10 15

<210> 1060
<211> 14
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 1060
Ser Gly Cys Arg Thr Trp Gln Cys Tyr Trp His Glu Phe Gly
1 5 10

<210> 1061
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1061
Asn Lys Cys Arg Thr Trp Gln Cys Tyr Trp His Glu Tyr Gly
1 5 10

<210> 1062
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1062
Ser Gly Cys Arg Thr Trp Glu Cys Tyr Trp His Glu Tyr Gly
1 5 10

<210> 1063
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1063
Asp Ala Cys Arg Thr Trp Glu Cys Tyr Trp His Lys Phe Gly
1 5 10

<210> 1064
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1064
Pro Glu Cys Arg Thr Trp Glu Cys Tyr Trp His Lys Phe Gly
1 5 10

<210> 1065
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1065
Gln Val Cys Gln Thr Trp Glu Cys Tyr Trp Arg Glu Phe Gly
1 5 10

<210> 1066
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1066
Asp Arg Cys Val Thr Trp Glu Cys Tyr Trp Arg Glu Phe Gly
1 5 10

<210> 1067
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1067
Ala Asp Gln Cys Arg Thr Trp Gln Cys Tyr Trp His Glu Phe Gly
1 5 10 15

<210> 1068
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1068
Lys Glu Asn Cys Arg Thr Trp Glu Cys Tyr Trp Arg Glu Phe Gly
1 5 10 15

<210> 1069
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1069
Val Gln Glu Cys Ser Thr Trp Gln Cys Tyr Trp Arg Thr Phe Gly
1 5 10 15

<210> 1070
<211> 15

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1070
Gly Glu Glu Cys Ser Thr Trp Gln Cys Tyr Trp Arg Lys Phe Gly
1 5 10 15

<210> 1071
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1071
Asp Gly Ser Cys Arg Thr Trp Gln Cys Tyr Trp His Gln Phe Gly
1 5 10 15

<210> 1072
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1072
Asn Ala Asp Cys His Ser Trp Glu Cys Tyr Trp Arg Glu Phe Gly
1 5 10 15

<210> 1073
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1073
Glu Arg Asn Cys Ser Thr Trp Glu Cys Tyr Trp Arg Ala Phe Gly
1 5 10 15

<210> 1074
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1074
Arg Val Gly Cys Ser Thr Trp Glu Cys Tyr Trp Arg Glu Phe Gly
1 5 10 15

<210> 1075
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1075
Lys Ala Asn Cys Arg Thr Trp Gln Cys Tyr Trp Arg Lys Phe Glu
1 5 10 15

<210> 1076
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1076
Tyr Glu Asp Cys Arg Thr Trp Gln Cys Tyr Trp Glu Asn Phe Gly
1 5 10 15

<210> 1077
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1077
Cys Gln Thr Trp Gln Cys Tyr Trp Arg Asn Phe Gly Asp Ser
1 5 10

<210> 1078
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1078
Cys Gln Thr Trp Gln Cys Tyr Trp Arg Asn Phe Glu Ser Gly
1 5 10

<210> 1079
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1079
Cys Gln Asp Trp Gln Cys Tyr Trp Arg Glu Phe Gly Pro Gly
1 5 10

<210> 1080
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1080
Cys Gln Asp Trp Gln Cys Tyr Trp Arg Ser Phe Gly Pro Gln
1 5 10

<210> 1081
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1081
Cys Gln Thr Trp Gln Cys Tyr Trp Arg Thr Leu Gly Pro Ser
1 5 10

<210> 1082
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1082
Cys Arg Thr Trp Gln Cys Tyr Trp Gln Asn Phe Gly
1 5 10

<210> 1083
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1083
Cys Gly Thr Trp Gln Cys Tyr Trp Arg Thr Phe Gly Pro Ser
1 5 10

<210> 1084
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1084

Cys Ser Thr Trp Gln Cys Tyr Trp His Lys Phe Gly Asn Glu
1 5 10

<210> 1085
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1085
Cys Arg Thr Trp Glu Cys Tyr Trp Arg Thr Tyr Gly Pro Ser
1 5 10

<210> 1086
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1086
Cys Arg Thr Trp Gln Cys Tyr Trp Trp Glu Asn Ser Gln Met
1 5 10

<210> 1087
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1087
Cys Gln Thr Trp Gln Cys Tyr Trp Arg Glu Phe Gly Gly Gly
1 5 10

