NOVEL α4β7 PEPTIDE DIMER ANTAGONISTS

FIELD OF THE INVENTION

[0001] The present invention relates to novel compounds having activity useful for treating conditions which arise or are exacerbated by integrin binding, pharmaceutical compositions comprising the compounds, methods of treatment using the compounds, and methods of blocking or disrupting integrin binding.

BACKGROUND OF THE INVENTION

[0002] Integrins are noncovalently associated α/β heterodimeric cell surface receptors involved in numerous cellular processes ranging from cell adhesion and migration to gene regulation (Dubree, et al., Selective α4β7 Integrin Antagonist and Their Potential as Anti-inflammatory Agents, *J. Med. Chem.* 2002, 45, 3451-3457). Differential expression of integrins can regulate a cell's adhesive properties, allowing different leukocyte populations to be recruited to specific organs in response to different inflammatory signals. If left unchecked, integrins-mediated adhesion process can lead to chronic inflammation and autoimmune disease.

[0003] The α4 integrins, α4β1 and α4β7, play essential roles in lymphocyte migration throughout the gastrointestinal tract. They are expressed on most leukocytes, including B and T lymphocytes, where they mediate cell adhesion via binding to their respective primary ligands, vascular cell adhesion molecule (VCAM), and mucosal addressin cell adhesion molecule (MAdCAM), respectively. The proteins differ in binding specificity in that VCAM binds both α4β1 and to a lesser extent α4β7, while MAdCAM is highly specific for α4β7.In addition to pairing with the α4 subunit, the β7 subunit also forms a heterodimeric complex with αE subunit to form αEβ7, which is primarily expressed on intraepithelial lymphocytes (IEL) in the intestine, lung and genitourinary tract. αEβ7 is also expressed on dendritic cells in the gut. The αEβ7 heterodimer binds to E-cadherin on the epithelial cells. The IEL cells are thought to provide a mechanism for immune surveillance within the epithelial compartment. Therefore, blocking αEβ7 and α4β7 together may be a useful method for treating inflammatory conditions of the intestine

[0004] Inhibitors of specific integrins-ligand interactions have been shown effective as anti-inflammatory agents for the treatment of various autoimmune diseases. For example, monoclonal antibodies displaying high binding affinity for α4β7 have displayed therapeutic benefits for gastrointestinal auto-inflammatory/autoimmune diseases, such as Crohn's

disease, and ulcerative colitis. *Id.* However, these therapies interfered with α4β1 integrin-ligand interactions thereby resulting in dangerous side effects to the patient. Therapies utilizing small molecule antagonists have shown similar side effects in animal models, thereby preventing further development of these techniques.

[0005] Accordingly, there is a need in the art for an integrin antagonist molecule having high affinity for the α4β7 integrin and high selectivity against the α4β1 integrin, as a therapy for various gastrointestinal autoimmune diseases.

[0006] Such an integrin antagonist molecule is disclosed herein.

SUMMARY OF THE INVENTION

[0007] The present invention has been developed in response to the present state of the art, and in particular, in response to the problems and needs in the art that have not yet been fully solved by currently available integrin antagonists that are selective for α4β7. Thus, the present invention provides α4β7 antagonist dimer peptides for use as anti-inflammatory and/or immunosuppressive agents. Further, the present invention provides α4β7 antagonist dimer peptide for use in treating a condition that is associated with a biological function of α4β7 to tissues expressing MAdCAM.

[0008] The invention relates to a novel class of peptidic compounds exhibiting integrin antagonist activity. The present invention further relates to a novel class of peptidic compounds exhibiting high specificity for α4β7 integrin. Compounds of the present invention comprise two paired subunits that are linked together by their C- or N-terminus via a linking moiety. Each subunit of the present invention further comprises two natural or unnatural amino acids that are capable of bridging to form a cyclized structure. Thus, the compounds of the present invention comprise dimerized peptides, each subunit of the dimer forming a cyclized structure through at least one of a disulfide salt bridge, an amide bond, or an equivalent connection. This feature provides increased stability to the compound when administered orally as a therapeutic agent. This feature further provides for increased specificity and potency as compared to non-cyclized analogs.

[0009] In one aspect, the present invention provides a dimer compound comprising two linked subunits of Formula (I):

$$Xaa^{1}\text{-}Xaa^{2}\text{-}Xaa^{3}\text{-}Xaa^{4}\text{-}Xaa^{5}\text{-}Xaa^{6}\text{-}Xaa^{7}\text{-}Xaa^{8}\text{-}Xaa^{9}\text{-}Xaa^{10}\text{-}Xaa^{11}\text{-}Xaa^{12}\text{-}Xaa^{13}\text{-}Xaa^{14}$$

(SEQ ID NO:1), or a pharmaceutically acceptable salt thereof, wherein each subunit comprises a disulfide or lactam bond between Xaa^{4} and Xaa^{10}, and further wherein Formula (I) represents a monomer subunit of a dimer molecule, wherein the monomer subunits are

linked to form a dimer molecule in accordance with the present invention, and wherein Xaa^1 is absent, or Xaa^1 is selected from the group consisting of hydrogen, Gln, Asp, Pro, Gly, His, Ala, Ile, Phe, Lys, Arg, Asn, Glu, Leu, Val, Tyr, Ser, Trp, Met, Thr, suitable isostere, and corresponding D-amino acids. Xaa^2 is absent, or Xaa^2 is selected from the group consisting of Gln, Asp, Pro, Gly, His, Ala, Ile, Phe, Lys, Arg, Asn, Glu, Leu, Val, Tyr, Trp , Met, Thr, a suitable isostere and corresponding D-amino acids. Xaa^3 is absent, or Xaa^3 is selected from the group consisting of an Gln, Asp, Pro, Gly, His, Ala, Ile, Phe, Lys, Arg, Asn, Glu, Leu, Val, Tyr, Trp , Met, Ser and Thr, a suitable isostere and corresponding D-amino acids.

[0010] Xaa^4 is selected from the group consisting of Cys, Pen, Asp, Glu, HGlu, β-Asp, β-Glu, Lys, HLys, Orn, Dap, Dab, a suitable isostere and corresponding D-amino acids. Xaa^5 is selected from the group consisting of Gln, Asp, Pro, Gly, His, Ala, Ile, Phe, Lys, Arg, Asn, Glu, Leu, Val, Tyr, Trp, Met, Thr, HArg, Dap, Dab, N(alpha)Me-Arg, Arg-Me-sym, Arg-Me-asym, 4-Guan, Cit, Cav, and suitable isostere replacements. Xaa^6 is selected from the group consisting of Ser, Gln, Asn, Asp, Pro, Gly, His, Ala, Ile, Phe, Lys, Arg, Glu, Leu, Val, Tyr, Trp, Met, and suitable isostere replacements. Xaa^7 is selected from the group consisting of Asp, N-Me-Asp and a suitable isostere replacement for Asp. Xaa^8 is selected from the group consisting of Thr, Gln, Ser, Asp, Pro, Gly, His, Ala, Ile, Phe, Lys, Arg, Asn, Glu, Val, Tyr, Trp, Leu, Met, and N-Methyl amino acids including N-Me-Thr. Xaa^9 is selected from the group consisting of Gln, Asn, Asp, Pro, Gly, Ala, Phe, Leu, Glu, Ile, Val, HLeu, n-Butyl Ala, n-Pentyl Ala, n-Hexyl Ala, Nle, cyclobutyl-Ala, HCha, N-Me-Leu, and suitable isostere replacements. Xaa^{10} is selected from the group consisting of Cys, Asp, Lys, Glu, Pen, HAsp, HGlu, HLys, Orn, β-Asp, β-Glu, Dap, and Dab. Xaa^{11} is selected from the group consisting of Gly, Gln, Asn, Asp, Ala, Ile, Leu, Val, Met, Thr, Lys, Trp, Tyr, His, Glu, Ser, Arg, Pro, Phe, Sar, 1-Nal, 2-Nal, HPhe, Phe(4-F), O-Me-Tyr, dihydro-Trp, Dap, Dab, Dab(Ac), Orn, D-Orn, N-Me-Orn, N-Me-Dap, D-Dap, D-Dab, Bip, Ala(3,3diphenyl), Biphenyl-Ala, aromatic ring substituted Phe, aromatic ring substituted Trp, aromatic ring substituted His, hetero aromatic amino acids, N-Me-Lys, N-Me-Lys(Ac), 4-Me-Phe, and corresponding D-amino acids and suitable isostere replacements.

[0011] In some embodiments, Xaa^{12} is absent, or Xaa^{12} is selected from the group consisting of Glu, Amide, Lys, COOH, $CONH_2$, Gln, Pro, Gly, His, Ala, Ile, Phe, Lys, Arg, Leu, Val, Tyr, Trp, Met, Gla, Ser, Asn, D-Glu, β-HGlu, 2-Nal, 1-Nal, D-Asp, Bip, β-HPhe, β-Glu, D-Tyr, D-Lys, Dap, Dab, Orn, D-Orn, N-Me-Orn, N-Me-Dap, N-Me-Dab, N-Me Lys, D-Dap, D-Dab, suitable isosteres, and corresponding D-amino acids. Xaa^{13} may be absent, or

Xaa^{13} is selected from the group consisting of Gln, Pro, Gly, His, Ala, Ile, Phe, Lys, Arg, Leu, Val, Tyr, Trp, Met, Glu, Ser, Asn, Gla, Dap, Dab, Orn, D-Orn, D-Lys, N-Me-Orn, N-Me-Dap, N-Me-Dab, N-Me-Lys, D-Dap, D-Dab, COOH, $CONH_2$, suitable isosteres, and corresponding D-amino acids. Further, in some embodiments Xaa^{14} is absent, or Xaa^{14} is selected from the group consisting of natural amino acids, suitable isostere replacements, corresponding D-amino acids, and corresponding N-Methyl amino acids.

[0012] For some embodiments, Xaa^{1}-Xaa^{5}, Xaa^{7}-Xaa^{9}, and Xaa^{11}-Xaa^{12} are N(alpha)Methylated. Xaa^{5} may further be Arg-Me-sym or Arg-Me-asym, and Xaa^{11} may be O-Me-Tyr, N-Me-Lys(Ac), or 4-Me-Phe. In some instances, Xaa^{1}-Xaa^{4}, and Xaa^{11}-Xaa^{14} are acylated. For example, in some instances one or more residues at positions Xaa^{1}-Xaa^{4}, and Xaa^{11}-Xaa^{14} are acylated with an acylating organic compound selected from the group consisting of 2-me-Trifluorobutyl, Trifluoropentyl, Acetyl, Octonyl, Butyl, Pentyl, Hexyl, Palmityl, Trifluoromethyl butyric, cyclopentane carboxylic, cyclopropylacetic, 4-fluorobenzoic, 4-fluorophenyl acetic, 3-Phenylpropionic, tetrahedro-2H-pyran-4carboxylic, succinic acid, and glutaric acid.

[0013] In some embodiments Xaa^{1}, Xaa^{2}, Xaa^{3}, Xaa^{12}, Xaa^{13} or Xaa^{14} are modified with a suitable linker moiety to form a homo- or hetero-dimer molecule, wherein Formula (I) comprises a dimer formed from two subunits joined by a suitable C- or N-terminal linker selected from the group consisting of DIG, DIG-OH, PEG13, PEG25, PEG1K, PEG2K, PEG3.4K, PEG4K, PEG5K, IDA, IDA-Palm, IDA-Boc, IDA-Ac, IDA-Isovaleric acid, Triazine, Triazine-Boc, Isophthalic acid, 1,3-phenylenediacetic acid, 1,4-phenylenediacetic acid, cyclopropylacetic acid, 4-fluoorobenzoic acid, 4-fluorophenylacetic acid, 3-phenylpropionic acid, succinic acid, biotin, glutaric acid, Azelaic acid, Pimelic acid, Dodecanedioic acid, suitable aliphatics, suitable aromatics, heteroaromatics, and polyethylene glycols having a molecular weight from approximately 400Da to approximately 40,000Da.

[0014] One having skill in the art will appreciate that the C- and N-terminal linker moieties disclosed herein are non-limiting examples of suitable, and that the present invention may include any suitable linker moiety. Thus, some embodiments of the present invention comprises a homo- or heterodimer molecule comprised of two monomer subunits selected from the peptide molecules represented by SEQ ID NOs: 1-146, wherein the C- or N-termini of the respective monomers are linked by any suitable linker moiety to provide a dimer molecule having integrin antagonist activity.

[0015] In another aspect, the present invention provides a composition for treating a patient in need of integrin-antagonist therapy comprising a compound of Formula (I) in combination with a pharmaceutically acceptable carrier.

[0016] Yet another aspect of the present invention provides a composition for treating a patient in need of α4β7-specific antagonist therapy comprising a compound of Formula (I) having high selectivity for α4β7 integrin in combination with a pharmaceutically acceptable carrier.

[0017] Yet another aspect of the present invention provides a composition for treating a patient in need of α4β7 -specific antagonist therapy comprising a compound of Formula (I) having high selectivity for α4β7 against α4β1 integrins in combination with a pharmaceutically acceptable carrier.

[0018] Yet another aspect of the present invention provides a composition for treating a patient in need of α4β7 -specific antagonist therapy comprising a compound of Formula (I) having high selectivity for α4β7 against αEβ7 integrins in combination with a pharmaceutically acceptable carrier.

[0019] Yet another aspect of the present invention provides a composition for treating a patient in need of α4β7 -specific antagonist therapy comprising a compound of Formula (I) having low selectivity for α4β7 against αEβ7 integrins in combination with a pharmaceutically acceptable carrier.

[0020] Yet another aspect of the present invention provides a method for treating a patient in need of integrin-antagonist therapy comprising administering to the patient a therapeutically effective amount of a compound of Formula (I).

[0021] Still, yet another aspect of the present invention provides a composition for the treatment of a disease from ulcerative colitis, Crohn's disease, Celiac disease (nontropical Sprue), enteropathy associated with seronegative arthropathies, microscopic or 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, or pouchitis resulting after proctocolectomy and ileoanal anastomosis, and various forms of gastrointestinal cancer. In another embodiment, the condition is pancreatitis, insulin-dependent diabetes mellitus, mastitis, cholecystitis, cholangitis, pericholangitis, chronic bronchitis, chronic sinusitis, asthma or graft versus host disease. In addition, these compounds may be useful in the

prevention or reversal of these diseases when used in combination with currently available therapies, medical procedures, and therapeutic agents.

[0022] In yet another aspect, the present invention provides a diagnostic method for visualizing and diagnosing a disease comprising administering an orally stable compound of Formula (I) that is further labeled with at least one of a chelating group and a detectable label for use as an *in vivo* imaging agent for non-invasive diagnostic procedures.

BRIEF DESCRIPTION OF THE DRAWINGS

[0023] In order that the manner in which the above-recited and other features and advantages of the invention are obtained will be readily understood, a more particular description of the invention briefly described above will be rendered by reference to specific embodiments thereof which are illustrated in the appended drawings. Understanding that these drawings depict only typical embodiments of the invention and are not therefore to be considered to be limiting of its scope, the invention will be described and explained with additional specificity and detail through the use of the accompanying drawings in which:

[0024] Figure 1 is a schematic showing C and N-terminal dimerizations.

[0025] Figure 2 is a schematic showing a pair of integrin antagonist monomer subunits according to SEQ ID NO: 47, wherein the subunits are aligned and linked at their respective C-termini by a DIG linker in accordance with a representative embodiment of the present invention.

[0026] Figure 3 is a chart demonstrating stability data for integrin antagonist homodimer molecules represented by SEQ ID NOs: 46, 55, 74 and 93 in accordance with various representative embodiment of the present invention.

[0027] Figure 4 is a chart demonstrating potency and selectivity for integrin antagonist monomer and homodimer molecules represented by SEQ ID NOs: 51, 43. 48, 47, 50, and 94 in accordance with a representative selection of various embodiments of the present invention.

SEQUENCE LISTING

[0028] The amino acid sequences listed in the accompanying sequence listing are shown using three letter code for amino acids, as defined in 37 C.F.R. 1.822. Only the monomer subunit sequences are shown, however it is understood that the monomer subunits are dimerized to form peptide dimer molecules, in accordance with the present teaching and as shown generally in Figures 1 and 2. The monomer subunits are dimerized by a suitable linker moiety, as defined herein. Some of the monomer subunits are shown having C- and N-

termini that both comprise free amine. Thus, a user must modify the monomer subunit to eliminate either the C- or N-terminal free amine, thereby permitting dimerization at the remaining free amine. Further, in some instances a terminal end of one or more monomer subunits is acylated with an acylating organic compound selected from the group consisting of 2-me-Trifluorobutyl, Trifluoropentyl, Acetyl, Octonyl, Butyl, Pentyl, Hexyl, Palmityl, Trifluoromethyl butyric, cyclopentane carboxylic, cyclopropylacetic, 4-fluorobenzoic, 4-fluorophenyl acetic, 3-Phenylpropionic, tetrahedro-2H-pyran-4carboxylic, succinic acid, and glutaric acid. In some instances, monomer subunits comprise both a free carboxy terminal and a free amino terminal, whereby a user may selectively modify the subunit to achieve dimerization at a desired terminus. One having skill in the art will therefore appreciate that the monomer subunits of the instant invention may be selectively modified to achieve a single, specific amine for a desired dimerization.

[0029] It is further understood that the C-terminal residues of the monomer subunits disclosed herein are amides, unless otherwise indicated. Further, it is understood that dimerization at the C-terminal is facilitated by using a suitable amino acid with a side chain having amine functionality, as is generally understood in the art. Regarding the N-terminal residues, it is generally understood that dimerization may be achieved through the free amine of the terminal residue, or may be achieved by using a suitable amino acid side chain having a free amine, as is generally understood in the art.

[0030] In the accompanying sequence listing:

[0031] SEQ ID NO: 1 shows a monomer subunit of a dimer compound of Formula (I).

[0032] SEQ ID NO: 2 shows a monomer subunit of a dimer compound of Formula (II).

[0033] SEQ ID NOs: 1-38, 46-52, 54-135, and 137-146 show amino acid sequences of monomer subunits that are dimerized to form various dimer compounds in accordance with the present invention, wherein these sequences have been substituted with an N(alpha)methylated arginine.

[0034] SEQ ID NO: 136 shows an amino acid sequence of a monomer subunit that is dimerized to form a dimer compound in accordance with the present invention, wherein this sequence has been substituted with an N(alpha)methylated lysine.

[0035] SEQ ID NOs: 1-38 are general sequences that may be dimerized at their respective C- or N-termini to form various dimer compounds in accordance with the present invention.

[0036] SEQ ID NOs: 39-45, 47, 48, 51-58, 61, 63, 65-86, 88-97, and 102-146 show amino acid sequences of monomer subunits that may be dimerized at their respective C-termini to form various dimer compounds in accordance with the present invention. Generally, these amino acid sequences are acylated at their N-termini prior to dimerization using one of the acylating organic compounds and methods disclosed herein, including but not limited to cyclopropylacetic acid, 4-Fluorobenzoic acid, 4-fluorophenylacetic acid, 3-Phenylpropionic acid, Succinic acid, Glutaric acid, Cyclopentane carboxylic acid, 3,3,3-trifluoropropeonic acid, 3-Fluoromethylbutyric acid, Tetrahedro-2H-Pyran-4-carboxylic acid.

[0037] SEQ ID NOs: 46, 49, 50, 59, 60, 62, 64, 87, and 98-101 102-103, 113 -119 show amino acid sequences of monomer subunits that may be dimerized at their respective N-termini to form various dimer compounds in accordance with the present invention.

DETAILED DESCRIPTION OF THE PREFERRED EMBODIMENTS

[0038] As used herein, the singular forms "a," "and" and "the" include plural references unless the context clearly dictates otherwise.

[0039] As used in the present specification the following terms have the meanings indicated:

[0040] The term "peptide," as used herein, refers broadly to a sequence of two or more amino acids joined together by peptide bonds. It should be understood that this term does not connote a specific length of a polymer of amino acids, nor is it intended to imply or distinguish whether the polypeptide is produced using recombinant techniques, chemical or enzymatic synthesis, or is naturally occurring.