<210> 1088
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1088
Cys Gln Thr Trp Gln Cys Tyr Trp Arg Thr His Gly Asp Arg
1 5 10

<210> 1089
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1089
Cys Arg Asp Trp Gln Cys Tyr Trp Leu Ser Arg Pro
1 5 10

<210> 1090
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (9)..(9)
<223> Lys(Palm)

<400> 1090
Cys Gln Thr Trp Gln Cys Tyr Trp Lys Glu Asn Gly
1 5 10

<210> 1091
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (9)..(9)
<223> Lys(PEG8)

<400> 1091
Cys Gln Thr Trp Gln Cys Tyr Trp Lys Glu Asn Gly
1 5 10

<210> 1092
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (9)..(9)
<223> hLeu

<400> 1092
Cys Gln Thr Trp Gln Cys Tyr Trp Leu Glu Gln Gly
1 5 10

<210> 1093
<211> 12

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (7)..(7)
<223> D-Tyr

<220>
<221> MOD_RES
<222> (9)..(9)
<223> hLeu

<400> 1093
Cys Gln Thr Trp Gln Cys Tyr Trp Leu Glu Asn Gly
1 5 10

<210> 1094
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (7)..(7)
<223> N-MeTyr

<220>
<221> MOD_RES
<222> (9)..(9)
<223> hLeu

<400> 1094
Cys Gln Thr Trp Gln Cys Tyr Trp Leu Glu Asn Gly
1 5 10

<210> 1095
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Tic-OH

<220>
<221> MOD_RES
<222> (9)..(9)
<223> hLeu

<400> 1095
Cys Gln Thr Trp Gln Cys Xaa Trp Leu Glu Asn Gly
1 5 10

<210> 1096
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (9)..(9)
<223> hLeu

<400> 1096
Cys Gln Thr Trp Gln Cys Glu Trp Leu Glu Asn Gly
1 5 10

<210> 1097
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (9)..(9)
<223> hLeu

<400> 1097
Cys Gln Thr Trp Gln Cys Thr Trp Leu Glu Asn Gly
1 5 10

<210> 1098
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Cha

<220>
<221> MOD_RES
<222> (9)..(9)
<223> hLeu

<400> 1098
Cys Gln Thr Trp Gln Cys Xaa Trp Leu Glu Asn Gly
1 5 10

<210> 1099
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (9)..(9)
<223> alpha-MeLeu

<400> 1099
Cys Gln Thr Trp Gln Cys Tyr Trp Leu Glu Asn Gly
1 5 10

<210> 1100
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (9)..(9)
<223> D-Leu

<400> 1100
Cys Gln Thr Trp Gln Cys Tyr Trp Leu Glu Asn Gly
1 5 10

<210> 1101
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (9)..(9)
<223> hLeu

<220>
<221> MOD_RES
<222> (13)..(13)
<223> D-Lys

<400> 1101
Cys Gln Thr Trp Gln Cys Tyr Trp Leu Glu Asn Gly Lys
1 5 10

<210> 1102

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

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (9)..(9)
<223> hLeu

<400> 1102
Cys Gln Thr Trp Gln Cys Tyr Trp Leu Glu Asn Gly
1 5 10

<210> 1103
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (9)..(9)
<223> hLeu

<400> 1103
Cys Gln Thr Trp Gln Cys Tyr Trp Leu Glu Asn Glu
1 5 10

<210> 1104
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (9)..(9)
<223> hLeu

<400> 1104
Cys Gln Thr Trp Gln Cys Tyr Trp Leu Glu Asn Arg
1 5 10

<210> 1105
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (9)..(9)
<223> hLeu

<400> 1105
Cys Gln Thr Trp Gln Cys Tyr Trp Leu Glu Asn Phe
1 5 10

<210> 1106
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (9)..(9)
<223> hLeu

<400> 1106
Cys Gln Thr Trp Gln Cys Tyr Trp Leu Glu Asn Pro
1 5 10

<210> 1107
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (9)..(9)
<223> hLeu

<400> 1107
Cys Gln Thr Trp Gln Cys Tyr Trp Leu Glu Asn Gln
1 5 10

<210> 1108
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (9)..(9)
<223> hLeu

<400> 1108
Cys Gln Thr Trp Gln Cys Tyr Trp Leu Glu Asn Leu

2821483_1
1 5 10

<210> 1109
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (9)..(9)
<223> hLeu