[0041] The term "DRP," as used herein, refers to disulfide rich peptides.

[0042] The term "dimer," as used herein, refers broadly to a peptide comprising two or more subunits, wherein the subunits are DRPs that are linked at their C- or N-termini. Dimers of the present invention may include homodimers and heterodimers and function as integrin antagonists.

[0043] The term "L-amino acid," as used herein, refers to the "L" isomeric form of a peptide, and conversely the term "D-amino acid" refers to the "D" isomeric form of a peptide. The amino acid residues described herein are preferred to be in the "L" isomeric

form, however, residues in the "D" isomeric form can be substituted for any L-amino acid residue, as long as the desired functional is retained by the peptide.

[0044] The term "NH2," as used herein, refers to the free amino group present at the amino terminus of a polypeptide. The term "OH," as used herein, refers to the free carboxy group present at the carboxy terminus of a peptide. Further, the term "Ac," as used herein, refers to Acetyl protection through acylation of the C- or N-terminus of a polypeptide.

[0045] The term "carboxy," as used herein, refers to $-CO_2H$.

[0046] The term "isostere replacement," as used herein, refers to any amino acid or other analog moiety having chemical and/or structural properties similar to a specified amino acid.

[0047] The term "cyclized," as used herein, refers to a reaction in which one part of a polypeptide molecule becomes linked to another part of the polypeptide molecule to form a closed ring, such as by forming a disulfide bridge or other similar bond.

[0048] The term "subunit," as used herein, refers to one of a pair of polypeptides monomers that are joined at the C- or N- terminus to form a dimer peptide composition.

[0049] The term "dimer," as used herein, refers to a chemical entity consisting of two structurally similar monomers joined by terminus bonds and/or a terminus linker.

[0050] The term "linker," as used herein, refers broadly to a chemical structure that is capable of linking together a plurality of peptide monomer subunits to form a dimer.

[0051] The term "receptor," as used herein, refers to chemical groups of molecules on the cell surface or in the cell interior that have an affinity for a specific chemical group or molecule. Binding between dimer peptides and targeted integrins can provide useful diagnostic tools.

[0052] The term "integrin-related diseases," as used herein, refer to indications that manifest as a result of integrin binding, and which may be treated through the administration of an integrin antagonist.

[0053] The term "pharmaceutically acceptable salt," as used herein, represents salts or zwitterionic forms of the compounds of the present invention which are water or oil-soluble or dispersible, which are suitable for treatment of diseases without undue toxicity, irritation, and allergic response; which are commensurate with a reasonable benefit/risk ratio, and which are effective for their intended use. The salts can be prepared during the final isolation and purification of the compounds or separately by reacting an amino group with a suitable acid. Representative acid addition salts include acetate, adipate, alginate, citrate, aspartate,

benzoate, benzenesulfonate, bisulfate, butyrate, camphorate, camphorsulfonate, digluconate, glycerophosphate, hemisulfate, heptanoate, hexanoate, formate, fumarate, hydrochloride, hydrobromide, hydroiodide, 2-hydroxyethansulfonate (isethionate), lactate, maleate, mesitylenesulfonate, methanesulfonate, naphthylenesulfonate, nicotinate, 2-naphthalenesulfonate, oxalate, pamoate, pectinate, persulfate, 3-phenylproprionate, picrate, pivalate, propionate, succinate, tartrate, trichloroacetate, trifluoroacetate, phosphate, glutamate, bicarbonate, para-toluenesulfonate, and undecanoate. Also, amino groups in the compounds of the present invention can be quaternized with methyl, ethyl, propyl, and butyl chlorides, bromides, and iodides; dimethyl, diethyl, dibutyl, and diamyl sulfates; decyl, lauryl, myristyl, and steryl chlorides, bromides, and iodides; and benzyl and phenethyl bromides. Examples of acids which can be employed to form therapeutically acceptable addition salts include inorganic acids such as hydrochloric, hydrobromic, sulfuric, and phosphoric, and organic acids such as oxalic, maleic, succinic, and citric.

[0054] The term "N(alpha)Methylation", as used herein, describes the methylation of the alpha amine of an amino acid, also generally termed as an N-methylation.

[0055] The term "sym methylation" or "Arg-Me-sym", as used herein, describes the symmetrical methylation of the two nitrogens of the guanidine group of arginine. Further, the term "asym methylation" or "Arg-Me-asym" describes the methylation of a single nitrogen of the guanidine group of arginine.

[0056] The term "acylating organic compounds", as used herein refers to various compounds with carboxylic acid functionality that are used to acylate the N-terminus of an amino acid subunit prior to forming a C-terminal dimer. Non-limiting examples of acylating organic compounds include cyclopropylacetic acid, 4-Fluorobenzoic acid, 4-fluorophenylacetic acid, 3-Phenylpropionic acid, Succinic acid, Glutaric acid, Cyclopentane carboxylic acid, 3,3,3-trifluoropropeonic acid, 3-Fluoromethylbutyric acid, Tetrahedro-2H-Pyran-4-carboxylic acid.

[0057] All peptide sequences are written according to the generally accepted convention whereby the α-N-terminal amino acid residue is on the left and the α-C-terminal is on the right. As used herein, the term "α-N-terminal" refers to the free α-amino group of an amino acid in a peptide, and the term "α-C-terminal" refers to the free α-carboxylic acid terminus of an amino acid in a peptide.

[0058] For the most part, the names of naturally occurring and non-naturally occurring aminoacyl residues used herein follow the naming conventions suggested by the

IUPAC Commission on the Nomenclature of Organic Chemistry and the IUPAC-IUB Commission on Biochemical Nomenclature as set out in "Nomenclature of α-Amino Acids (Recommendations, 1974)" Biochemistry, 14(2), (1975). To the extent that the names and abbreviations of amino acids and aminoacyl residues employed in this specification and appended claims differ from those suggestions, they will be made clear to the reader. Some abbreviations useful in describing the invention are defined below in the following Table 1.

[0059] **TABLE 1**

Abbreviation	Definition
DIG	DIGlycolic acid (Linker)
Dap	Diaminopropionic acid
Dab	Diaminobutyric acid
Pen	Penicillamine
Sar	Sarcosine
Cit	Citroline
Cav	Cavanine
4-Guan	4-Guanidine-Phenylalanine
N-Me-Arg; N(alpha)Methylation	N-Methyl-Arginine
Ac-	Acetyl
2-Nal	2-Napthylalanine
1-Nal	1-Napthylalanine
Bip	Biphenylalanine
O-Me-Tyr	Tyrosine (O-Methyl)
N-Me-Lys	N-Methyl-Lysine
N-Me-Lys (Ac)	N-e-Acetyl-D-lysine
Ala (3,3 diphenyle)	3,3 diphenyl alanine
NH2	Free Amine

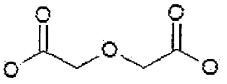
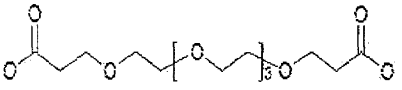
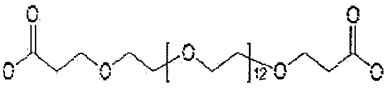
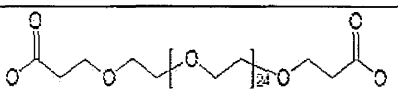
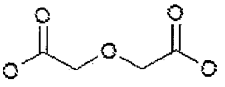
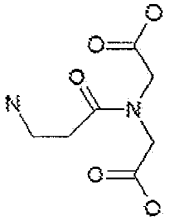
CONH2	Amide
COOH	Acid
Phe (4-F)	4-Fluoro-Phenylanine
PEG13	Bifunctional PEG linker with 13 PolyEthylene Glycol units
PEG25	Bifunctional PEG linker with 25 PolyEthylene Glycol units
PEG1K	Bifunctional PEG linker with PolyEthylene Glycol Mol wt of 1000Da
PEG2K	Bifunctional PEG linker with PolyEthylene Glycol Mol wt of 2000Da
PEG3.4K	Bifunctional PEG linker with PolyEthylene Glycol Mol wt of 3400Da
PEG5K	Bifunctional PEG linker with PolyEthylene Glycol Mol wt of 5000Da
IDA	β-Ala-Iminodiacetic acid (Linker)
IDA-Palm	β-Ala (Palmityl)-Iminodiacetic acid
HPhe	Homo Phenylalanine
Ahx	Aminohexanoic acid
DIG-OH	Glycolic monoacid
Triazine	Amino propyl Triazine di-acid
Boc-Triazine	Boc-Triazine di-acid
Trifluorobutyric acid	Acylated with 4,4,4-Trifluorobutyric acid
2-Methly-trifluorobutyric acid	acylated with 2-methy-4,4,4-Butyric acid
Trifluorpentanoic acid	Acylated with 5,5,5-Trifluoropentnoic acid
1,4- Phenylenediacetic acid	*para*- Phenylenediacetic acid (Linker)
1,3 - Phenylenediacetic acid	*meta* - Phenylenediacetic acid (Linker)
DTT	Dithiothreotol
Nle	Norleucine
β-HTrp	β-homoTrypophane

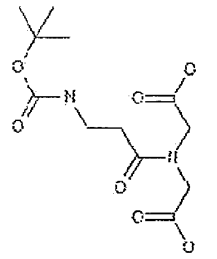
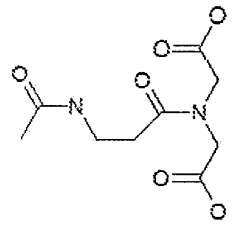
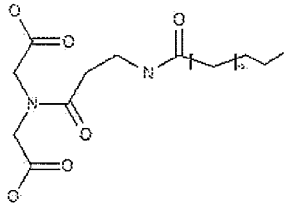
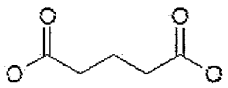
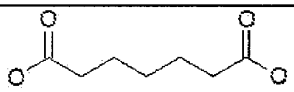
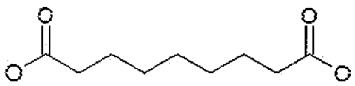
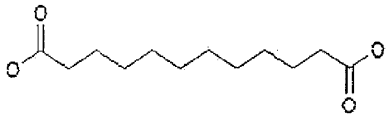
β-HPhe	β-homophenylalanine
Phe(4-CF3)	4-Trifluoromethyl Phenylalanine
β-Glu	β-Glutamic acid
β-HGlu	β-homoglutamic acid
2-2-Indane	2-Aminoindane-2-carboxylic acid
1-1-Indane	1-Aminoindane-1-carboxylic acid
HCha	homocyclohexyl Alanine
Cyclobutyl	Cyclobutylalanine
β-HPhe	β-homophenylalanine
HLeu	Homoleucine
Gla	Gama-Carboxy-Glutamic acid

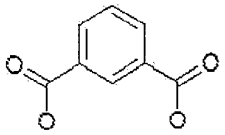
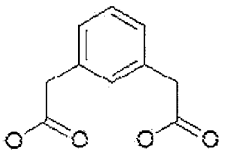
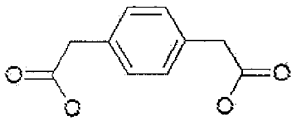
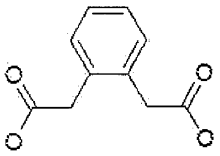
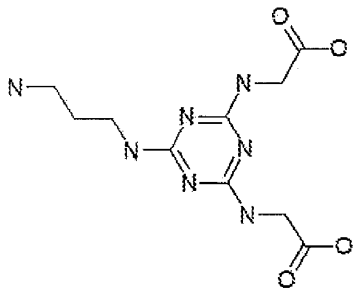
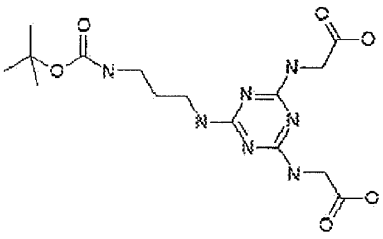
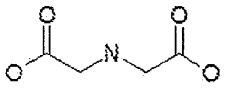
[0060] The present invention relates generally to peptides that have been shown to have integrin antagonist activity. In particular, the present invention relates to various peptide dimers comprising hetero- or homo-monomer subunits that each form cyclized structures through disulfide bonds. The monomer subunits are linked at either their C- or N-termini, as shown in Figure 1. The cyclized structure of each subunit has been shown to increase potency and selectivity of the dimer molecules, as discussed below. A non-limiting, representative illustration of the cyclized structure is shown in Figure 2.

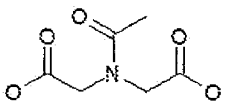
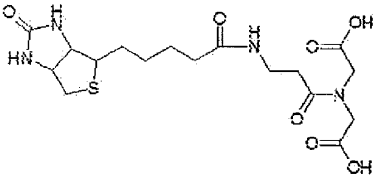
[0061] The linker moieties of the present invention may include any structure, length, and/or size that is compatible with the teachings herein. In at least one embodiment, a linker moiety is selected from the non-limiting group consisting of DIG, PEG4, PEG4-biotin, PEG13, PEG25, PEG1K, PEG2K, PEG3.4K, PEG4K, PEG5K, IDA, ADA, Boc-IDA, Glutaric acid, Isophthalic acid, 1,3-phenylenediacetic acid, 1,4-phenylenediacetic acid, 1,2-phenylenediacetic acid, Triazine, Boc-Triazine, IDA-biotin, PEG4-Biotin, AADA, suitable aliphatics, aromatics, heteroaromatics, and polyethylene glycol based linkers having a molecular weight from approximately 400Da to approximately 40,000Da. Non-limiting examples of suitable linker moieties are provided in Table 2.

[0062] **TABLE 2**

Abbrivation	Discription	Structure
DIG	DIGlycolic acid,	
PEG4	Bifunctional PEG linker with 4 PolyEthylene Glycol units	
PEG13	Bifunctional PEG linker with 13 PolyEthylene Glycol units	
PEG25	Bifunctional PEG linker with 25 PolyEthylene Glycol units	
PEG1K	Bifunctional PEG linker with PolyEthylene Glycol Mol wt of 1000Da	
PEG2K	Bifunctional PEG linker with PolyEthylene Glycol Mol wt of 2000Da	
PEG3.4K	Bifunctional PEG linker with PolyEthylene Glycol Mol wt of 3400Da	
PEG5K	Bifunctional PEG linker with PolyEthylene Glycol Mol wt of 5000Da	
DIG	DIGlycolic acid,	
IDA	β-Ala-Iminodiacetic acid	

Boc-IDA	Boc-β-Ala-Iminodiacetic acid	
Ac-IDA	Ac-β-Ala-Iminodiacetic acid	
IDA-Palm	Palmityl-β-Ala-Iminodiacetic acid	
GTA	Glutaric acid	
PMA	Pemilic acid	
AZA	Azelaic acid	
DDA	Dodecanedioic acid	

IPA	Isopthalic aicd	
1,3-PDA	1,3- Phenylenediacetic acid	
1,4-PDA	*1,4*- Phenylenediacetic acid	
1,2-PDA	1,2 - Phenylenediacetic acid	
Triazine	Amino propyl Triazine di-acid	
Boc-Triazine	Boc-Triazine di-acid	
ADA	Amino diacetic acid	

AADA	n-Acetyl amino acetic acid	
PEG4-Biotin	PEG4-Biotin (Product number 10199, QuantaBioDesign)	
IDA-Biotin	N-Biotin-β-Ala-Iminodiacetic acid	

[0063] The present invention further includes various peptides that have been substituted with various modified amino acids. For example, some peptides include Dab, Dap, Pen, Sar, Cit, Cav, HLeu, 2-Nal, d-1-Nal, d-2-Nal, Bip, O-Me-Tyr, β-HTrp, β-HPhe, Phe (4-CF3), 2-2-Indane, 1-1-Indane, Cyclobutyl, β-HPhe, HLeu, Gla, Phe(4-NH2), HPhe, 1-Nal, Nle, homo amino acids, D-amino acids, 3-3-diPhe, cyclobutyl-Ala, HCha, Bip, β-HPhe, β-Glu, 4-Guan, and various N-methylated amino acids. One having skill in the art will appreciate that additional substitutions may be made to achieve similar desired results, and that such substitutions are within the teaching and spirit of the present invention.

[0064] In one aspect, the present invention relates to dimer compounds, each subunit of the dimer compound comprising the structure of Formula (I) Xaa^1-Xaa^2-Xaa^3-Xaa^4-Xaa^5-Xaa^6-Xaa^7-Xaa^8-Xaa^9-Xaa^{10}-Xaa^{11}-Xaa^{12}-Xaa^{13}-Xaa^{14} SEQ ID NO: 1), wherein Xaa^1-Xaa^2-Xaa^3-Xaa^4-Xaa^5-Xaa^6-Xaa^7-Xaa^8-Xaa^9-Xaa^{10} (SEQ ID NO: 2), or a pharmaceutically acceptable salt thereof, further represent a subunit of a homo- or heterodimer molecule, wherein each subunit of the dimer molecule comprises 10 amino acids, and wherein Xaa^1-Xaa^{10} of Formula (II) corresponds to Xaa^4-Xaa^{13} of Formula (I).

Further, each subunit of Formula (I) and Formula (II) comprises a disulfide or lactam bond between Xaa^4 and Xaa^{10}, and Xaa1 and Xaa^7, respectively.

[0065] Some sequences of the present invention are derived from the general sequences provided in Formula (I) and Formula (II). For example, the N-terminus of a decapeptide represented by Xaa^4-Xaa^{13} of Formula (I) can be modified by one to three suitable groups, as represented by Xaa^1, Xaa^2, and Xaa^3 of Formula (I). The N-terminus may further be acylated. In some instances, the N-terminus further comprises a suitable linker moiety to facilitate linking together two monomer subunits to form an N-terminal dimer molecule.

[0066] Similarly, the C-terminus of the decapeptide represented by Formula (I) can be modified by a suitable group. The C-terminus may further be acylated. In some instances, the C-terminus further comprises a suitable linker moiety to facilitate linking together two monomer subunits to form a C-terminal dimer molecule.

[0067] In some embodiments, Xaa^1, Xaa^2, and Xaa^3 of Formula (I) are absent. In other embodiments, Xaa^1 is absent, and Xaa^2 and Xaa^3 represent suitable groups for modifying the N-terminus of the decapeptide, wherein the decapeptide is represented by residues Xaa^4-Xaa^{13} of Formula (I), and residues Xaa^1-Xaa^{10} of Formula (II). Further, in some embodiments Xaa^1 and Xaa^2 are absent, and Xaa^3 represents a single suitable group for modifying the N-terminus of the decapeptide subunit.

[0068] With continued reference to the general formula of Formula (I), Xaa^1 is an amino acyl residue selected from the group consisting of Gln, Asp, Pro, Gly, His, Ala, Ile, Phe, Lys, Arg, Asn, Glu, Leu, Val, Tyr, Trp, Met, Thr, suitable isosteres, and corresponding D-amino acids. In some embodiments, Xaa^1 is acylated or free NH_2. In other embodiments, Xaa^1 is absent.

[0069] Xaa^2 is an amino acyl residue selected from the group consisting of Gln, Asp, Pro, Gly, His, Ala, Ile, Phe, Lys, Arg, Asn, Glu, Leu, Val, Ser, Tyr, Trp, Met, Thr, suitable isosteres, and corresponding D-amino acids. When Xaa^1 is absent, Xaa^2 is the N-terminus.

[0070] Xaa^3 is an amino acyl residue selected from the group consisting of Gln, Asp, Pro, Gly, His, Ala, Ile, Phe, Lys, Arg, Asn, Glu, Leu, Val, Tyr, Trp, Met, Thr, Ser, and corresponding D-amino acids. When Xaa^1 and Xaa^2 are absent, Xaa^3 is the N-terminus. In other embodiments, Xaa^1-Xaa^3 are absent, wherein Xaa^4 is the N-terminus.

[0071] In some embodiments, the N-terminal residue of Formula (I) further comprises a linker moiety selected from the group consisting of DIG, DIG-OH, PEG13, PEG25,

PEG1K, PEG2K, PEG3.4K, PEG4K, PEG5K, IDA, IDA-Palm, IDA-Boc, IDA-Isovaleric acid, Triazine, Triazine-Boc, Isophthalic acid, 1,3-phenylenediacetic acid, 1,4-phenylenediacetic acid, cyclopropylacetic acid, 4-fluoorobenzoic acid, 4-fluorophenylacetic acid, 3-phenylpropionic acid, succinic acid, biotin, glutaric acid, Azelaic acid, Pimelic acid, Dodecanedioic acid, suitable aliphatics, suitable aromatics, heteroaromatics, and polyethylene glycols having a molecular weight from approximately 400Da to approximately 40,000Da. Further, in some embodiments Xaa^1-Xaa^4 are acylated.

[0072] In some embodiments, Xaa^4 is an amino acyl residue or analog selected from the group consisting of Cys, Pen, Asp, Glu, HGlu, β-Asp, β-Glu, Lys, HLys, Orn, Dap, and Dab. When Xaa^{10} is Lys, HLys, Orn, Dap or Dab, suitable groups for Xaa^4 are Asp, Glu, and HGlu. When Xaa^{10} is Asp, Glu, HGlu, suitable groups for Xaa^4 are Lys, HLys, Orn, Dap, and Dab.

[0073] When Xaa^4 and Xaa^{10} are either Cys or Pen, each subunit of the dimer is cyclized though a disulfide bond between Xaa^4 and Xaa^{10}. When Xaa^4 is Lys, HLys, Orn, Dap, or Dab, and when Xaa^{10} is Asp, HAsp, Glu, and HGlu, each subunit of the dimer is cyclized through a lactam bond between Xaa^4 and Xaa^{10}. Preferably, in one embodiment Xaa^4 is Cys. In another embodiment, preferably Xaa^4 is Pen.

[0074] Xaa^5 is an amino acyl residue or analog selected from the group consisting of Gln, Asn, Asp, Pro, Gly, His, Ala, Ile, Phe , Lys, Arg, Glu, Leu, Val, Tyr, Trp, Met, Thr, HArg, Dap, Dab, N-Me-Arg, Arg-Me-sym, Arg-Me-asym, Phe(4-NH2), 4-Guan, Cit, Cav, and suitable isostere replacements. In some embodiments, Xaa^5 is N(alpha)Methylated. Preferably, Xaa^5 is N-Me-Arg. In other embodiments, preferably Xaa^5 is Arg.

[0075] Xaa^6 is an amino acyl residue or analog selected from the group consisting of Ser, Gln, Asn, Asp, Pro, Gly, His, Ala, Ile, Phe, Lys, Arg, Glu, Leu, Val, Thr, Tyr, Trp, Met, and suitable isostere replacements. Preferably, Xaa^6 is Ser or Gly.

[0076] Xaa^7 is an amino acyl residue or analog selected from the group consisting of Asp, N-Me-Asp, and suitable isostere replacements. In some embodiments, Xaa^7 is N(alpha)Methylated. Preferably, Xaa^7 is Asp.

[0077] Xaa^8 is an amino acyl residue or analog selected from the group consisting of Thr, Gln, Ser, Asn, Asp, Pro, Gly, His, Ala, Ile, Phe , Lys, Arg, Glu, Val, Tyr, Trp, Leu, Met, N-Me-Thr and suitable isostere replacements. In some embodiments, Xaa^8 is N(alpha)Methylated. Preferably, Xaa^8 is Thr.

[0078] Xaa^9 is an amino acyl residue or analog selected from the group consisting of Gln, Asn, Asp, Pro, Gly, Ala, Phe, Leu, Glu, Ile, Val, HLeu, n-Butyl Ala, n-Pentyl Ala, n-Hexyl Ala, N-Me-Leu, amino acids with hydrophobic side chains, and suitable isostere replacements. In some embodiments, Xaa^9 is N(alpha)Methylated. Preferably, Xaa^9 is Leu.

[0079] Xaa^{10} is an amino acyl residue selected from the group consisting of Cys, Asp, Pen, Lys, Glu, HLys, HAsp, HGlu, Orn, Dap, and Dab. In some embodiments, Xaa^{10} is selected from the group consisting of Asp, HAsp, Glu, and HGlu, when Xaa^4 is Lys, Dap, Dab, HLys, or Orn. In other embodiments, Xaa^{10} selected from the group consisting of Lys, HLys, Orn, Dap, or Dab when Xaa^4 is Asp, HAsp, Glu, or HGlu. In at least one embodiment, Xaa^{10} is Pen. When Xaa^{10} and Xaa^4 are both either Cys or Pen, each subunit of the dimer is cyclized through a disulfide bond between Xaa^4 and Xaa^{10}. When Xaa^{10} is Asp, HAsp, Glu, or HGlu, and when Xaa^4 is Lys, HLys, Orn, Dap, or Dab, each subunit of the dimer is cyclized through a lactam bond between Xaa^4 and Xaa^{10}. When Xaa^{11} is absent, Xaa^{10} is the C-terminus of the subunit. Preferably, in one embodiment Xaa^{10} is Pen. In another embodiment, Xaa^{10} is preferably Cys.

[0080] Xaa^{11} is an amino acyl residue selected from the group consisting of Gly, Gln, Asn, Asp, Ala, Ile, Leu, Val, Met, Thr, Lys, Trp, Tyr, His, Glu, Ser, Arg, Pro, Phe, Sar, 1-Nal, 2-Nal, D-1-Nal, D-2-Nal, HPhe, Phe(4-F), O-Me-Tyr, dihydro-Trp, Dap, Dab, Orn, D-Orn, N-Me-Orn, N-Me-Dap, N-Me-Dab, N-Me Lys, D-Dap, D-Dab, D-Lys, N-Me-D-Lys, Bip, Ala(3,3diphenyl), Biphenyl-Ala, D-Phe, D-Trp, D-Tyr, D-Glu, D-His, D-Lys, 3,3-diPhe, β-HTrp, F(4CF3), 4-Me-Phe, 2-2 Indane, Phe (2,4 Cl2), Phe (3,4 Cl2), 1-1 Indane, aromatic ring substituted Phe, aromatic ring substituted Trp, aromatic ring substituted His, hetero aromatic amino acids, N-Me-Lys, N-Me-Lys(Ac), 4-Me-Phe, and corresponding D-amino acids and suitable isostere replacements. In at least one embodiment, Xaa^{11} and Xaa^{12} are absent. When Xaa^{12} and Xaa^{13} are absent, Xaa^{11} is the C-terminus of the subunit. When Xaa^{11} is the C-terminus of the subunit, Xaa^{11} may be modified to include a linker moiety in accordance with the present invention. Preferably, Xaa^{11} is Trp. In other embodiments Xaa^{11} is N(alpha)Methylated. Further, in some embodiments Xaa^{11} is acylated.

[0081] Xaa^{12} is an amino acyl residue selected from the group consisting of Glu, Lys, Gln, Pro, Gly, His, Ala, Ile, Phe, Lys, Arg, Leu, Val, Tyr, Trp, Met, Ser, Asn, Asp, Gla, Dap, Dab, Orn, D-Orn, N-Me-Orn, N-Me-Dap, N-Me-Dab, N-Me Lys, D-Dap, D-Dab, D-Lys, N-Me-D-Lys, N-Me-Glu, , 2-Nal. 1-Nal, Bip, Beta-HPhe, β-Glu, Phe(4-CF3), D-Asp suitable isosters, and corresponding D-amino acids. When Xaa^{13} and Xaa^{14} are absent, Xaa^{12} is the C-

terminus of the subunit. In some embodiments Xaa^{12} is absent. When Xaa^{12} is the C-terminus of the subunit, Xaa^{12} may be modified to include a linker moiety in accordance with the present invention. Further, in some embodiments Xaa^{12} is N(alpha)Methylated. Further in some embodiments Xaa^{12} selected from the group consisting of Lys, D-Lys, and N-Me-Lys. Preferably, Xaa^{12} is Glu, D-Glu, β-HGlu, and Asp.

[0082] Xaa^{13} is an amino acyl residue selected from the group consisting of Gln, Pro, Gly, His, Ala, Ile, Phe, Lys, Arg, Leu, Val, Tyr, Trp, Met, Glu, Ser, Asn, Gla, Dap, Dab, Orn, D-Orn, N-Me-Orn, N-Me-Dap, N-Me-Dab, N-Me Lys, D-Dap, D-Dab, D-Lys, N-Me-D-Lys, suitable isosteres, and corresponding D-amino acids. In some embodiments, when Xaa^{14} is absent, Xaa^{13} is the C-terminus. When Xaa^{13} is the C-terminus of the subunit, Xaa^{13} may be modified to include a linker moiety in accordance with the present invention. In at least one embodiment, Xaa^{13} is Lys. In other embodiments, Xaa^{13} is absent. Further, in some embodiments Xaa^{13} is N(alpha)Methylated. Further still, in some embodiments Xaa^{13} is acylated. Further still, in some embodiments Xaa^{13} is D-Lys.

[0083] Xaa^{14} is an amino acyl residue selected from the group consisting of natural amino acids, Dap, Dab, Orn, D-Orn, N-Me-Orn, N-Me-Dap, N-Me-Dab, N-Me Lys, D-Dap, D-Dab, D-Lys, N-Me-D-Lys, suitable isostere replacements, corresponding D-amino acids, and corresponding N-Methyl amino acids. In at least one embodiment, Xaa^{14} is absent. In at least one embodiment, Xaa^{14} is the C-terminus. When Xaa^{14} is the C-terminus of the subunit, Xaa14 may be modified to include a linker moiety in accordance with the present invention. Further, in some embodiments Xaa^{14} is N(alpha)Methylated.

[0084] In some embodiments, the C-terminal residue of Formula (I) further comprises a linker moiety selected from the group consisting of DIG, PEG13, PEG25, PEG1K, PEG2K, PEG3.4K, PEG4K, PEG5K, IDA, IDA-Palm, IDA-Boc, IDA-Isovaleric acid, Triazine, Triazine-Boc, Isophthalic acid, 1,3-phenylenediacetic acid, 1,4-phenylenediacetic acid, glutaric acid, Azelaic acid, Pimelic acid, Dodecanedioic acid, suitable aliphatics, aromatics, heteroaromatics, and polyethylene glycol based linkers having a molecular weight from approximately 400Da to approximately 40,000Da.

[0085] Some embodiments of the present invention further include a peptide homodimer or heterodimer molecule, wherein each subunit of the dimer molecule comprises an amino acid sequence represented by at least one of SEQ ID NOs: 1-146. Other embodiments comprise a peptide homodimer or heterodimer molecule, wherein each subunit of the dimer molecule comprises an amino acid sequence comprising an N(alpha)methylated

arginine residue, as represented by at least one of SEQ ID NOs: 1-38, 46-52, 54-135, and 137-146. At least one embodiment comprises a peptide homodimer or heterodimer molecule, wherein at least one subunit of the dimer molecule comprises an amino acid sequence comprising an N(alpha)Methylated lysine residue, as represented by SEQ ID NO: 136.

[0086] Further, some embodiments of the present invention comprise a peptide homodimer or hetereodimer molecule, wherein each subunit of the dimer molecule is cyclized through a disulfide bond, as represented by at least one of SEQ ID NOs: 1-146. In other embodiments, a peptide homo- or heterodimer molecule is provided, wherein each subunit of the dimer molecule is cyclized through a lactam bond, as represented by at least one of SEQ ID NOs: 1 and 2, wherein Xaa4 and Xaa10 are selected from the group consisting of Lys, HLys, Orn, Dap, Dab, Asp, HAsp, Glu and HGlu.

[0087] *Dimer Structure and Biological Activity*

[0088] The present invention provides various novel antagonist disulfide peptide dimers. These compounds have been tested to more clearly characterize the increased affinity for α4β7 binding, increased selectivity against α4β1, and increased stability in simulated intestinal fluid (SIF). These novel antagonist molecules demonstrate high binding affinity with α4β7, thereby preventing binding between α4β7 and the MAdCAM ligand. Accordingly, these antagonist peptides have shown to be effective in eliminating and/or reducing the inflammation process in various experiments.

[0089] The present invention thus provides various dimer peptide compounds which bind or associate with the α4β7 integrin, in serum and SIF, to disrupt or block binding between α4β7 and the MAdCAM ligand. The various peptide compounds of the invention may be constructed solely of natural amino acids. Alternatively, the peptide compounds may include non-natural amino acids including, but not limited to, modified amino acids. Modified amino acids include natural amino acids which have been chemically modified to include a group, groups, or chemical moiety not naturally present on the amino acid. The peptide compounds of the invention may additionally include D-amino acids. Still further, the peptide compounds of the invention may include amino acid analogs.

[0090] Some antagonist disulfide dimers have been shown to be gastrointestinal stable and provide high levels of specificity and affinity for the α4β7 integrin. Some implementations of the present invention provide a disulfide dimer comprising a half-life of greater than 60 minutes when exposed to simulated intestinal fluids (SIF). Some

implementations further provide a DRP comprising a half-life from approximately 1 minute to approximately 60 minutes.

[0091] The compounds of the present invention are homo- or heterodimers formed by linking two subunit monomers at their C- or N-termini. Dimerization of the monomer subunits represented by SEQ ID NOs: 1-146 demonstrate increased potency over their non-dimerized, monomer analogs. Some dimer compounds of the present invention demonstrated further increased potency as a result of substituting various natural amino acyl residues with N-methylated analog residues. For example, SEQ ID NOs.: 1-38, 46-52, 54-135, and 137-146 represent subunit monomers sequences that were substituted with N(alpha)methylated arginine. Further still, some dimer compounds of the present invention comprise monomer subunits that undergo independent cyclization, whereby the cyclized structures demonstrate increased stability over their non-cyclized monomer and dimer analogs. Specific examples and data illustrating these improvements are provided in Figures 3 and 4.

[0092] Referring now to Figure 3, a chart is provided which includes various data illustrating increased stability for various non-limiting sample homodimer molecules in accordance with the instant invention. Simulated Intestinal Fluid (SIF) Stability assays were performed for the majority of the instant monomer peptides, and their respective homodimer molecules. A selective sampling of these results is provided in Figure 3.

[0093] According to the protocols discussed herein, applicant successfully synthesized, purified and dimerized the majority of the integrin antagonist dimer molecules represented by SEQ ID NOs: 39-146 to form homodimers.

[0094] Dimerization of the monomer disulfide peptide subunits generally demonstrated increase stability, as compared to the monomer disulfide subunit peptides. Further, substitutions at arginine with N-Me-Arg increased half-life substantially in SIF, as demonstrated by the N(alpha)Methylated and non-methylated variations of SEQ ID NO: 46. In some embodiments, substitution of Cys with Penicillamine (Pen) increased stability significantly in simulated intestinal fluids (SIF), as demonstrated by SEQ ID NOs: 55, 74 and 93 when compared to SEQ ID NO: 46 with Cys. The substitution of Cys with Pen also increased stability under reduced conditions (DTT) indicating improved gastric stability.

[0095] Referring now to Figure 4, a chart is provided which includes various data illustrating increased potency and selectivity for various non-limiting sample homodimer molecules in accordance with the instant invention. Potency assays were performed for all of the monomer peptides, and their respective homodimer molecules, represented by SEQ ID

NOs: 39-146. Selectivity assays were performed for majority of the monomer peptides, and their respective homodimer molecules, represented by SEQ ID NOs: 39-146. A selective sampling of these results is provided in Figure 4 wherein the homodimer peptides are represented by Samples 2, 4, 5, 7, 9, 11, 13, 15, 16, 17 and 19, and the respective monomer subunits molecules are represented by Samples 1, 3, 6, 8, 10, 12, 14, and 18. Through dimerization, significant improvement in potency was achieved for α4β7 in ELISA as well as cell adhesion assays. In addition, dimerization lead to significant improvement achieved in selectivity against α4β1 through improved potency for α4β7. The peptides also demonstrate low efficacy for α4β1 when compared to α4β7, thereby indicating selectivity against α4β7.

[0096] According to the protocols discussed herein, applicant successfully synthesized, purified and dimerized majority of the integrin antagonist dimer molecules represented by SEQ ID NOs: 39-146 to form homodimers. Each of these molecules was subjected to an α4β7-MAdCAM Competition ELISA assay, an α4β1-VCAM Competition ELISA assay, an α4β7-MadCAM cell adhesion assay. For many sequences, these assays were also performed on both the monomer subunit and dimer molecules. A small sampling of these results is provided in Figure 4.

[0097] Dimerization of the monomer disulfide peptides subunits generally demonstrated increased affinity for a4b7 and/or decreased affinity for a4b1 leading to increased selectivity against a4b1, as compared to the monomer disulfide subunit peptides.

[0098] Upon C- and N-terminal dimerization, a significant improvement in potency for α4β7 was also observed. In addition dimerization also lead to either decrees of potency for α4β1 or no significant change in potency leading to increased selectivity for α4β7 in ELISA and cell adhesion assays. When Arg is replaced with N-Me-Arg, a significant improvement in potency for α4β7 was shown in both ELISA and cell adhesion assays. N(alpha)methylation further demonstrated increased molecular stability. One having skill in the art will appreciate that methylated isosteres of arginine may further demonstrate similar increases in potency and/or stability.

[0099] Compositions

[0100] As discussed above, integrins are heterodimers that function as cell adhesion molecules. The α4 integrins, α4β1 and α4β7, play essential roles in lymphocyte migration throughout the gastrointestinal tract. They are expressed on most leukocytes, including B and T lymphocytes, monocytes, and dendritic cells, where they mediate cell adhesion via binding to their respective primary ligands, namely vascular cell adhesion molecule (VCAM) and

mucosal addressin cell adhesion molecule (MAdCAM). VCAM and MAdCAM differ in binding specificity, in that VCAM binds both $\alpha4\beta1$ and $\alpha4\beta7$, while MAdCAM is highly specific for $\alpha4\beta7$.

[0101] Differences in the expression profiles of VCAM and MAdCAM provide the most convincing evidence of their role in inflammatory diseases. Both are constitutively expressed in the gut; however, VCAM expression extends into peripheral organs, while MAdCAM expression is confined to organs of the gastrointestinal tract. In addition, elevated MAdCAM expression in the gut has now been correlated with several gut-associated inflammatory diseases, including Crohn's disease, ulcerative colitis, and hepatitis C.

[0102] The compounds of the invention, including but not limited to those specified in the examples, possess integrin-antagonist activity. In one embodiment, the condition or medical indication comprises at least one of Inflammatory Bowel Disease (IBD), ulcerative colitis, Crohn's disease, Celiac disease (*nontropical Sprue)*, enteropathy associated with seronegative arthropathies, microscopic or 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, or pouchitis resulting after proctocolectomy and ileoanal anastomosis and various forms of gastrointestinal cancer, osteoporosis, arthritis, multiple sclerosis, chronic pain, weight gain, and depression. In another embodiment, the condition is pancreatitis, insulin-dependent diabetes mellitus, mastitis, cholecystitis, cholangitis, pericholangitis, chronic bronchitis, chronic sinusitis, asthma or graft versus host disease. In addition, these compounds may be useful in the prevention or reversal of these diseases when used in combination with currently available therapies, medical procedures, and therapeutic agents.

[0103] The compounds of the invention may be used in combination with other compositions and procedures for the treatment of disease. Additionally, the compounds of the present invention may be combined with pharmaceutically acceptable excipients, and optionally sustained-release matrices, such as biodegradable polymers, to form therapeutic compositions.

[0104] *Methods of Treatment*

[0105] In some embodiments, the present invention provides a method for treating an individual afflicted with a condition or indication characterized by integrin binding, wherein

the method comprises administering to the individual an integrin antagonist dimer molecule according to Formulas (I) or (II). In one embodiment, a method is provided for treating an individual afflicted with a condition or indication characterized by inappropriate trafficking of cells expressing α4β7 to tissues comprising cells expressing MAdCAM, comprising administering to the individual an α4β7-antagonist dimer molecule according to at least one of Formula (I) and Formula (II) in an amount sufficient to inhibit (partially or fully) the trafficking of cells expressing α4β7 to tissues comprising cells expressing MAdCAM.