<400> 1109
Cys Gln Thr Trp Gln Cys Tyr Trp Leu Glu Glu Gly
1 5 10

<210> 1110
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (9)..(9)
<223> hLeu

<400> 1110
Cys Gln Thr Trp Gln Cys Tyr Trp Leu Glu Arg Gly
1 5 10

<210> 1111
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (1)..(3)
<223> Any amino acid or absent

<220>
<221> MOD_RES
<222> (4)..(4)
<223> 2-allylglycine, 2-(3'-butenyl)glycine, 2-(4'-pentenyl)glycine, or 2-(5'-hexenyl)glycine

<220>
<221> MOD_RES
<222> (5)..(5)
<223> Ala, Arg, Sarc, alpha-MeOrn, alpha-MeSer, Cit, Dap, Dab,

Dap(Ac), Gly, Lys, Asn, N-MeGln, N-MeArg, Orn or Gln

<220>
<221> MOD_RES
<222> (6)..(6)
<223> Asp, Thr or Asn

<220>
<221> MOD_RES
<222> (8)..(8)
<223> Val, Gln or Glu

<220>
<221> MOD_RES
<222> (9)..(9)
<223> 2-allylglycine, 2-(3'-butenyl)glycine, 2-(4'-pentenyl)glycine or 2-(5'-hexenyl)glycine

<220>
<221> MOD_RES
<222> (11)..(11)
<223> Trp, 1-Nal, 2-Nal, Phe(3,4-OMe2) 5-Hydroxy-Trp, Phe(3,4-Cl2) or Tyr(3-t-Bu)

<220>
<221> MOD_RES
<222> (13)..(13)
<223> Thr, Sarc, Glu, Phe, Arg, Leu, Lys, Beta-hAla, Val, Aib, Lys(Ac), Cit, Asp, Dab, Dap, Glu, hArg, Lys, Asn, Orn or Gln

<220>
<221> MOD_RES
<222> (15)..(15)
<223> Gly, Ser, Thr, Gln, Ala, Sarc, Beta-Ala, Glu, Arg or Asn

<220>
<221> MOD_RES
<222> (16)..(20)
<223> Any amino acid or absent

<400> 1111
Xaa Xaa Xaa Gly Xaa Xaa Trp Xaa Gly Tyr Xaa His Xaa Phe Xaa Xaa
1 5 10 15

Xaa Xaa Xaa Xaa
20

<210> 1112
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (1)..(3)
<223> Any amino acid or absent

<220>
<221> MOD_RES
<222> (5)..(5)

<223> Ala, Arg, Glu, Phe, Leu, Thr, Ser, Aib, Sarc, alpha-MeOrn, alpha-MeSer, Cit, Dap, Dab, Dap(Ac), Gly, Lys, Asn, N-MeGln, N-MeArg, Orn or Gln

<220>
<221> MOD_RES
<222> (6)..(6)
<223> Asp, Thr, Asn or Phe

<220>
<221> MOD_RES
<222> (8)..(8)
<223> Val, Gln, Glu or Lys

<220>
<221> MOD_RES
<222> (11)..(11)
<223> Trp, 1-Nal, 2-Nal, Phe(3,4-OMe2), 5-Hydroxy-Trp, Phe(3,4-Cl2) or Tyr(3-t-Bu)

<220>
<221> MOD_RES
<222> (13)..(13)
<223> Thr, Sarc, Glu, Phe, Arg, Leu, Lys, Beta-hAla, Val, Aib, Lys(Ac), Cit, Asp, Dab, Dap, Glu, hArg, Lys, Asn, Orn, Gln or absent

<220>
<221> MOD_RES
<222> (14)..(14)
<223> Phe, Tyr, Asn, Arg, Gln, Lys(Ac), His, Dap(Ac), Dab(Ac), Asp or absent

<220>
<221> MOD_RES
<222> (15)..(15)
<223> Gly, Ser, Thr, Gln, Ala, Sarc, beta-Ala, Glu, Arg, Asn or absent

<220>
<221> MOD_RES
<222> (16)..(20)
<223> Any amino acid or absent

<400> 1112
Xaa Xaa Xaa Cys Xaa Xaa Trp Xaa Cys Tyr Xaa His Xaa Xaa Xaa Xaa
1 5 10 15