[0106] In some embodiments, the present invention provides a method whereby a pharmaceutical composition comprising an integrin antagonist dimer molecule according to Formula (I) is administered to a patient as a first treatment. In another embodiment, the method further comprises administering to the subject a second treatment. In another embodiment, the second treatment is administered to the subject before and/or simultaneously with and/or after the pharmaceutical composition is administered to the subject. In other embodiment, the second treatment comprises an anti-inflammatory agent. In another embodiment, the second pharmaceutical composition comprises an agent selected from the group consisting of non-steroidal anti-inflammatory drugs, steroids, and immune modulating agents. In another embodiment, the method comprises administering to the subject a third treatment.

[0107] In one embodiment, a method is provided for treating an individual afflicted with a condition or indication characterized by α4β7 integrin binding, wherein the method comprises administering to the individual an effective amount of an α4β7 integrin antagonist dimer molecule containing subunits selected from SEQ ID NOs: 1-146. In some instances, an α4β7 integrin antagonist dimer molecule having subunits selected from and corresponding to SEQ ID NOs: 1-146, and having high specificity for α4β7 is administered to an individual as part of a therapeutic treatment for a condition or indication characterized by α4β7 integrin binding. Some embodiments of the present invention further provide a method for treating an individual with an α4β7 integrin antagonist dimer molecule that is suspended in a sustained-release matrix. A sustained-release matrix, as used herein, is a matrix made of materials, usually polymers, which are degradable by enzymatic or acid-base hydrolysis or by dissolution. Once inserted into the body, the matrix is acted upon by enzymes and body fluids. A sustained-release matrix desirably is chosen from biocompatible materials such as liposomes, polylactides (polylactic acid), polyglycolide (polymer of glycolic acid), polylactide co-glycolide (copolymers of lactic acid and glycolic acid) polyanhydrides,

poly(ortho)esters, polypeptides, hyaluronic acid, collagen, chondroitin sulfate, carboxylic acids, fatty acids, phospholipids, polysaccharides, nucleic acids, polyamino acids, amino acids such as phenylalanine, tyrosine, isoleucine, polynucleotides, polyvinyl propylene, polyvinylpyrrolidone and silicone. A preferred biodegradable matrix is a matrix of one of either polylactide, polyglycolide, or polylactide co-glycolide (co-polymers of lactic acid and glycolic acid).

[0108] In some aspects, the invention provides a pharmaceutical composition for oral delivery. The various embodiments and dimer compositions of the instant invention may be prepared for oral administration according to any of the methods, techniques, and/or delivery vehicles described herein. Further, one having skill in the art will appreciate that the dimer compositions of the instant invention may be modified or integrated into a system or delivery vehicle that is not disclosed herein, yet is well known in the art and compatible for use in oral delivery of small dimer peptide molecules.

[0109] Oral dosage forms or unit doses compatible for use with the dimer peptides of the present invention may include a mixture of dimer peptide active drug components, and nondrug components or excipients, as well as other non-reusable materials that may be considered either as an ingredient or packaging. Oral compositions may include at least one of a liquid, a solid, and a semi-solid dosage forms. In some embodiments, an oral dosage form is provided comprising an effective amount of dimer peptide having subunits selected from and corresponding to SEQ ID NOs: 1-146, wherein the dosage form comprises at least one of a pill, a tablet, a capsule, a gel, a paste, a drink, a syrup, ointment, and suppository. In some instances, an oral dosage form is provided that is designed and configured to achieve delayed release of the peptide dimer in the subjects small intestine and/or colon

[0110] In one embodiment, an oral pharmaceutical composition according to Formula (I) comprises an enteric coating that is designed to delay release of the peptide dimer in the small intestine. In at least some embodiments, a pharmaceutical composition is provided which comprises a peptide dimer compound having subunits selected from and corresponding to SEQ ID NOs: 1-146, and a protease inhibitor, such as aprotinin, in a delayed release pharmaceutical formulation. In some instances it is preferred that a pharmaceutical composition of the instant invention comprise an enteric coat that is soluble in gastric juice at a pH of about 5.0 or higher. In at least one embodiment, a pharmaceutical composition is provided comprising an enteric coating comprising a polymer having dissociable carboxylic groups, such as derivatives of cellulose, including hydroxypropylmethyl cellulose phthalate,

cellulose acetate phthalate and cellulose acetate trimellitate and similar derivatives of cellulose and other carbohydrate polymers.

[0111] In one embodiment, a pharmaceutical composition having subunits selected from and corresponding to SEQ ID NOs: 1-146 is provided in an enteric coating, the enteric coating being designed to protect and release the pharmaceutical composition in a controlled manner within the subjects lower gastrointestinal system, and to avoid systemic side effects. In addition to enteric coatings, the dimer peptides of the instant invention may be encapsulated, coated, engaged or otherwise associated within any compatible oral drug delivery system or component. For example, in some embodiments a dimer peptide of the present invention is provided in a lipid carrier system comprising at least one of polymeric hydrogels, nanoparticles, microspheres, micelles, and other lipid systems.

[0112] To overcome peptide degradation in the small intestine, some implementations of the present invention comprise a hydrogel polymer carrier system in which a peptide dimer in accordance with the present invention is contained, whereby the hydrogel polymer protect the peptide dimer from proteolysis in the small intestine and/or colon. The peptide dimers of the present invention may further be formulated for compatible use with a carrier system that is designed to increase the dissolution kinetics and enhance intestinal absorption of the dimer peptides. These methods include the use of liposomes, micelles and nanoparticles to increase GI tract permeation of peptides.

[0113] Various bioresponsive systems may also be combined with one or more peptide dimers of the present invention to provide a pharmaceutical agent for oral delivery. In some embodiments, a peptide dimer of the instant invention is used in combination with a bioresponsive system, such as hydrogels and mucoadhesive polymers with hydrogen bonding groups (e.g., PEG, poly(methacrylic) acid [PMAA], cellulose, Eudragit®, chitosan and alginate) to provide a therapeutic agent for oral administration. Other embodiments include a method for optimizing or prolonging drug residence time for a peptide dimer disclosed herein, wherein the surface of the peptide dimer surface is modified to comprise mucoadhesive properties through hydrogen bonds, polymers with linked mucins or/and hydrophobic interactions. These modified dimer molecules may demonstrate increase drug residence time within the subject, in accordance with a desired feature of the invention. Moreover, targeted mucoadhesive systems may specifically bind to receptors at the enterocytes and M-cell surfaces, thereby further increasing the uptake of particles containing the dimer peptide.

[0114] Other embodiments comprise a method for oral delivery of a dimer peptide having subunits selected from and corresponding to SEQ ID NOs: 1-146, wherein the dimer peptide is used in combination with permeation enhancers that promote the transport of the dimer peptides across the intestinal mucosa by increasing paracellular or transcellular permeation. For example, in one embodiment a permeation enhancer is combined with a dimer peptide having subunits selected from and corresponding to SEQ ID NOs: 1-146, wherein the permeation enhancer comprises at least one of a long-chain fatty acid, a bile salt, an amphiphilic surfactant, and a chelating agent. In one embodiment, a permeation enhancer comprising sodium N-[hydroxybenzoyl)amino] caprylate is used to form a weak noncovalent association with the dimer peptide of the instant invention, wherein the permeation enhancer favors membrane transport and further dissociation once reaching the blood circulation. In another embodiment, a peptide dimer of the present invention is conjugated to oligoarginine, thereby increasing cellular penetration of the dimer peptides into various cell types. Further, in at least one embodiment a noncovalent bond is provided between a dimer peptide having subunits selected from and corresponding to SEQ ID NOs: 1-146 and a permeation enhancer selected from the group consisting of a cyclodextrin (CD) and a dendrimers, wherein the permeation enhancer reduces peptide aggregation and increasing stability and solubility for the peptide dimer molecule.

[0115] Other embodiments of the invention provide a method for treating an individual with an $\alpha 4\beta 7$ integrin antagonist dimer molecule having an increased half-life. In one aspect, the present invention provides an integrin antagonist dimer molecule having a half-life of at least several hours to one day *in vitro* or *in vivo* (e.g., when administered to a human subject) sufficient for daily (q.d.) or twice daily (b.i.d.) dosing of a therapeutically effective amount. In another embodiment, the dimer molecule has a half-life of three days or longer sufficient for weekly (q.w.) dosing of a therapeutically effective amount. Further, in another embodiment the dimer molecule has a half-life of eight days or longer sufficient for bi-weekly (b.i.w.) or monthly dosing of a therapeutically effective amount. In another embodiment, the dimer molecule is derivatized or modified such that is has a longer half-life as compared to the underivatized or unmodified dimer molecule. In another embodiment, the dimer molecule contains one or more chemical modifications to increase serum half-life.

[0116] When used in at least one of the treatments or delivery systems described herein, a therapeutically effective amount of one of the compounds of the present invention may be employed in pure form or, where such forms exist, in pharmaceutically acceptable

salt form. As used herein, a "therapeutically effective amount" of the compound of the invention is meant to describe a sufficient amount of the peptide dimer compound to treat an integrin-related disease, (for example, to reduce inflammation associated with IBD) at a desired benefit/risk ratio applicable to any medical treatment. It will be understood, however, that the total daily usage of the compounds and compositions of the present invention will be decided by the attending physician within the scope of sound medical judgment. The specific therapeutically effective dose level for any particular patient will depend upon a variety of factors including: a) the disorder being treated and the severity of the disorder; b) activity of the specific compound employed; c) the specific composition employed, the age, body weight, general health, sex and diet of the patient; d) the time of administration, route of administration, and rate of excretion of the specific compound employed; e) the duration of the treatment; f) drugs used in combination or coincidental with the specific compound employed, and like factors well known in the medical arts. For example, it is well within the skill of the art to start doses of the compound at levels lower than those required to achieve the desired therapeutic effect and to gradually increase the dosage until the desired effect is achieved.

[0117] Alternatively, a compound of the present invention may be administered as pharmaceutical compositions containing the compound of interest in combination with one or more pharmaceutically acceptable excipients. A pharmaceutically acceptable carrier or excipient refers to a non-toxic solid, semi-solid or liquid filler, diluent, encapsulating material or formulation auxiliary of any type. The compositions may be administered parenterally, intracisternally, intravaginally, intraperitoneally, intrarectally, topically (as by powders, ointments, drops, suppository, or transdermal patch), or buccally. The term "parenteral" as used herein refers to modes of administration which include intravenous, intramuscular, intraperitoneal, intrasternal, subcutaneous, intradermal and intraarticular injection and infusion.

[0118] Pharmaceutical compositions for parenteral injection comprise pharmaceutically acceptable sterile aqueous or nonaqueous solutions, dispersions, suspensions or emulsions, as well as sterile powders for reconstitution into sterile injectable solutions or dispersions just prior to use. Examples of suitable aqueous and nonaqueous carriers, diluents, solvents or vehicles include water, ethanol, polyols (such as glycerol, propylene glycol, polyethylene glycol, and the like), carboxymethylcellulose and suitable mixtures thereof, vegetable oils (such as olive oil), and injectable organic esters such as ethyl

oleate. Proper fluidity may be maintained, for example, by the use of coating materials such as lecithin, by the maintenance of the required particle size in the case of dispersions, and by the use of surfactants.

[0119] These compositions may also contain adjuvants such as preservative, wetting agents, emulsifying agents, and dispersing agents. Prevention of the action of microorganisms may be ensured by the inclusion of various antibacterial and antifungal agents, for example, paraben, chlorobutanol, phenol sorbic acid, and the like. It may also be desirable to include isotonic agents such as sugars, sodium chloride, and the like. Prolonged absorption of the injectable pharmaceutical form may be brought about by the inclusion of agents which delay absorption, such as aluminum monostearate and gelatin.

[0120] Injectable depot forms are made by forming microencapsule matrices of the drug in biodegradable polymers such as polylactide-polyglycolide, poly(orthoesters), poly(anhydrides), and (poly)glycols, such as PEG. Depending upon the ratio of drug to polymer and the nature of the particular polymer employed, the rate of drug release can be controlled. Depot injectable formulations are also prepared by entrapping the drug in liposomes or microemulsions which are compatible with body tissues.

[0121] The injectable formulations may be sterilized, for example, by filtration through a bacterial-retaining filter, or by incorporating sterilizing agents in the form of sterile solid compositions which can be dissolved or dispersed in sterile water or other sterile injectable medium just prior to use.

[0122] Topical administration includes administration to the skin or mucosa, including surfaces of the lung and eye. Compositions for topical lung administration, including those for inhalation and intranasal, may involve solutions and suspensions in aqueous and non-aqueous formulations and can be prepared as a dry powder which may be pressurized or non-pressurized. In non-pressurized powder compositions, the active ingredient in finely divided form may be used in admixture with a larger-sized pharmaceutically acceptable inert carrier comprising particles having a size, for example, of up to 100 micrometers in diameter. Suitable inert carriers include sugars such as lactose.

[0123] Alternatively, the composition may be pressurized and contain a compressed gas, such as nitrogen or a liquefied gas propellant. The liquefied propellant medium and indeed the total composition is preferably such that the active ingredient does not dissolve therein to any substantial extent. The pressurized composition may also contain a surface active agent, such as a liquid or solid non-ionic surface active agent or may be a solid anionic

surface active agent. It is preferred to use the solid anionic surface active agent in the form of a sodium salt.

[0124] A further form of topical administration is to the eye. A compound of the invention is delivered in a pharmaceutically acceptable ophthalmic vehicle, such that the compound is maintained in contact with the ocular surface for a sufficient time period to allow the compound to penetrate the corneal and internal regions of the eye, as for example the anterior chamber, posterior chamber, vitreous body, aqueous humor, vitreous humor, cornea, iris/ciliary, lens, choroid/retina and sclera. The pharmaceutically acceptable ophthalmic vehicle may, for example, be an ointment, vegetable oil or an encapsulating material. Alternatively, the compounds of the invention may be injected directly into the vitreous and aqueous humour.

[0125] Compositions for rectal or vaginal administration are preferably suppositories which may be prepared by mixing the compounds of this invention with suitable non-irritating excipients or carriers such as cocoa butter, polyethylene glycol or a suppository wax which are solid at room temperature but liquid at body temperature and therefore melt in the rectum or vaginal cavity and release the active compound.

[0126] Compounds of the present invention may also be administered in the form of liposomes. As is known in the art, liposomes are generally derived from phospholipids or other lipid substances. Liposomes are formed by mono- or multi-lamellar hydrated liquid crystals that are dispersed in an aqueous medium. Any non-toxic, physiologically acceptable and metabolizable lipid capable of forming liposomes can be used. The present compositions in liposome form can contain, in addition to a compound of the present invention, stabilizers, preservatives, excipients, and the like. The preferred lipids are the phospholipids, including the phosphatidyl cholines (lecithins) and serines, both natural and synthetic. Methods to form liposomes are known in the art.

[0127] Total daily dose of the compositions of the invention to be administered to a human or other mammal host in single or divided doses may be in amounts, for example, from 0.0001 to 300 mg/kg body weight daily and more usually 1 to 300 mg/kg body weight.

[0128] *Non-invasive Detection of Intestinal Inflammation*

[0129] The peptides of the invention may be used for detection, assessment and diagnosis of intestinal inflammation by microPET imaging using an orally stable compound having subunits selected from and corresponding to SEQ ID NOs: 1-146, and that is further labeled with at least one of a chelating group and a detectable label as part of a non-invasive

diagnostic procedure. In one embodiment, an integrin antagonist dimer molecule is conjugated with a bifunctional chelator to provide an orally stable dimer molecule. In another embodiment, an integrin antagonist dimer molecule is radiolabeled to provide an orally stable dimer molecule. The orally stable, chelated or radiolabeled dimer molecule is then administered to a subject orally or rectally. In one embodiment, the orally stable dimer molecule is included in drinking water. Following uptake of the dimer molecules, microPET imaging may be used to visualize inflammation throughout the subject's bowels and digestive track.

[0130] *Synthesis of Peptide Subunits*

[0131] The monomer peptide subunits of the present invention may be synthesized by many techniques that are known to those skilled in the art. Novel and unique monomer subunits were synthesized, purified, and dimerized using the techniques provided herein.

[0132] The peptides of the present invention were synthesized using the Merrifield solid phase synthesis techniques on Protein Technology's Symphony multiple channel synthesizer. The peptides were assembled using HBTU (O-Benzotriazole-N,N,N',N'-tetramethyl-uronium-hexafluoro-phosphate), Diisopropylethylamine(DIEA) coupling conditions. For some amino acid couplings PyAOP(7-Azabenzotriazol-1-yloxy)tripyrrolidinophosponium hexafluorophosphate) and DIEA conditions were used. Rink Amide MBHA resin (100-200mesh, 0.57mmol/g) is used for peptide with C-terminal amides and pre-loaded Wang Resin with N-a-Fmoc protected amino acid is used for peptide with C-terminal acids. The coupling reagents (HBTU and DIEA premixed) were prepared at 100mmol concentration. Similarly amino acids solutions were prepared at 100mmol concentration. The peptides were assembled using standard Symphony protocols.

[0133] *Assembly*

The peptide sequences were assembled as follows: Resin (250mg, 0.14mmol) in each reaction vial was washed twice with 4ml of DMF followed by treatment with 2.5ml of 20% 4-methyl piperidine (Fmoc de-protection) for 10min. The resin was then filtered and washed two times with DMF (4ml) and re-treated with N-methyl piperifine for additional 30 minute. The resin was again washed three times with DMF (4ml) followed by addition 2.5ml of amino acid and 2.5ml of HBTU-DIEA mixture. After 45min of frequent agitations, the resin was filtered and washed three timed with DMF (4ml each). For a typical peptide of the present invention, double couplings were performed for first 25 amino acid, and triple couplings were performed for the remaining residues. After completing the coupling reaction,

the resin was washed three times with DMF (4ml each) before proceeding to the next amino acid coupling.

[0134] *Cleavage*

[0135] Following completion of the peptide assembly, the peptide was cleaved from the resin by treatment with cleavage reagent, such as reagent K (82.5% trigluoroacetic acid, 5% water, 5% thioanisole, 5% phenol, 2.5% 1,2-ethanedithiol). The cleavage reagent was able to successfully cleave the peptide from the resin, as well as all remaining side chain protecting groups.

[0136] The cleaved were precipitated in cold diethyl ether followed by two washings with ethyl ether. The filtrate was poured off and a second aliquot of cold ether was added, and the procedure repeated. The crude peptide was dissolved in a solution of acetonitrile:water (7:3 with 1% TFA) and filtered. The quality of linear peptide was then verified using electrospray ionization mass spectrometry (ESI-MS) (Micromass/Waters ZQ) before being purified.

[0137] *Disulfide Bond Formation via Oxidation*

[0138] 50mg of crude, cleaved peptide was dissolved in 20ml of water:acetonitrile. Saturated Iodine in acetic acid was then added drop wise with stirring until yellow color persisted. The solution was stirred for 15 minutes and the reaction was monitored with analytic HPLC and LCMS. When the reaction was completed, solid ascorbic acid was added until the solution became clear. The solvent mixture was then purified by first being diluted with water and then loaded onto a reverse phase HPLC machine (Luna C18 support, 10u, 100A, Mobile phase A: water containing 0.1% TFA, mobile phase B: Acetonitrile (ACN) containing 0.1% TFA, gradient began with 5% B, and changed to 50% B over 60 minutes at a flow rate of 15ml/min). Fractions containing pure product were then freeze-dried on a lyophilyzer.

[0139] *Lactam Bond Formation*

[0140] 100mg of crude, cleaved peptide (approx. 0.12mmol) was dissolved in 100ml of anhydrous dichloromethane. HOBt (1-Hydroxybenzotriazole hydrate) (0.24mmol, 2 equivalents) was added followed by DIEA (N,N-Diisopropylethylamine) (1.2mmol, 10equivalents) and TBTU (O-(Benzotriazol-1-yl)-N,N,N',N'-tetramethyluronium tetrafluoroborate)(0.24 mmol, 2 equivalents). The mixture was stirred overnight and followed the reaction by HPLC. When the reaction was completed, dichloromethane was evaporated and diluted with water and Acetonitrile and then loaded onto a reverse phase HPLC machine

(Luna C18 support, 10u, 100A, Mobile phase A: water containing 0.1% TFA, mobile phase B: Acetonitrile (ACN) containing 0.1% TFA, gradient began with 5% B, and changed to 50% B over 60 minutes at a flow rate of 15ml/min). Fractions containing pure product were then freeze-dried on a lyophilyzer.

[0141] *Purification*

[0142] Analytical reverse-phase, high performance liquid chromatography (HPLC) was performed on a Gemini C18 column (4.6 mm x 250 mm) (Phenomenex). Semi-Preparative reverse phase HPLC was performed on a Gemini 10 μm C18 column (22 mm x 250 mm) (Phenomenex) or Jupiter 10 μm, 300 A ° C18 column (21.2 mm x 250 mm) (Phenomenex). Separations were achieved using linear gradients of buffer B in A (Mobile phase A: water containing 0.15% TFA, mobile phase B: Acetonitrile (ACN) containing 0.1% TFA), at a flow rate of 1 mL/min (analytical) and 15 mL/min (preparative). Separations were achieved using linear gradients of buffer B in A (Mobile phase A: water containing 0.15% TFA, mobile phase B: Acetonitrile (ACN) containing 0.1% TFA), at a flow rate of 1 mL/min (analytical) and 15mL/min (preparative).

[0143] *Linker Activation and Dimerization*

[0144] Small Scale DIG Linker Activation Procedure: 5mL of NMP was added to a glass vial containing IDA diacid (304.2 mg, 1 mmol), N-hydroxysuccinimide (NHS, 253.2 mg, 2.2 eq. 2.2mmol) and a stirring bar. The mixture was stirred at room temperature to completely dissolve the solid starting materials. N, N'-Dicyclohexylcarbodiimide (DCC, 453.9mg, 2.2 eq., 2.2 mmol) was then added to the mixture. Precipitation appeared within 10 min and the reaction mixture was further stirred at room temperature overnight. The reaction mixture was then filtered to remove the precipitated dicyclohexylurea (DCU). The activated linker was kept in a closed vial prior to use for dimerization. The nominal concentration of the activated linker was approximately 0.20 M.

[0145] For dimerization using PEG linkers, there is no pre-activation step involved. Commercially available pre-activated bi-functional PEG linkers were used.

[0146] Dimerization Procedure: 2mL of anhydrous DMF was added to a vial containing peptide monomer (0.1 mmol). The pH of the peptide was the adjusted to 8~9 with DIEA. Activated linker (IDA or PEG13, PEG 25) (0.48eq relative to monomer, 0.048 mmol) was then added to the monomer solution. The reaction mixture was stirred at room temperature for one hour. Completion of the dimerization reaction was monitored using analytical HPLC. The time for completion of dimerization reaction varied depending upon

the linker. After completion of reaction, the peptide was precipitated in cold ether and centrifuged. The supernatant ether layer was discarded. The precipitation step was repeated twice. The crude dimer was then purified using reverse phase HPLC (Luna C18 support, 10u, 100A, Mobile phase A: water containing 0.1% TFA, mobile phase B: Acetonitrile (ACN) containing 0.1% TFA, gradient of 15%B and change to 45%B over 60min, flow rate 15ml/min). Fractions containing pure product were then freeze-dried on a lyophilyzer.

[0147] *Simulated Intestinal Fluid (SIF) Stability Assay*

[0148] Studies were carried out in simulated intestinal fluid (SIF) to evaluate gastric stability of the dimer molecules of the instant invention. 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 had been pre-warmed to 37°C.

[0149] 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, and 60 minutes), 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 was 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. A small sampling of the results of these studies is provided and discussed in connection Figure 3, above.

EXAMPLES

[0150] *α4β7-MAdCAM Competition ELISA*

[0151] A nickel coated plate (Pierce # 15442) was coated with recombinant human integrin α4β7 (R&D Systems #5397-A30) at 800ng/well and incubated at room temperature with shaking for 1hr. The solution was then remove by shaking and blocked with assay buffer (50mM Tris-HCl pH7.6, 150mM NaCl, 1mM $MnCl_2$, 0.05% Tween-20 and 0.5% BSA) at 250ul/well. The plate was then incubated at room temperature for 1hr. Each well was washed 3 times with wash buffer (50mM Tris-HCl pH7.6, 100mM NaCl, 1mM $MnCl_2$,

0.05% Tween-20). To each well was added 25ul of a serial dilution (3-fold dilutions in assay buffer) of peptides starting at 20μM or lower concentration. 25 ul of recombinant human MAdCAM-Fc chimera (R&D Systems #6056-MC) was then added to each well at a fixed concentration 20nM. The final starting peptide concentration was 10μM, and the final MAdCAM-1 concentration was 10nM. The plates were then incubated at room temperature for 1hr to reach binding equilibrium. The wells were then washed three times with wash buffer. 50ul of mouse anti-human IgG1-HRP (Invitrogen # A10648) diluted in 1:2000 in assay buffer was then added to each well. The wells were incubated at room temperature for 45 min with shaking. The wells were then washed 3 times with wash buffer. 100ul of TMB were then added to each well and closely observe during development time. The reaction was stopped with 2N H_2SO_4 and absorbance was read at 450nm.

[0152] *α4β1-VCAM Competition ELISA*

[0153] A Nunc MaxiSorp plate was coated with rh VCAM-1/CD106 Fc chimera (R&D #862-VC) at 400ng/well in 50ul per well in 1XPBS and incubated overnight at 4° C. The solution was removed by shaking and then blocked with 250ul of 1% BSA in 1XPBS per well. The wells were then incubated at room temperature for 1hr with shaking. Each well was then washed once with wash buffer (50mM Tris-HCl pH7.6, 100mM NaCL, 1mM $MnCl_2$, 0.05% Tween-20). 25ul of serial dilutions of peptides starting at 200μM or lower concentration in assay buffer (Assay buffer: 50mM Tris-HCl pH7.6, 100mM NaCl, 1mM $MnCl_2$, 0.05% Tween-20) was added to each well. Additionally, 25 ul of α4β1 (R&D Systems #5668-A4) was added to each well at a fixed concentration of 20nM. The final peptide and α4β1 concentrations were 100μM and 10nM, respectively. The plates were then incubated at 37°C for 2hr. The solution was then removed by shaking and each well was washed three times with wash buffer. 50ul of 9F10 antibody at 4ug/ml (purified mouse anti-human CD49d, BD Bioscience Cat# 555502) was then added to each well, and the plate was incubated at room temperature for 1hr with shaking. The solution was again removed by shaking, and each well was washed three times with wash buffer. 50ul of peroxidase-conjugated AffiniPure Goat anti-mouse IgG (Jackson immune research cat #115-035-003) diluted in 1:5000 in assay buffer was added to each well. The plate was incubated at room temperature for 30 min with shaking. Each well was then washed 3 times with wash buffer. 100ul of TMB was then added to each well and closely observe during developing time. The reaction was stepped with 2N H_2SO_4 and absorbance was read at 450nm.

[0154] *Example 3: α4β7-MAdCAM Cell Adhesion Assay*

[0155] RPMI 8866 cells (Sigma #95041316) are cultured in RPMI 1640 HEPES medium (Invitrogen #22400-089) supplemented with 10% serum (Fetal Bovine Serum, Invitrogen # 16140-071), 1 mM sodium pyruvate (Invitrogen #11360-070), 2mM L-glutamine (Invitrogen # 25030-081) and Penicillin-Streptomycin (Invitrogen # 15140-122) at 100 units of penicillin and 100 µg of streptomycin per ml. The cells are washed two times in DMEM medium (ATCC #30-2002) supplemented with 0.1% BSA, 10 mM HEPES pH 7 and 1 mM $MnCl_2$. The cells are re-suspended in supplemented DMEM medium at a density of 4 X 10^6 cells/ml.

[0156] A Nunc MaxiSorp plate was coated with rh MAdCAM-1/ Fc Chimera (R&D 6056-MC) at 200 ng per well in 50 ul per well in 1XPBS and incubated at 4°C overnight. The solution was then removed by shaking, blocked with 250 ul per well PBS containing 1% BSA, and incubated at 37°C for 1 hr. The solution was removed by shaking. Peptides are diluted by serial dilution in a final volume of 50 ul per well (2X concentration). To each well, 50 ul of cells (200,000 cells) are added and the plate is incubated at 37°C, 5% CO_2 for 30-45 min to allow cell adhesion. The wells are washed manually three times (100 ul per wash) with supplemented DMEM. After the final wash, 100ul/well of supplemented DMEM and 10ul/well of MTT reagent (ATTC cat# 30-1010K) are added. The plate is incubated at 37°C, 5% CO2 for 2-3hrs until a purple precipitate is visible. 100ul of Detergent Reagent (ATTC cat# 30-1010K) is added to each well. The plate is covered from the light, wrapped in Parafilm to prevent evaporation, and left overnight at room temperature in the dark. The plate is shaken for 5 min and the absorbance at 570 nm is measured. To calculate the dose response, the absorbance value of control wells not containing cells is subtracted from each test well.

[0157] *Example 4: α4β1-VCAM Cell Adhesion Assay*

[0158] Jurkat E6.1 cells (Sigma #88042803) are cultured in RPMI 1640 HEPES medium (Invitrogen #22400-089) supplemented with 10% serum (Fetal Bovine Serum, Invitrogen # 16140-071), 1 mM sodium pyruvate (Invitrogen #11360-070), 2mM L-glutamine (Invitrogen # 25030-081) and Penicillin-Streptomycin (Invitrogen # 15140-122) at 100 units of penicillin and 100 µg of streptomycin per ml. The cells are washed two times in DMEM medium (ATCC #30-2002) supplemented with 0.1% BSA, 10 mM HEPES pH 7 and 1 mM $MnCl_2$. The cells are re-suspended in supplemented DMEM medium at a density of 4 X 10^6 cells/ml.

[0159] A Nunc MaxiSorp plate was coated with rh VCAM-1/CD106 Fc chimera (R&D #862-VC) at 400 ng per well in 50 ul per well in 1XPBS and incubated at 4°C overnight. The solution was then removed by shaking, blocked with 250 ul per well PBS containing 1% BSA, and incubated at 37°C for 1 hr. The solution was removed by shaking. peptides are diluted by serial dilution in a final volume of 50 ul per well (2X concentration). To each well, 50 ul of cells (200,000 cells) are added and the plate is incubated at 37°C, 5% CO_2 for 30-45 min to allow cell adhesion. The wells are washed manually three times (100 ul per wash) with supplemented DMEM. After the final wash, 100ul/well of supplemented DMEM and 10ul/well of MTT reagent (ATTC cat# 30-1010K) are added. The plate is incubated at 37°C, 5% CO2 for 2-3hrs until a purple precipitate is visible. 100ul of Detergent Reagent (ATTC cat# 30-1010K) is added to each well. The plate is covered from the light, wrapped in Parafilm to prevent evaporation, and left overnight at room temperature in the dark. The plate is shaken for 5 min and the absorbance at 570 nm is measured. To calculate the dose response, the absorbance value of control wells not containing cells is subtracted from each test well.

[0160] The present invention may be embodied in other specific forms without departing from its structures, methods, or other essential characteristics as broadly described herein and claimed hereinafter. The described embodiments are to be considered in all respects only as illustrative, and not restrictive. The scope of the invention is, therefore, indicated by the appended claims, rather than by the foregoing description. All changes that come within the meaning and range of equivalency of the claims are to be embraced within their scope.

CLAIMS

1. A peptide dimer compound comprising two peptide monomer subunits of Formula (I) Xaa^1-Xaa^2-Xaa^3-Xaa^4-Xaa^5-Xaa^6-Xaa^7-Xaa^8-Xaa^9-Xaa^{10}-Xaa^{11}-Xaa^{12}-Xaa^{13}-Xaa^{14}, or a pharmaceutically acceptable salt thereof, wherein

Xaa^1 is selected from the group consisting of absent, Gln, , Asp, Pro, Gly, His, Ala, Ile, Phe, Lys, Arg, Asn, Glu, Leu, Val, Tyr, Trp, Ser, Met, Thr, a suitable isostere, and a corresponding D-amino acid;

Xaa^2 is selected from the group consisting of absent, Gln, , Asp, Pro, Gly, His, Ala, Ile, Phe, Lys, Arg, Asn, Glu, Leu, Val, Tyr, Trp, Ser, Met, Thr, a suitable isostere, and a corresponding D-amino acid;

Xaa^3 is selected from the group consisting of absent, Gln, , Asp, Pro, Gly, His, Ala, Ile, Phe, Lys, Arg, Asn, Glu, Leu, Val, Tyr, Trp, Met, Thr, Ser, a suitable isostere, and a corresponding D-amino acid;

Xaa^4 is selected from the group consisting of Cys, Asp, Glu, Lys, Pen, HGlu, HLys, Orn, Dap, Dab, βAsp, βGlu, HGlu, HLys, a suitable isostere, and a corresponding D-amino acid;

Xaa^5 is selected from the group consisting of Gln, Asn, Asp, Pro, Gly, His, Ala, Ile, Phe, Lys, Arg, Glu, Leu, Val, Tyr, Trp, Met, Thr, hArg, 4-Guan, Phe(4-NH2), Cit, Cav, Dap, Dab, a suitable isostere, and a corresponding D-amino acid;

Xaa^6 is selected from the group consisting of Ser, Gln, Asn, Asp, Pro, Gly, His, Ala, Ile, Phe, Lys, Arg, Glu, Leu, Val, Thr, Trp, Tyr, Met, a suitable isostere replacement and a corresponding D-amino acid;

Xaa^7 is selected from the group consisting of Asp, and a suitable isostere replacement;

Xaa^8 is selected from the group consisting of Thr, Gln, Ser, Asn, Asp, Pro, Gly, His, Ala, Ile, Phe, Lys, Arg, Glu, Val, Tyr, Trp, Leu, Met, a suitable isostere, and a corresponding D-amino acid;

Xaa^9 is selected from the group consisting of Gln, Asn, Asp, Pro, Gly, Ala, Phe, Leu, Glu, Ile, Val, HLeu, n-Butyl Ala, n-Pentyl Ala, n-Hexyl Ala, Nle, cyclobutyl-Ala, HCha, a suitable isostere, and a corresponding D-amino acid;

Xaa^{10} is selected from the group consisting of Cys, Asp, Lys, Glu, Pen, HAsp, HGlu, HLys, Orn, Dap, Dab, HLys, a suitable isostere, and a corresponding D-amino acid;

Xaa^{11} is selected from the group consisting of absent, Gly, Gln, Asn, Asp, Ala, Ile, Leu, Val, Met, Thr, Lys, Trp, Tyr, His, Glu, Ser, Arg, Pro, Phe, Sar, 1-Nal, 2-Nal, HPhe,

Phe(4-F), dihydro-Trp, Dap, Dab, Orn, D-Orn, D-Dap, D-Dab, Bip, Ala(3,3 diphenyl), Biphenyl-Ala, D-Phe, D-Trp, D-Tyr, D-Glu, D-His, D-Lys, 3,3-diPhe, β-HTrp, F(4-CF3), O-Me-Tyr, 4-Me-Phe, an aromatic ring substituted Phe, an aromatic ring substituted Trp, an aromatic ring substituted His, a hetero aromatic amino acid, N-Me-Lys, N-Me-Lys(Ac), 4-Me-Phe, a corresponding D-amino acid; a suitable isostere; and a suitable linker moiety.

Xaa^{12} is selected from the group consisting of absent, Glu, Lys, Gln, Pro, Gly, His, Ala, Ile, Phe, Arg, Leu, Val, Tyr, Trp, Met, Gla, Ser, Asn, Asp, Dap, Dab, Orn, D-Orn, D-Dap, D-Dab, β-HGlu, 2-Nal, 1-Nal, Bip, β-HPhe, βGlu, a suitable isostere, a suitable linker moiety, and a corresponding D-amino acid;

Xaa^{13} is selected from the group consisting of absent, Gln, Pro, Gly, His, Ala, Ile, Phe, Lys, Arg, Leu, Val, Tyr, Trp, Met, Glu, Gla, Ser, Asn, Dap, Dab, Orn, D-Orn, D-Dap, D-Dab, absent, a suitable isostere, and a corresponding D-amino acid; and

Xaa^{14} is selected from the group consisting of absent, a natural amino acid, a suitable isostere, and a corresponding D-amino acid,

wherein the peptide dimer compound further comprises at least one of a disulfide bond and a lactam bond between Xaa^{4} and Xaa^{10}.

2. The peptide dimer compound of claim 1 further comprising a suitable linker moiety selected from the group consisting of DIG, DIG-OH, PEG13, PEG25, PEG1K, PEG2K, PEG3.4K, PEG4K, PEG5K, IDA, IDA-Palm, IDA-Boc, IDA-Isovaleric acid, Triazine, Triazine-Boc, Isophthalic acid, 1,3-phenylenediacetic acid, 1,4-phenylenediacetic acid, cyclopropylacetic acid, 4-fluoorobenzoic acid, 4-fluorophenylacetic acid, 3-phenylpropionic acid, succinic acid, biotin, glutaric acid, Azelaic acid, Pimelic acid, Dodecanedioic acid, suitable aliphatics, suitable aromatics, heteroaromatics, and polyethylene glycols having a molecular weight from approximately 400Da to approximately 40,000Da.

3. The peptide dimer compound of claim 2, wherein the N-terminus of each monomer subunit is joined by a suitable linker moiety to provide an N-terminus dimer compound.

4. The peptide dimer compound of claim 2, wherein the C-terminus of each monomer sumbunit is joined by a suitable linker moiety to provide a C-terminus dimer compound.

5. The peptide dimer compound of claim 1, further comprising a disulfide bond between Xaa^{4} and Xaa^{10}.

6. The peptide dimer compound of claim 1, further comprising a lactam bond between Xaa^{4} and Xaa^{10}.

7. The peptide dimer compound of claim 1, further comprising N(alpha)methylation at one or more positions selected from the group consisting of Xaa^3, Xaa^5, Xaa^7-Xaa^9, and Xaa^{11}-Xaa^{13}.

8. The peptide dimer compound of claim 1, further comprising acylation at one or more position selected from the group consisting of Xaa^1-Xaa^3 and Xaa^{11}-Xaa^{14}.

9. The peptide dimer compound of claim 1, wherein when Xaa^{10} is selected from the group consisting of Asp, HAsp, Glu, and HGlu, HLys, Xaa^4 is selected from the group consisting of Lys, Dap, Dab, HLys, Orn, and HGlu, and when Xaa^{10} is selected from the group consisting of Lys, Dap, Dab, HLys, Orn, and HGlu, Xaa^4 is selected from the group consisting of Asp, HAsp, Glu, HGlu, and HLys.

10. The peptide dimer compound of claim 1, further comprising a lactam bond between Xaa^4 and Xaa^{10}.

11. The peptide dimer compound of claim 1, wherein when Xaa^4 is selected from the group consisting of Asp, HAsp, Glu, HGlu, and HLys, and when Xaa^{10} is selected from the group consisting of Lys, Dap, Dab, HLys, Orn, and HGlu, Xaa^4 and Xaa^{10} are cyclized through an amide bond.

12. A method for treating inflammatory bowel disease in a patient, comprising administering to the patient an effective amount of a peptide dimer compound of claim 1.

13. The method of claim 12, wherein the inflammatory bowel disease is selected from a group consisting of ulcerative colitis.

14. The method of claim 12, wherein the inflammatory bowel disease is Crohn's disease.

15. The method of claim 12, wherein the peptide dimer compound inhibits binding of $\alpha 4\beta 7$ to MAdCAM.

16. A method for treating a human having an inflammatory bowel disease, comprising the steps of administering to the human an effective amount of a peptide dimer according to the composition of claim 1.

17. The method of claim 16, further comprising a step wherein the peptide dimer is administered as an initial does followed by one or more subsequent doses and the minimum interval between any two doses is a period of less than 1 day, and wherein each of the doses comprises an effective amount of the peptide dimer.