Xaa Xaa Xaa Xaa
20

<210> 1113
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (1)..(3)
<223> Any amino acid or absent

<220>
<221> MOD_RES
<222> (5)..(5)
<223> Ala, Arg, Sarc, alpha-MeOrn, alpha-MeSer, Cit, Dap, Dab, Dap(Ac), Gly, Lys, Asn, N-MeGln, N-MeArg, Orn or Gln

<220>
<221> MOD_RES
<222> (6)..(6)
<223> Asp, Thr or Asn

<220>
<221> MOD_RES
<222> (8)..(8)
<223> Val, Gln or Glu

<220>
<221> MOD_RES
<222> (11)..(11)
<223> Trp, 1-Nal, 2-Nal, Phe(3,4-OMe2), 5-Hydroxy-Trp, Phe(3,4-Cl2) or Tyr(3-t-Bu)

<220>
<221> MOD_RES
<222> (13)..(13)
<223> Thr, Sarc, Glu, Phe, Arg, Leu, Lys, beta-hAla, Val, Aib, Lys(Ac), Cit, Asp, Dab, Dap, Glu, hArg, Lys, Asn, Orn, Gln or absent

<220>
<221> MOD_RES
<222> (15)..(15)
<223> Gly, Ser, Thr, Gln, Ala, Sarc, beta-Ala, Glu, Arg, Asn or absent

<220>
<221> MOD_RES
<222> (16)..(20)
<223> Any amino acid or absent

<400> 1113
Xaa Xaa Xaa Cys Xaa Xaa Trp Xaa Cys Tyr Xaa His Xaa Phe Xaa Xaa
1 5 10 15

Xaa Xaa Xaa Xaa
20

<210> 1114
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (1)..(3)
<223> Any amino acid or absent

<220>
<221> MOD_RES
<222> (5)..(6)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (8)..(8)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (10)..(10)
<223> Tyr, 1-Nal, 2-Nal, Phe(3,4-F2), Phe(3,4-Cl2), Phe(3-Me),
Phe[4-(2-aminoethoxy)], Phe[4-(2-(acetyl-aminoethoxy)],
Phe(4-Br), Phe(4-CONH2), Phe(4-Cl), Phe(4-CN),
Phe(4-guanidino) Phe(4-Me), Phe(4-NH2), Phe(4-N3),

<220>
<221> MOD_RES
<222> (10)..(10)
<223> continued from above; Phe(4-OMe) or Phe(4-OBzl)

<220>
<221> MOD_RES
<222> (11)..(11)
<223> Trp, 1-Nal, Phe(3,4-OMe2), 5-Hydroxy-Trp, Phe(3,4-Cl2) or
Tyr(3-t-Bu)

<220>
<221> MOD_RES
<222> (12)..(12)
<223> Arg, Lys, His, hArg, Cit, Orn, 1-Nal, D-Ala, D-Leu, D-Phe,
D-Asn, D-Asp, Agp, Leu, Beta-hLeu, Aib, Beta-hAla, Beta-hVal,
Beta-hArg, hLeu, Dap, 4-amino-4-carboxy-tetrahydropyran, Achc,
Acpc, Acbc, Acvc, Agp, Aib, alpha-DiethylGly, alpha-MeLys,

<220>
<221> MOD_RES
<222> (12)..(12)
<223> continued from above; alpha-MeLys(Ac), alpha-Me-Leu,
alpha-MeOrn, alpha-MeSer, alpha-MeVal, Cha, Cit, Cpa,
D-Asn, Glu, hArg or Lys

<220>
<221> MOD_RES
<222> (13)..(13)
<223> Cha, Ogl, Aib, Leu, Val, Dab, Glu, Lys, Beta-hLeu, Beta-hAla,
Beta-hVal, Beta-Glu, Lys(Ac), Cit, Asp, Dab, Dap, Glu, hArg,
Lys, Asn, Orn, Lys(Ac) or Gln

<220>
<221> MOD_RES
<222> (14)..(14)
<223> Phe, Tic, Asn, Tyr, Asn, Arg, Gln, Lys(Ac), His, Dap(Ac),
Dab(Ac) or Asp

<220>
<221> MOD_RES
<222> (16)..(16)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (17)..(17)
<223> D-Lys

<220>
<221> MOD_RES
<222> (18)..(19)
<223> Any amino acid or absent

<400> 1114
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1 5 10 15

Lys Xaa Xaa