18. The method of claim 16, wherein the effective amount of peptide dimer is sufficient to achieve at least one of the following selected from the group consisting of: a) about 50% or greater saturation of MAdCAM binding sites on $\alpha 4\beta 7$ integrin molecules; b) about 50% or

greater inhibition of α4β7 integrin expression on the cell surface; and c) about 50% or greater saturation of MAdCAM binding sites on α4β7 molecules and about 50% or greater inhibition of α4β7 integrin expression on the cell surface, wherein i) the saturation is maintained for a period consistent with a dosing frequency of no more than twice daily; ii) the inhibition is maintained for a period consistent with a dosing frequency of no more than twice daily; or iii) the saturation and the inhibition are each maintained for a period consistent with a dosing frequency of no more than twice daily;

19. The method of claim 16, wherein the peptide dimer is administered orally.

20. The method of claim 16, wherein the peptide dimer is administered parenterally.

21. The method of claim 16, wherein the peptide dimer is administered topically.

22. The method of claim 16, wherein the peptide dimer comprises two monomer subunits selected from the group consisting of SEQ ID NO: 39-146.

23. The method of claim 16, further comprising a step for administering the peptide dimer to the human at an interval sufficient to ameliorate the inflammatory bowel disease.

24. A method for treating a human afflicted with a condition that is associated with a biological function of α4β7, the method comprising administering to the human a peptide dimer according to the composition of claim 1.

25. The method of claim 24, further comprising a step for administering the peptide dimer to the human at an interval sufficient to ameliorate the condition.

26. The method of claim 25, wherein the interval is selected from the group consisting of around the clock, hourly, every four hours, once daily, twice daily, three times daily, four times daily, every other day, weekly, bi-weekly, and monthly.

27. A method for stabilizing a peptide dimer compound according to claim 1, the method comprising a step for substituting Xaa^4 and Xaa^{10} with an amino acid residue selected from the group consisting of Cys and Pen, wherein Xaa^4 and Xaa^{10} form a cyclized structure through a disulfide bond.

28. A method for stabilizing a peptide dimer compound of Formula (II)

Xaa^1-Xaa^2-Xaa^3-Xaa^4-Xaa^5-Xaa^6-Xaa^7-Xaa^8-Xaa^9-Xaa^{10}, or a pharmaceutically acceptable salt thereof, wherein the method comprises a step for substituting Xaa^1 and Xaa^7 with compatible amino acid residues that are capable of forming a cyclized structure through at least one of disulfide bond or lactam bond.

29. The method of claim 28, wherein the compatible amino acids are selected from the group consisting of Cys and Pen, wherein Xaa^1 and Xaa^7 form a cyclized structure through a disulfide bond.

30. The method of claim 28, wherein when Xaa^4 is selected from the group consisting of Lys, HLys, Orn, Dap, and Dab, and when Xaa^{10} is selected from the group consisting of Asp, Glu, HGlu, β-Asp, and β-Glu, Xaa^4 and Xaa^{10} are cyclized through an lactam bond

31. A pharmaceutical composition comprising a peptide dimer compound according to at least one of Formula (I) and Formula (II).

32. The composition of claim 31, further comprising an enteric coating.

33. The composition of claim 32, wherein the enteric coating protects and releases the pharmaceutical composition within a subject's lower gastrointestinal system.

34. A method for treating a condition in a subject comprising administering the pharmaceutical composition of claim 32 to the subject, wherein the condition is treatable by reducing the activity (partially or fully) of α4β7 in the subject.

35. The method of claim 34, wherein the subject is a human being.

36. The method of claim 34, wherein the condition is an inflammatory condition of the gastrointestinal system.

37. A method for treating a human afflicted with a condition that is associated with a biological function α4β7 and comprising administering to the individual a peptide dimer of Formula (I) in an amount sufficient to inhibit (partially or fully) the biological function of α4β7 to tissues expressing MAdCAM.

38. A method for treating a human afflicted with a condition that is associated with a biological function of α4β7 and comprising administering to the individual a peptide dimer of Formula (I) in an effective amount sufficient to at least partially inhibit the biological function of α4β7 to tissues expressing MAdCAM.

39. The method of claim 37, wherein the condition is inflammatory bowel disease.

40. The method of claim 37, wherein the condition is selected from the group consisting of 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, and graft versus host disease.

41. The method of claim 37, wherein the peptide dimer is administered to the individual by a form of administration selected from the group consisting of oral, intravenous, peritoneal, intradermal, subcutaneous, intramuscular, intrathecal, inhalation, vaporization, nebulization, sublingual, buccal, parenteral, rectal, vaginal, and topical.

42. A method for treating an individual with an α4β7 integrin antagonist dimer molecule according to at least one of Formula (I) and Formula (II), wherein the α4β7 integrin antagonist dimer molecule comprises an increased half-life.

43. The method of claim 42, wherein the increased half-life is at least one day *in vitro* or *in vivo*.

44. The method of claim 42, wherein when the increased half-life is equal to or greater than a period consistent with no more frequent than twice daily dosing *in vivo*, the α4β7 integrin antagonist dimer molecule comprises a pharmaceutical preparation that is administered orally.

45. The method of claim 42, wherein when the increased half-life is from approximately 12 hours to greater than 24 *in vivo*, the α4β7 integrin antagonist dimer molecule comprises a pharmaceutical preparation that is administered parenterally.

46. The method of claim 42, wherein when the increased half-life is from approximately 12 hours to greater than 24 hours *in vivo*, the α4β7 integrin antagonist dimer molecule comprises a pharmaceutical preparation that is administered topically.

47. A method for increasing SIF stability of peptide dimer molecule according to SEQ ID NOs: 1-146, comprising a step for substituting N-Me-Arg for one or more unmethylated arginine residues.

48. A method for increasing SIF stability of a peptide dimer molecule according to SEQ ID NOs: 1-146, comprising a step for substituting Pen for one or more cysteine residues.

49. A method for increasing redox stability of a peptide dimer molecule according to SEQ ID NOs: 1-146, comprising a step for substituting Pen for one or more cysteine residues.

50. A method for increasing potency of a peptide molecule for a4b7 according to SEQ ID NOs: 1-146, comprising forming a dimer molecule through a C- or N-terminal dimerization.

SEQUENCE LISTING

<110> Bhandari, Ashok
Mattheakis, Larry C.
Patel, Dinesh V.

<120> NOVEL a4b7 PEPTIDE DIMER ANTAGONISTS

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<223> Dap, Dab, Orn, D-Orn, D-Dap, D-Dab, D-Lys, D-Glu, Beta-HGlu,
2-Nal, 1-Nal, D-Asp, Bip, Beta-HPhe, Beta-Glu, D-Tyr, Beta-HGlu,
Gla

<220>
<221> MOD_RES
<222> (12)..(12)
<223> N(alpha)METHYLATION

<220>
<221> VARIANT
<222> (13)..(13)
<223> absent, Gln, Pro, Gly, His, Ala, Ile, Phe, Lys, Arg, Leu, Val,
Tyr, Trp, Met, Glu, Ser, Asn

<220>
<221> MOD_RES

<222> (13)..(13)
<223> Dap, Dab, Orn, D-Orn, D-Dap, D-Dab, D-Lys, Gla

<220>
<221> MOD_RES
<222> (13)..(13)
<223> ACETYLATION

<220>
<221> MOD_RES
<222> (13)..(13)
<223> N(alpha)METHYLATION

<220>
<221> MOD_RES
<222> (14)..(14)
<223> ACETYLATION

<220>
<221> VARIANT
<222> (14)..(14)
<223> absent, can be any naturally occuring amino acid

<220>
<221> MOD_RES
<222> (14)..(14)
<223> N(alpha)METHYLATION

<400> 1

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10

<210> 2
<211> 10
<212> PRT
<213> Unknown

<220>
<223> Synthetic Construct

<220>
<221> VARIANT
<222> (1)..(1)
<223> Cys, Asp, Glu, Lys

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Pen, HGlu, HLys, Orn, Dap, Dab

<220>
<221> MOD_RES
<222> (1)..(1)
<223> ACETYLATION

<220>
<221> DISULFID
<222> (1)..(7)
<223> Disulfide bond between Xaa at position 1 and Xaa at position 7

<220>
<221> LACTAM
<222> (1)..(7)

<220>

<221> VARIANT
<222> (2)..(2)
<223> Gln, Asn, Asp, Pro, Gly, His, Ala, Ile, Phe, Lys, Arg, Glu, Leu, Val, Tye, Trp, Met, Thr

<220>
<221> MOD_RES
<222> (2)..(2)
<223> HArg, Dap, Dab, 4-Guan, Cit, Cav

<220>
<221> MOD_RES
<222> (2)..(2)
<223> N(alpha)METHYLATION; N-Me-Arg; Arg-Me-sym; Arg-Me-asym

<220>
<221> VARIANT
<222> (3)..(3)
<223> Ser, Thr, Gln, Asn, Asp, Pro, Gly, His, Ala, Ile, Phe, Lys, Arg, Glu, Leu, Val, Tyr, Trp, Met

<220>
<221> MOD_RES
<222> (4)..(4)
<223> N(alpha)METHYLATION

<220>
<221> VARIANT
<222> (4)..(4)
<223> Asp

<220>
<221> MOD_RES
<222> (5)..(5)
<223> N(alpha)METHYLATION

<220>
<221> VARIANT
<222> (5)..(5)
<223> Thr, Gln, Ser, Asn, Asp, Pro, Gly, His, Ala, Ile, Phe, Lys, Arg, Glu, Val, Tyr, Trp, Met

<220>
<221> MOD_RES
<222> (6)..(6)
<223> HLeu, n-Butyl Ala, n-Pentyl Ala

<220>
<221> MOD_RES
<222> (6)..(6)
<223> N(alpha)METHYLATION

<220>
<221> VARIANT
<222> (6)..(6)
<223> Gln, Asn, Asp, Pro, Gly, Ala, Phe, Leu, Glu, Ile, Val

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Pen, HLys, Orn, HGlu, Dap, Dab

<220>
<221> VARIANT
<222> (7)..(7)
<223> Cys, Asp, Lys, Glu

<220>

<221> VARIANT
<222> (8)..(8)
<223> Gly, Gln, Asn, Asp, Ala, Ile, Leu, Val, Met, Thr, Lys, Trp, Tyr, His, Glu, Ser, Arg, Pro, Phe

<220>
<221> MOD_RES
<222> (8)..(8)
<223> Sar, 1-Nal, 2-Nal, HPhe, Phe(4-F), dihydro-Trp, Dap, Dab, Orn, D-Orn, D-Dap, D-Dab, Bip, Ala(3,3 diphenyl), Biphenyl-Ala, D-Phe, D-Trp, D-Tyr, D-Glu, D-His, D-Lys, 3,3-diPhe, Beta-HTrp, F(4-CF3), O-Me-Tyr, 4-Me-Phe, Phe(2,4-Cl2), Phe(3,4-Cl2),

<220>
<221> MOD_RES
<222> (8)..(8)
<223> 1,1-Indane, 2,2-Indane, D-HPhe

<220>
<221> MOD_RES
<222> (8)..(8)
<223> N(alpha)METHYLATION

<220>
<221> MOD_RES
<222> (8)..(10)
<223> ACETYLATION

<220>
<221> MOD_RES
<222> (9)..(9)
<223> Dap, Dab, Orn, D-Orn, D-Dap, D-Dab, D-Lys, D-Glu, Beta-HGlu, 2-Nal, 1-Nal, D-Asp, Bip, Beta-HPhe, Beta-Glu, D-Tyr, Beta-HGlu

<220>
<221> MOD_RES
<222> (9)..(9)
<223> N(alpha)METHYLATION

<220>
<221> VARIANT
<222> (9)..(9)
<223> absent, Glu, Lys, Gln, Pro, Gly, His, Ala, Asp, Ile, Phe, Arg, Leu, Val, Tyr, Trp, Met, Ser, Asn

<220>
<221> VARIANT
<222> (10)..(10)
<223> absent, Gln, Pro, Gly, His, Ala, Ile, Phe, Lys, Arg, Leu, Val, Tyr, Trp, Met, Glu, Ser, Asn

<220>
<221> MOD_RES
<222> (10)..(10)
<223> Dap, Dab, Orn, D-Orn, D-Dap, D-Dab, D-Lys, Gla

<220>
<221> MOD_RES
<222> (10)..(10)
<223> N(alpha)METHYLATION

<400> 2

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10

<210> 3
<211> 9
<212> PRT
<213> Unknown

<220>
<223> Synthetic Construct

<220>
<221> MOD_RES
<222> (1)..(1)
<223> ACETYLATION

<220>
<221> DISULFID
<222> (1)..(7)
<223> Disulfide bond between Cys at position 1 and Cys at position 7

<220>
<221> MOD_RES
<222> (2)..(2)
<223> N(alpha)METHYLATION

<220>
<221> VARIANT
<222> (3)..(3)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> VARIANT
<222> (5)..(6)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> VARIANT
<222> (8)..(9)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> MOD_RES
<222> (9)..(9)
<223> ACETYLATION

<220>
<221> MOD_RES
<222> (9)..(9)
<223> N(alpha)METHYLATION

<220>
<221> MOD_RES
<222> (9)..(9)
<223> D-Lys, Dap, Dab, Orn, D-Orn, D-Dab, D-Dap

<400> 3

Cys Arg Xaa Asp Xaa Xaa Cys Xaa Xaa
1 5

<210> 4
<211> 9
<212> PRT
<213> Unknown

<220>
<223> Synthetic Construct

<220>
<221> DISULFID
<222> (1)..(7)
<223> Disulfide bond between Cys at position 1 and Xaa at position 7

<220>
<221> MOD_RES
<222> (1)..(1)
<223> ACETYLATION

<220>
<221> MOD_RES
<222> (2)..(2)
<223> N(alpha)METHYLATION

<220>
<221> VARIANT
<222> (3)..(3)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> VARIANT
<222> (5)..(6)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Pen

<220>
<221> VARIANT
<222> (8)..(9)
<223> Can be any naturally occurring amino acid

<220>
<221> MOD_RES
<222> (9)..(9)
<223> N(alpha)METHYLATION

<220>
<221> MOD_RES
<222> (9)..(9)
<223> ACYLATION

<220>
<221> MOD_RES
<222> (9)..(9)
<223> ACETYLATION

<220>
<221> MOD_RES
<222> (9)..(9)
<223> D-Lys, Dap, Dab, Orn, D-Orn, D-Dab, D-Dap

<400> 4

Cys Arg Xaa Asp Xaa Xaa Xaa Xaa Xaa
1 5

<210> 5
<211> 9
<212> PRT
<213> Unknown

<220>

<223> Synthetic Construct

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Pen

<220>
<221> MOD_RES
<222> (1)..(1)
<223> ACETYLATION

<220>
<221> DISULFID
<222> (1)..(7)
<223> Disulfide bond between Xaa at position 1 and Cys at position 7

<220>
<221> MOD_RES
<222> (2)..(2)
<223> N(alpha)METHYLATION

<220>
<221> VARIANT
<222> (3)..(3)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> VARIANT
<222> (5)..(6)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> VARIANT
<222> (8)..(9)
<223> Xaa can be any naturally occurring amino acid

<220>
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<222> (9)..(9)
<223> N(alpha)METHYLATION

<220>
<221> MOD_RES
<222> (9)..(9)
<223> ACETYLATION

<220>
<221> MOD_RES
<222> (9)..(9)
<223> D-Lys, Dap, Dab, Orn, D-Orn, D-Dab, D-Dap

<400> 5

Xaa Arg Xaa Asp Xaa Xaa Cys Xaa Xaa
1 5

<210> 6
<211> 9
<212> PRT
<213> Unknown

<220>
<223> Synthetic Construct

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Pen

<220>
<221> MOD_RES
<222> (1)..(1)
<223> ACETYLATION

<220>
<221> DISULFID
<222> (1)..(7)
<223> Disulfide bond between Xaa at position 1 and Xaa at position 7

<220>
<221> MOD_RES
<222> (2)..(2)
<223> N(alpha)METHYLATION

<220>
<221> VARIANT
<222> (3)..(3)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> VARIANT
<222> (5)..(6)
<223> Xaa can be any naturally occurring amino acid

<220>
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<222> (7)..(7)
<223> Pen

<220>
<221> VARIANT
<222> (8)..(9)
<223> Xaa can be any naturally occurring amino acid

<220>
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<222> (9)..(9)
<223> ACETYLATION

<220>
<221> MOD_RES
<222> (9)..(9)
<223> N(alpha)METHYLATION

<220>
<221> MOD_RES
<222> (9)..(9)
<223> D-Lys, Dap, Dab, Orn, D-Orn, D-Dab, D-Dap

<400> 6

Xaa Arg Xaa Asp Xaa Xaa Xaa Xaa Xaa
1 5

<210> 7
<211> 10
<212> PRT
<213> Unknown

<220>
<223> Synthetic Construct

<220>
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<222> (1)..(1)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> MOD_RES
<222> (1)..(1)
<223> ACETYLATION

<220>
<221> DISULFID
<222> (2)..(8)

<220>
<221> DISULFID
<222> (2)..(8)
<223> Disulfide bond between Cys at position 2 and Cys at position 8

<220>
<221> MOD_RES
<222> (3)..(3)
<223> N(alpha)METHYLATION

<220>
<221> VARIANT
<222> (4)..(4)
<223> Xaa can be any naturally occurring amino acid

<220>
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<222> (6)..(7)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> VARIANT
<222> (9)..(10)
<223> Xaa can be any naturally occurring amino acid

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

<220>
<221> MOD_RES
<222> (10)..(10)
<223> N(alpha)METHYLATION

<220>
<221> MOD_RES
<222> (10)..(10)
<223> D-Lys, Dap, Dab, Orn, D-Orn, D-Dab, D-Dap

<400> 7

Xaa Cys Arg Xaa Asp Xaa Xaa Cys Xaa Xaa
1 5 10

<210> 8
<211> 10
<212> PRT
<213> Unknown

<220>

<223> Synthetic Construct

<220>
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<223> Xaa can be any naturally occurring amino acid

<220>
<221> MOD_RES
<222> (1)..(1)
<223> ACETYLATION

<220>
<221> DISULFID
<222> (2)..(8)
<223> Disulfide bond between Cys at position 2 and Xaa at position 8

<220>
<221> MOD_RES
<222> (3)..(3)
<223> N(alpha)METHYLATION

<220>
<221> VARIANT
<222> (4)..(4)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> VARIANT
<222> (6)..(7)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> MOD_RES
<222> (8)..(8)
<223> Pen

<220>
<221> VARIANT
<222> (9)..(10)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> MOD_RES
<222> (10)..(10)
<223> ACETYLATION

<220>
<221> MOD_RES
<222> (10)..(10)
<223> N(alpha)METHYLATION

<220>
<221> MOD_RES
<222> (10)..(10)
<223> D-Lys, Dap, Dab, Orn, D-Orn, D-Dab, D-Dap

<400> 8

Xaa Cys Arg Xaa Asp Xaa Xaa Xaa Xaa Xaa
1 5 10

<210> 9
<211> 10
<212> PRT
<213> Unknown

<220>
<223> Synthetic Construct

<220>
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<223> Xaa can be any naturally occurring amino acid

<220>
<221> MOD_RES
<222> (1)..(1)
<223> ACETYLATION

<220>
<221> MOD_RES
<222> (2)..(2)
<223> Pen

<220>
<221> DISULFID
<222> (2)..(8)
<223> Disulfide bond between Xaa at position 2 and Cys at position 8

<220>
<221> MOD_RES
<222> (3)..(3)
<223> N(alpha)METHYLATION

<220>
<221> VARIANT
<222> (4)..(4)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> VARIANT
<222> (6)..(7)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> VARIANT
<222> (9)..(10)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> MOD_RES
<222> (10)..(10)
<223> ACETYLATION

<220>
<221> MOD_RES
<222> (10)..(10)
<223> N(alpha)METHYLATION

<220>
<221> MOD_RES
<222> (10)..(10)
<223> D-Lys, Dap, Dab, Orn, D-Orn, D-Dab, D-Dap

<400> 9

Xaa Xaa Arg Xaa Asp Xaa Xaa Cys Xaa Xaa
1 5 10

<210> 10
<211> 10

<212> PRT
<213> Unknown

<220>
<223> Synthetic Construct

<220>
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<223> Xaa can be any naturally occurring amino acid

<220>
<221> MOD_RES
<222> (1)..(1)
<223> ACETYLATION

<220>
<221> MOD_RES
<222> (2)..(2)
<223> Pen

<220>
<221> DISULFID
<222> (2)..(8)
<223> Disulfide bond between Xaa at position 2 and Xaa at position 8

<220>
<221> MOD_RES
<222> (3)..(3)
<223> N(alpha)METHYLATION

<220>
<221> VARIANT
<222> (4)..(4)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> VARIANT
<222> (6)..(7)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> MOD_RES
<222> (8)..(8)
<223> Pen

<220>
<221> VARIANT
<222> (9)..(10)
<223> Xaa can be any naturally occurring amino acid

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

<220>
<221> MOD_RES
<222> (10)..(10)
<223> N(alpha)METHYLATION

<220>
<221> MOD_RES
<222> (10)..(10)
<223> D-Lys, Dap, Dab, Orn, D-Orn, D-Dab, D-Dap

<400> 10

Xaa Xaa Arg Xaa Asp Xaa Xaa Xaa Xaa Xaa
1 5 10

<210> 11
<211> 10
<212> PRT
<213> Unknown

<220>
<223> Synthetic Construct

<220>
<221> MOD_RES
<222> (1)..(1)
<223> ACETYLATION

<220>
<221> DISULFID
<222> (1)..(7)
<223> Disulfide bond between Cys at position 1 and Cys at position 7

<220>
<221> MOD_RES
<222> (2)..(2)
<223> N(alpha)METHYLATION

<220>
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<222> (3)..(3)
<223> Xaa can be any naturally occurring amino acid

<220>
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<222> (5)..(5)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> VARIANT
<222> (6)..(6)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> VARIANT
<222> (8)..(10)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> MOD_RES
<222> (10)..(10)
<223> N(alpha)METHYLATION

<220>
<221> MOD_RES
<222> (10)..(10)
<223> D-Lys, Dap, Dab, Orn, D-Orn, D-Dab, D-Dap

<220>
<221> MOD_RES
<222> (10)..(10)
<223> ACETYLATION

<400> 11

Cys Arg Xaa Asp Xaa Xaa Cys Xaa Xaa Xaa
1 5 10

<210> 12
<211> 10
<212> PRT
<213> Unknown

<220>
<223> Synthetic Construct

<220>
<221> MOD_RES
<222> (1)..(1)
<223> ACETYLATION

<220>
<221> DISULFID
<222> (1)..(7)
<223> Disulfide bond between Cys at position 1 and Xaa at position 7

<220>
<221> MOD_RES
<222> (2)..(2)
<223> N(alpha)METHYLATION

<220>
<221> VARIANT
<222> (3)..(3)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> VARIANT
<222> (5)..(5)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> VARIANT
<222> (6)..(6)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Pen

<220>
<221> VARIANT
<222> (8)..(10)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> MOD_RES
<222> (10)..(10)
<223> ACETYLATION

<220>
<221> MOD_RES
<222> (10)..(10)
<223> N(alpha)METHYLATION

<220>
<221> MOD_RES
<222> (10)..(10)
<223> D-Lys, Dap, Dab, Orn, D-Orn, D-Dab, D-Dap

<400> 12

Cys Arg Xaa Asp Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10

<210> 13
<211> 10
<212> PRT
<213> Unknown

<220>
<223> Synthetic Construct

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Pen

<220>
<221> MOD_RES
<222> (1)..(1)
<223> ACETYLATION

<220>
<221> DISULFID
<222> (1)..(7)
<223> Disulfide bond between Xaa at position 1 and Cys at position 7

<220>
<221> MOD_RES
<222> (2)..(2)
<223> N(alpha)METHYLATION

<220>
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<222> (3)..(3)
<223> Xaa can be any naturally occurring amino acid

<220>
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<222> (5)..(6)
<223> Xaa can be any naturally occurring amino acid

<220>
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<222> (8)..(10)
<223> Xaa can be any naturally occurring amino acid

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

<220>
<221> MOD_RES
<222> (10)..(10)
<223> N(alpha)METHYLATION

<220>
<221> MOD_RES
<222> (10)..(10)
<223> D-Lys, Dap, Dab, Orn, D-Orn, D-Dab, D-Dap

<400> 13

Xaa Arg Xaa Asp Xaa Xaa Cys Xaa Xaa Xaa
1 5 10

<210> 14
<211> 10
<212> PRT
<213> Unknown

<220>
<223> Synthetic Construct

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Pen

<220>
<221> MOD_RES
<222> (1)..(1)
<223> ACETYLATION

<220>
<221> DISULFID
<222> (1)..(7)
<223> Disulfide bond between Xaa at position 1 and Xaa at position 7

<220>
<221> MOD_RES
<222> (2)..(2)
<223> N(alpha)METHYLATION

<220>
<221> VARIANT
<222> (3)..(3)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> VARIANT
<222> (5)..(6)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Pen

<220>
<221> VARIANT
<222> (8)..(10)
<223> Xaa can be any naturally occurring amino acid

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

<220>
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<222> (10)..(10)
<223> N(alpha)METHYLATION

<220>
<221> MOD_RES
<222> (10)..(10)
<223> D-Lys, Dap, Dab, Orn, D-Orn, D-Dab, D-Dap

<400> 14

Xaa Arg Xaa Asp Xaa Xaa Xaa Xaa Xaa Xaa

1 5 10

<210> 15
<211> 11
<212> PRT
<213> Unknown

<220>
<223> Synthetic Construct

<220>
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<222> (1)..(1)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> MOD_RES
<222> (1)..(1)
<223> ACETYLATION

<220>
<221> DISULFID
<222> (2)..(8)
<223> Disulfide bond between Cys at position 2 and Cys at position 8

<220>
<221> MOD_RES
<222> (3)..(3)
<223> N(alpha)METHYLATION

<220>
<221> VARIANT
<222> (4)..(4)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> VARIANT
<222> (6)..(7)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> VARIANT
<222> (9)..(11)
<223> Xaa can be any naturally occurring amino acid

<220>
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<222> (11)..(11)
<223> ACETYLATION

<220>
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<223> D-Lys, Dap, Dab, Orn, D-Orn, D-Dab, D-Dap

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1 5 10

<210> 16
<211> 11
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<223> D-Lys, Dap, Dab, Orn, D-Orn, D-Dab, D-Dap

<400> 16

Xaa Cys Arg Xaa Asp Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10

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<223> D-Lys, Dap, Dab, Orn, D-Orn, D-Dab, D-Dap

<400> 17

Xaa Xaa Arg Xaa Asp Xaa Xaa Cys Xaa Xaa Xaa
1 5 10

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<400> 18

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1 5 10

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<223> D-Lys, Dap, Dab, Orn, D-Orn, D-Dab, D-Dap

<220>
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<223> ACETYLATION

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1 5 10

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<223> D-Lys, Dap, Dab, Orn, D-Orn, D-Dab, D-Dap

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1 5 10

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<223> Disulfide bond between Xaa at position 3 and Cys at position 9

<220>
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<223> D-Lys, Dap, Dab, Orn, D-Orn, D-Dab, D-Dap

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<400> 21

Xaa Xaa Xaa Arg Xaa Asp Xaa Xaa Cys Xaa Xaa Xaa
1 5 10

<210> 22
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<223> Pen

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<223> D-Lys, Dap, Dab, Orn, D-Orn, D-Dab, D-Dap

<220>
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<400> 22

Xaa Xaa Xaa Arg Xaa Asp Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10

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<220>
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<223> D-Lys, Dap, Dab, Orn, D-Orn, D-Dab, D-Dap

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<400> 23

Xaa Xaa Xaa Cys Arg Xaa Asp Xaa Xaa Cys Xaa Xaa Xaa
1 5 10

<210> 24
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<223> D-Lys, Dap, Dab, Orn, D-Orn, D-Dab, D-Dap

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<400> 24

Xaa Xaa Xaa Cys Arg Xaa Asp Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10

<210> 25
<211> 13
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<223> D-Lys, Dap, Dab, Orn, D-Orn, D-Dab, D-Dap

<400> 25

Xaa Xaa Xaa Xaa Arg Xaa Asp Xaa Xaa Cys Xaa Xaa Xaa
1 5 10

<210> 26
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<223> D-Lys, Dap, Dab, Orn, D-Orn, D-Dab, D-Dap

<400> 26

Xaa Xaa Xaa Xaa Arg Xaa Asp Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10

<210> 27
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<220>
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<223> D-Lys, Dap, Dab, Orn, D-Orn, D-Dab, D-Dap

<400> 27

Xaa Cys Arg Xaa Asp Xaa Xaa Cys
1 5

<210> 28
<211> 9
<212> PRT
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<223> D-Lys, Dap, Dab, Orn, D-Orn, D-Dab, D-Dap

<400> 28

Xaa Cys Arg Xaa Asp Xaa Xaa Xaa Xaa
1 5

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<220>
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<220>
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<223> D-Lys, Dap, Dab, Orn, D-Orn, D-Dab, D-Dap

<400> 29

Xaa Xaa Arg Xaa Asp Xaa Xaa Cys Xaa
1 5

<210> 30
<211> 9
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<220>
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<223> Pen

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<220>
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<220>
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<223> D-Lys, Dap, Dab, Orn, D-Orn, D-Dab, D-Dap

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Xaa Xaa Arg Xaa Asp Xaa Xaa Xaa Xaa
1 5

<210> 31
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<212> PRT
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<220>
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<223> D-Lys, Dap, Dab, Orn, D-Orn, D-Dab, D-Dap

<220>
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<400> 31

Xaa Xaa Cys Arg Xaa Asp Xaa Xaa Cys Xaa
1 5 10

<210> 32
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<212> PRT
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<223> Xaa can be any naturally occurring amino acid

<220>
<221> VARIANT
<222> (7)..(8)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> MOD_RES
<222> (9)..(9)
<223> Pen

<220>
<221> VARIANT
<222> (10)..(10)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> MOD_RES
<222> (10)..(10)
<223> ACETYLATION

<220>
<221> MOD_RES
<222> (10)..(10)
<223> N(alpha)METHYLATION

<220>
<221> MOD_RES
<222> (10)..(10)
<223> D-Lys, Dap, Dab, Orn, D-Orn, D-Dab, D-Dap

<400> 32

Xaa Xaa Cys Arg Xaa Asp Xaa Xaa Xaa Xaa
1 5 10

<210> 33
<211> 10
<212> PRT
<213> Unknown

<220>
<223> Synthetic Construct

<220>
<221> VARIANT
<222> (1)..(2)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> MOD_RES
<222> (1)..(1)
<223> ACETYLATION

<220>
<221> MOD_RES
<222> (3)..(3)
<223> Pen

<220>
<221> DISULFID
<222> (3)..(9)
<223> Disulfide bond between Xaa at position 3 and Cys at position 9

<220>
<221> MOD_RES
<222> (4)..(4)
<223> N(alpha)METHYLATION

<220>
<221> VARIANT
<222> (5)..(5)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> VARIANT

<222> (7)..(8)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> VARIANT
<222> (10)..(10)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> MOD_RES
<222> (10)..(10)
<223> ACETYLATION

<220>
<221> MOD_RES
<222> (10)..(10)
<223> N(alpha)METHYLATION

<220>
<221> MOD_RES
<222> (10)..(10)
<223> D-Lys, Dap, Dab, Orn, D-Orn, D-Dab, D-Dap

<400> 33

Xaa Xaa Xaa Arg Xaa Asp Xaa Xaa Cys Xaa
1 5 10

<210> 34
<211> 10
<212> PRT
<213> Unknown

<220>
<223> Synthetic Construct

<220>
<221> VARIANT
<222> (1)..(2)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> MOD_RES
<222> (1)..(1)
<223> ACETYLATION

<220>
<221> MOD_RES
<222> (3)..(3)
<223> Pen

<220>
<221> DISULFID
<222> (3)..(9)
<223> Disulfide bond between Xaa at position 3 and Xaa at position 9

<220>
<221> MOD_RES
<222> (4)..(4)
<223> N(alpha)METHYLATION

<220>
<221> VARIANT
<222> (5)..(5)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> VARIANT
<222> (7)..(8)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> MOD_RES
<222> (9)..(9)
<223> Pen

<220>
<221> VARIANT
<222> (10)..(10)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> MOD_RES
<222> (10)..(10)
<223> ACETYLATION

<220>
<221> MOD_RES
<222> (10)..(10)
<223> N(alpha)METHYLATION

<220>
<221> MOD_RES
<222> (10)..(10)
<223> D-Lys, Dap, Dab, Orn, D-Orn, D-Dab, D-Dap

<400> 34

Xaa Xaa Xaa Arg Xaa Asp Xaa Xaa Xaa Xaa
1 5 10

<210> 35
<211> 11
<212> PRT
<213> Unknown

<220>
<223> Synthetic Construct

<220>
<221> VARIANT
<222> (1)..(3)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> MOD_RES
<222> (1)..(1)
<223> ACETYLATION

<220>
<221> DISULFID
<222> (4)..(10)
<223> Disulfide bond between Cys at position 4 and Cys at position 10

<220>
<221> MOD_RES
<222> (5)..(5)
<223> N(alpha)METHYLATION

<220>
<221> VARIANT
<222> (6)..(6)

<223> Xaa can be any naturally occurring amino acid

<220>
<221> VARIANT
<222> (8)..(9)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> VARIANT
<222> (11)..(11)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> MOD_RES
<222> (11)..(11)
<223> N(alpha)METHYLATION

<220>
<221> MOD_RES
<222> (11)..(11)
<223> D-Lys, Dap, Dab, Orn, D-Orn, D-Dab, D-Dap

<220>
<221> MOD_RES
<222> (11)..(11)
<223> ACETYLATION

<400> 35

Xaa Xaa Xaa Cys Arg Xaa Asp Xaa Xaa Cys Xaa
1 5 10

<210> 36
<211> 11
<212> PRT
<213> Unknown

<220>
<223> Synthetic Construct

<220>
<221> VARIANT
<222> (1)..(3)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> MOD_RES
<222> (1)..(1)
<223> ACETYLATION

<220>
<221> DISULFID
<222> (4)..(10)
<223> Disulfide bond between Cys at position 4 and Xaa at position 10

<220>
<221> MOD_RES
<222> (5)..(5)
<223> N(alpha)METHYLATION

<220>
<221> VARIANT
<222> (6)..(6)
<223> Xaa can be any naturally occurring amino acid

<220>

<221> VARIANT
<222> (8)..(9)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> MOD_RES
<222> (10)..(10)
<223> Pen

<220>
<221> VARIANT
<222> (11)..(11)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> MOD_RES
<222> (11)..(11)
<223> ACETYLATION

<220>
<221> MOD_RES
<222> (11)..(11)
<223> N(alpha)METHYLATION

<220>
<221> MOD_RES
<222> (11)..(11)
<223> D-Lys, Dap, Dab, Orn, D-Orn, D-Dab, D-Dap

<400> 36

Xaa Xaa Xaa Cys Arg Xaa Asp Xaa Xaa Xaa Xaa
1 5 10

<210> 37
<211> 11
<212> PRT
<213> Unknown

<220>
<223> Synthetic Construct

<220>
<221> VARIANT
<222> (1)..(3)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> MOD_RES
<222> (1)..(1)
<223> ACETYLATION

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

<220>
<221> DISULFID
<222> (4)..(10)
<223> Disulfide bond between Xaa at position 4 and Cys at position 10

<220>
<221> MOD_RES
<222> (5)..(5)
<223> N(alpha)METHYLATION

<220>
<221> VARIANT
<222> (6)..(6)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> VARIANT
<222> (8)..(9)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> VARIANT
<222> (11)..(11)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> MOD_RES
<222> (11)..(11)
<223> ACETYLATION

<220>
<221> MOD_RES
<222> (11)..(11)
<223> N(alpha)METHYLATION

<220>
<221> MOD_RES
<222> (11)..(11)
<223> D-Lys, Dap, Dab, Orn, D-Orn, D-Dab, D-Dap

<400> 37

Xaa Xaa Xaa Xaa Arg Xaa Asp Xaa Xaa Cys Xaa
1 5 10

<210> 38
<211> 11
<212> PRT
<213> Unknown

<220>
<223> Synthetic Construct

<220>
<221> VARIANT
<222> (1)..(3)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> MOD_RES
<222> (1)..(1)
<223> ACETYLATION

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

<220>
<221> DISULFID
<222> (4)..(10)
<223> Disulfide bond between Xaa at position 4 and Xaa at position 10

<220>
<221> MOD_RES

<222> (5)..(5)
<223> N(alpha)METHYLATION

<220>
<221> VARIANT
<222> (6)..(6)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> VARIANT
<222> (8)..(9)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> MOD_RES
<222> (10)..(10)
<223> Pen

<220>
<221> MOD_RES
<222> (11)..(11)
<223> ACETYLATION

<220>
<221> VARIANT
<222> (11)..(11)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> MOD_RES
<222> (11)..(11)
<223> N(alpha)METHYLATION

<220>
<221> MOD_RES
<222> (11)..(11)
<223> D-Lys, Dap, Dab, Orn, D-Orn, D-Dab, D-Dap

<400> 38

Xaa Xaa Xaa Xaa Arg Xaa Asp Xaa Xaa Xaa Xaa
1 5 10

<210> 39
<211> 8
<212> PRT
<213> Unknown

<220>
<223> Synthetic Construct

<220>
<221> MOD_RES
<222> (1)..(1)
<223> ACETYLATION

<220>
<221> DISULFID
<222> (1)..(7)
<223> Disulfide bond between Cys at position 1 and Cys at position 7

<220>
<221> VARIANT
<222> (2)..(2)
<223> Arg, Tyr

<400> 39

Cys Xaa Ser Asp Thr Leu Cys Lys
1 5

<210> 40
<211> 10
<212> PRT
<213> Unknown

<220>
<223> Synthetic Construct

<220>
<221> MOD_RES
<222> (1)..(1)
<223> ACETYLATION

<220>
<221> DISULFID
<222> (1)..(7)
<223> Disulfide bond between Cys at position 1 and Cys at position 7

<400> 40

Cys Arg Ser Asp Thr Leu Cys Gly Glu Lys
1 5 10

<210> 41
<211> 8
<212> PRT
<213> Unknown

<220>
<223> Synthetic Construct

<220>
<221> MOD_RES
<222> (1)..(1)
<223> ACETYLATION

<220>
<221> DISULFID
<222> (2)..(8)
<223> Disulfide bond between Cys at position 2 and Cys at position 8

<400> 41

Lys Cys Arg Ser Asp Thr Leu Cys
1 5

<210> 42
<211> 10
<212> PRT
<213> Unknown

<220>
<223> Synthetic Construct

<220>
<221> MOD_RES
<222> (1)..(1)

<223> ACETYLATION

<220>
<221> DISULFID
<222> (2)..(8)
<223> Disulfide bond between Cys at position 2 and Cys at position 8

<400> 42

Lys Cys Arg Ser Asp Thr Leu Cys Gly Glu
1 5 10

<210> 43
<211> 9
<212> PRT
<213> Unknown

<220>
<223> Synthetic Construct

<220>
<221> MOD_RES
<222> (1)..(1)
<223> ACETYLATION

<220>
<221> DISULFID
<222> (1)..(7)
<223> Disulfide bond between Cys at position 1 and Cys at position 7

<220>
<221> MOD_RES
<222> (2)..(2)
<223> METHYLATION: Arg-Me-sym; Arg-Me-asym

<400> 43

Cys Arg Ser Asp Thr Leu Cys Gly Glu
1 5

<210> 44
<211> 9
<212> PRT
<213> Unknown

<220>
<223> Synthetic Construct

<220>
<221> MOD_RES
<222> (1)..(1)
<223> ACETYLATION

<220>
<221> DISULFID
<222> (1)..(7)
<223> Disulfide bond between Cys at position 1 and Cys at position 7

<220>
<221> MOD_RES
<222> (2)..(2)
<223> Dab, Cit, Cav, Dap

<400> 44

Cys Xaa Ser Asp Thr Leu Cys Gly Glu
1 5

<210> 45
<211> 9
<212> PRT
<213> Unknown

<220>
<223> Synthetic Construct

<220>
<221> MOD_RES
<222> (1)..(1)
<223> ACETYLATION

<220>
<221> DISULFID
<222> (1)..(7)
<223> Disulfide bond between Cys at position 1 and Cys at position 7

<400> 45

Cys His Ser Asp Thr Leu Cys Gly Glu
1 5

<210> 46
<211> 7
<212> PRT
<213> Unknown

<220>
<223> Synthetic Construct

<220>
<221> DISULFID
<222> (1)..(7)
<223> Disulfide bond between Cys at position 1 and Cys at position 7

<220>
<221> MOD_RES
<222> (2)..(2)
<223> N(alpha)METHYLATION

<400> 46

Cys Arg Ser Asp Thr Leu Cys
1 5

<210> 47
<211> 8
<212> PRT
<213> Unknown

<220>
<223> Synthetic Construct

<220>
<221> MOD_RES
<222> (1)..(1)
<223> ACETYLATION

<220>
<221> DISULFID
<222> (1)..(7)
<223> Disulfide bond between Cys at position 1 and Cys at position 7

<220>
<221> MOD_RES
<222> (2)..(2)
<223> N(alpha)METHYLATION, Arg-Me-sym, Arg-Me-asym

<220>
<221> MOD_RES
<222> (8)..(8)
<223> Dap, Dab, D-Lys

<220>
<221> MOD_RES
<222> (8)..(8)
<223> ACETYLATION

<400> 47

Cys Arg Ser Asp Thr Leu Cys Xaa
1 5

<210> 48
<211> 8
<212> PRT
<213> Unknown

<220>
<223> Synthetic Construct

<220>
<221> MOD_RES
<222> (1)..(1)
<223> ACETYLATION

<220>
<221> DISULFID
<222> (1)..(7)
<223> Disulfide bond between Cys at position 1 and Cys at position 7

<220>
<221> MOD_RES
<222> (2)..(2)
<223> N(alpha)METHYLATION

<220>
<221> MOD_RES
<222> (8)..(8)
<223> N(alpha)METHYLATION

<400> 48

Cys Arg Ser Asp Thr Leu Cys Lys
1 5

<210> 49
<211> 8
<212> PRT
<213> Unknown

<220>

<223> Synthetic Construct

<220>
<221> DISULFID
<222> (1)..(7)
<223> Disulfide bond between Cys at position 1 and Cys at position 7

<220>
<221> MOD_RES
<222> (2)..(2)
<223> N(alpha)METHYLATION

<220>
<221> MOD_RES
<222> (2)..(2)
<223> Guan, 4-Guan, Dap, Dab, Phe(4-NH2)

<220>
<221> MOD_RES
<222> (8)..(8)
<223> Dap, Dab, D-Lys

<220>
<221> MOD_RES
<222> (8)..(8)
<223> ACETYLATION

<400> 49

Cys Xaa Ser Asp Thr Leu Cys Xaa
1 5

<210> 50
<211> 7
<212> PRT
<213> Unknown

<220>
<223> Synthetic Construct

<220>
<221> DISULFID
<222> (1)..(7)
<223> Disulfide bond between Cys at position 1 and Cys at position 7

<220>
<221> MOD_RES
<222> (2)..(2)
<223> N(alpha)METHYLATION

<400> 50

Cys Arg Ser Asp Thr Leu Cys
1 5

<210> 51
<211> 10
<212> PRT
<213> Unknown

<220>
<223> Synthetic Construct

<220>
<221> MOD_RES
<222> (1)..(1)
<223> ACETYLATION

<220>
<221> DISULFID
<222> (1)..(7)
<223> Disulfide bond between Cys at position 1 and Cys at position 7

<220>
<221> MOD_RES
<222> (2)..(2)
<223> N(alpha)METHYLATION

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

<220>
<221> VARIANT
<222> (2)..(2)
<223> Arg

<220>
<221> MOD_RES
<222> (10)..(10)
<223> N(alpha)METHYLATION

<400> 51

Cys Xaa Ser Asp Thr Leu Cys Gly Glu Lys
1 5 10

<210> 52
<211> 9
<212> PRT
<213> Unknown

<220>
<223> Synthetic Construct

<220>
<221> MOD_RES
<222> (1)..(1)
<223> ACETYLATION

<220>
<221> DISULFID
<222> (1)..(7)
<223> Disulfide bond between Cys at position 1 and Cys at position 7

<220>
<221> MOD_RES
<222> (5)..(6)
<223> N(alpha)METHYLATION

<400> 52

Cys His Ser Asp Thr Leu Cys Gly Glu
1 5

<210> 53
<211> 10

<212> PRT
<213> Unknown

<220>
<223> Synthetic Construct

<220>
<221> MOD_RES
<222> (1)..(1)
<223> ACETYLATION

<220>
<221> DISULFID
<222> (1)..(7)
<223> Disulfide bond between Cys at position 1 and Cys at position 7

<220>
<221> MOD_RES
<222> (8)..(8)
<223> Sar

<400> 53

Cys Arg Ser Asp Thr Leu Cys Xaa Glu Lys
1 5 10

<210> 54
<211> 10
<212> PRT
<213> Unknown

<220>
<223> Synthetic Construct

<220>
<221> MOD_RES
<222> (1)..(1)
<223> ACETYLATION

<220>
<221> DISULFID
<222> (1)..(7)
<223> Disulfide bond between Cys at position 1 and Cys at position 7

<220>
<221> MOD_RES
<222> (2)..(2)
<223> N(alpha)METHYLATION

<220>
<221> MOD_RES
<222> (10)..(10)
<223> D-Lys, Dab, Dab (2-Me-trifluorobutyl), Dab (trifluorpentyl), Dab (Acetyl), Dab (Octonyl)

<400> 54

Cys Arg Ser Asp Thr Leu Cys Gly Glu Xaa
1 5 10

<210> 55
<211> 8
<212> PRT
<213> Unknown

<220>
<223> Synthetic Construct

<220>
<221> MOD_RES
<222> (1)..(1)
<223> ACETYLATION

<220>
<221> DISULFID
<222> (1)..(7)
<223> Disulfide bond between Cys at position 1 and Xaa at position 7

<220>
<221> MOD_RES
<222> (2)..(2)
<223> N(alpha)METHYLATION

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Pen

<220>
<221> MOD_RES
<222> (8)..(8)
<223> D-Lys

<400> 55

Cys Arg Ser Asp Thr Leu Xaa Xaa
1 5

<210> 56
<211> 8
<212> PRT
<213> Unknown

<220>
<223> Synthetic Construct

<220>
<221> MOD_RES
<222> (1)..(1)
<223> ACETYLATION

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

<220>
<221> DISULFID
<222> (2)..(8)
<223> Disulfide bond between Cys at position 2 and Xaa at position 8

<220>
<221> MOD_RES
<222> (3)..(3)
<223> N(alpha)METHYLATION

<220>
<221> MOD_RES
<222> (8)..(8)

<223> Pen

<400> 56

Xaa Cys Arg Ser Asp Thr Leu Xaa
1 5

<210> 57
<211> 9
<212> PRT
<213> Unknown

<220>
<223> Synthetic Construct

<220>
<221> MOD_RES
<222> (1)..(1)
<223> ACETYLATION

<220>
<221> DISULFID
<222> (1)..(7)
<223> Disulfide bond between Cys at position 1 and Xaa at position 7

<220>
<221> MOD_RES
<222> (2)..(2)
<223> N(alpha)METHYLATION

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Pen

<220>
<221> MOD_RES
<222> (9)..(9)
<223> D-Lys

<400> 57

Cys Arg Ser Asp Thr Leu Xaa Trp Xaa
1 5

<210> 58
<211> 9
<212> PRT
<213> Unknown

<220>
<223> Synthetic Construct

<220>
<221> MOD_RES
<222> (1)..(1)
<223> ACETYLATION

<220>
<221> DISULFID
<222> (1)..(7)
<223> Disulfide bond between Cys at position 1 and Xaa at position 7

<220>

<221> MOD_RES
<222> (2)..(2)
<223> N(alpha)METHYLATION

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Pen

<220>
<221> MOD_RES
<222> (9)..(9)
<223> D-Lys

<400> 58

Cys Arg Ser Asp Thr Leu Xaa Tyr Xaa
1 5

<210> 59
<211> 8
<212> PRT
<213> Unknown

<220>
<223> Synthetic Construct

<220>
<221> DISULFID
<222> (2)..(8)
<223> Disulfide bond between Cys at position 2 and Xaa at position 8

<220>
<221> MOD_RES
<222> (3)..(3)
<223> N(alpha)METHYLATION

<220>
<221> MOD_RES
<222> (8)..(8)
<223> Pen

<400> 59

Arg Cys Arg Ser Asp Thr Leu Xaa
1 5

<210> 60
<211> 8
<212> PRT
<213> Unknown

<220>
<223> Synthetic Construct

<220>
<221> DISULFID
<222> (2)..(8)
<223> Disulfide bond between Cys at position 2 and Xaa at position 8

<220>
<221> MOD_RES
<222> (3)..(3)
<223> N(alpha)METHYLATION

<220>
<221> MOD_RES
<222> (8)..(8)
<223> Pen

<400> 60

Leu Cys Arg Ser Asp Thr Leu Xaa
1 5

<210> 61
<211> 9
<212> PRT
<213> Unknown

<220>
<223> Synthetic Construct

<220>
<221> MOD_RES
<222> (1)..(1)
<223> ACETYLATION

<220>
<221> DISULFID
<222> (3)..(9)
<223> Disulfide bond between Cys at position 3 and Xaa at position 9

<220>
<221> MOD_RES
<222> (4)..(4)
<223> N(alpha)METHYLATION

<220>
<221> MOD_RES
<222> (9)..(9)
<223> Pen

<400> 61

Lys Leu Cys Arg Ser Asp Thr Leu Xaa
1 5

<210> 62
<211> 8
<212> PRT
<213> Unknown

<220>
<223> Synthetic Construct

<220>
<221> DISULFID
<222> (2)..(8)
<223> Disulfide bond between Cys at position 2 and Xaa at position 8

<220>
<221> MOD_RES
<222> (3)..(3)
<223> N(alpha)METHYLATION

<220>
<221> MOD_RES

<222> (8)..(8)
<223> Pen

<400> 62

His Cys Arg Ser Asp Thr Leu Xaa
1 5

<210> 63
<211> 9
<212> PRT
<213> Unknown

<220>
<223> Synthetic Construct

<220>
<221> MOD_RES
<222> (1)..(1)
<223> ACETYLATION

<220>
<221> DISULFID
<222> (3)..(9)
<223> Disulfide bond between Cys at position 3 and Xaa at position 9

<220>
<221> MOD_RES
<222> (4)..(4)
<223> N(alpha)METHYLATION

<220>
<221> MOD_RES
<222> (9)..(9)
<223> Pen

<400> 63

Lys His Cys Arg Ser Asp Thr Leu Xaa
1 5

<210> 64
<211> 8
<212> PRT
<213> Unknown

<220>
<223> Synthetic Construct

<220>
<221> DISULFID
<222> (2)..(8)
<223> Disulfide bond between Cys at position 3 and Xaa at position 9

<220>
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<223> N(alpha)METHYLATION

<220>
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<223> Pen

<400> 64

Glu Cys Arg Ser Asp Thr Leu Xaa
1 5

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<220>
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<220>
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<223> N(alpha)METHYLATION

<220>
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<223> Pen

<400> 65

Lys Glu Cys Arg Ser Asp Thr Xaa
1 5

<210> 66
<211> 9
<212> PRT
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<220>
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<223> Disulfide bond between Cys at position 3 and Xaa at position 9

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<220>
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<223> Pen

<400> 66

Lys Trp Cys Arg Ser Asp Thr Leu Xaa
1 5

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<220>
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<223> Pen

<400> 67

Pro Cys Arg Ser Asp Thr Leu Xaa
1 5

<210> 68
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<220>
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<220>

<221> MOD_RES
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<223> Pen

<400> 68

Lys Pro Cys Arg Ser Asp Thr Leu Xaa
1 5

<210> 69
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<220>
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<223> N(alpha)METHYLATION

<220>
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<223> Pen

<400> 69

Lys Ser Cys Arg Ser Asp Thr Leu Xaa
1 5

<210> 70
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<220>
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<220>
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<220>
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<223> Pen

<400> 70

Lys Asn Cys Arg Ser Asp Thr Leu Xaa
1 5

<210> 71
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<400> 71

Lys Tyr Cys Arg Ser Asp Thr Leu Xaa
1 5

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<223> Pen

<220>
<221> MOD_RES
<222> (9)..(9)
<223> D-Lys

<400> 72

Cys Arg Ser Asp Thr Leu Xaa Leu Xaa
1 5

<210> 73
<211> 9
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<220>
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<222> (7)..(7)
<223> Pen

<220>
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<223> D-Lys

<400> 73

Cys Arg Ser Asp Thr Leu Xaa His Xaa
1 5

<210> 74
<211> 9
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<223> Pen

<220>
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<223> D-Lys

<400> 74

Cys Arg Ser Asp Thr Leu Xaa Glu Xaa
1 5

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<212> PRT
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<223> Disulfide bond between Cys at position 1 and Xaa at position 7

<220>
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<222> (2)..(2)
<223> N(alpha)METHYLATION

<220>
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<223> Pen

<400> 75

Cys Arg Ser Asp Thr Leu Xaa Tyr Lys
1 5

<210> 76
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<212> PRT
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<220>
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<223> N(alpha)METHYLATION

<220>
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<223> Pen

<400> 76

Cys Arg Ser Asp Thr Leu Xaa Trp Lys
1 5

<210> 77
<211> 9
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<223> Pen

<220>
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<223> D-Lys

<400> 77

Cys Arg Ser Asp Thr Leu Xaa Arg Xaa
1 5

<210> 78
<211> 9
<212> PRT
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<223> Pen

<220>
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<223> D-Lys

<400> 78

Cys Arg Ser Asp Thr Leu Xaa Pro Xaa
1 5

<210> 79
<211> 9
<212> PRT
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<220>
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<223> Disulfide bond between Cys at position 1 and Xaa at position 7

<220>
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<222> (7)..(7)
<223> Pen

<220>
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<400> 79

Cys Arg Ser Asp Thr Leu Xaa Ser Xaa
1 5

<210> 80
<211> 9
<212> PRT
<213> Unknown

<220>
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<223> Disulfide bond between Cys at position 1 and Xaa at position 7

<220>
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<222> (7)..(7)
<223> Pen

<220>
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<223> D-Lys

<400> 80

Cys Arg Ser Asp Thr Leu Xaa Asn Xaa
1 5

<210> 81
<211> 10
<212> PRT
<213> Unknown

<220>
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<223> Disulfide bond between Cys at position 2 and Xaa at position 8

<220>
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<223> N(alpha)METHYLATION

<220>
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<222> (8)..(8)
<223> Pen

<220>
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<400> 81

Arg Cys Arg Ser Asp Thr Leu Xaa Xaa Lys
1 5 10

<210> 82
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<212> PRT
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<220>
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<220>
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<222> (8)..(8)
<223> Pen

<220>
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<223> 1-Nal

<400> 82

Glu Cys Arg Ser Asp Thr Leu Xaa Xaa Lys
1 5 10

<210> 83
<211> 10
<212> PRT
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<220>
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<220>
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<223> Pen

<400> 83

Arg Cys Arg Ser Asp Thr Leu Xaa Trp Lys
1 5 10

<210> 84
<211> 10
<212> PRT
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<220>
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<220>
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<220>
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<223> Pen

<400> 84

Glu Cys Arg Ser Asp Thr Leu Xaa Trp Lys

1 5 10

<210> 85
<211> 10
<212> PRT
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<220>
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<223> Pen

<400> 85

Arg Cys Arg Ser Asp Thr Leu Xaa Tyr Lys
1 5 10

<210> 86
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<212> PRT
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<400> 86

Glu Cys Arg Ser Asp Thr Leu Xaa Tyr Lys
1 5 10

<210> 87
<211> 8
<212> PRT
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<220>
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<223> Pen

<400> 87

Tyr Cys Arg Ser Asp Thr Leu Xaa
1 5

<210> 88
<211> 9
<212> PRT
<213> Unknown

<220>
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<220>
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<220>
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<220>
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<223> Pen

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

<220>
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<222> (9)..(9)
<223> D-Lys

<400> 88

Cys Arg Ser Asp Thr Leu Xaa Xaa Xaa
1 5

<210> 89
<211> 9
<212> PRT
<213> Unknown

<220>
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<220>
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<223> Disulfide bond between Cys at position 1 and Xaa at position 7

<220>
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<223> N(alpha)METHYLATION

<220>
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<223> Pen

<400> 89

Cys Arg Ser Asp Thr Leu Xaa His Lys
1 5

<210> 90
<211> 9
<212> PRT
<213> Unknown

<220>
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<220>
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<220>
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<222> (1)..(7)
<223> Disulfide bond between Xaa at position 1 and Xaa at position 7

<220>
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<220>
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<222> (7)..(7)
<223> Pen

<220>
<221> MOD_RES
<222> (9)..(9)
<223> D-Lys

<400> 90

Xaa Arg Ser Asp Thr Leu Xaa His Xaa
1 5

<210> 91
<211> 9
<212> PRT
<213> Unknown

<220>
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<223> Disulfide bond between Xaa at position 1 and Xaa at position 7

<220>
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<223> N(alpha)METHYLATION

<220>
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<223> Pen

<220>
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<222> (9)..(9)
<223> D-Lys

<400> 91

Xaa Arg Ser Asp Thr Leu Xaa Tyr Xaa
1 5

<210> 92
<211> 9
<212> PRT
<213> Unknown

<220>
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<220>
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<223> Pen

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<223> ACETYLATION

<220>
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<223> Disulfide bond between Xaa at position 1 and Xaa at position 7

<220>
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<223> N(alpha)METHYLATION

<220>
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<222> (7)..(7)
<223> Pen

<220>
<221> MOD_RES
<222> (9)..(9)
<223> D-Lys

<400> 92

Xaa Arg Ser Asp Thr Leu Xaa Trp Xaa
1 5

<210> 93
<211> 8
<212> PRT
<213> Unknown

<220>
<223> Synthetic Construct

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Pen

<220>
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<223> ACETYLATION

<220>
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<222> (1)..(7)

<223> Disulfide bond between Xaa at position 1 and Xaa at position 7

<220>
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<222> (2)..(2)
<223> N(alpha)METHYLATION

<220>
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<222> (7)..(7)
<223> Pen

<220>
<221> MOD_RES
<222> (8)..(8)
<223> D-Lys, D-Phe

<400> 93

Xaa Arg Ser Asp Thr Leu Xaa Xaa
1 5

<210> 94
<211> 8
<212> PRT
<213> Unknown

<220>
<223> Synthetic Construct

<220>
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<223> ACETYLATION

<220>
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<223> Disulfide bond between Cys at position 1 and Xaa at position 7

<220>
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<223> N(alpha)METHYLATION

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Pen

<220>
<221> MOD_RES
<222> (8)..(8)
<223> D-Lys

<400> 94

Cys Arg Ser Asp Thr Leu Xaa Xaa
1 5

<210> 95
<211> 8
<212> PRT
<213> Unknown

<220>
<223> Synthetic Construct

<220>
<221> MOD_RES
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<223> Pen

<220>
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<223> ACETYLATION

<220>
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<223> Disulfide bond between Xaa at position 1 and Cys at position 7

<220>
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<222> (2)..(2)
<223> N(alpha)METHYLATION

<220>
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<223> D-Lys

<400> 95

Xaa Arg Ser Asp Thr Leu Cys Xaa
1 5

<210> 96
<211> 9
<212> PRT
<213> Unknown

<220>
<223> Synthetic Construct

<220>
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<223> Disulfide bond between Cys at position 1 and Xaa at position 7

<220>
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<223> N(alpha)METHYLATION

<220>
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<222> (7)..(7)
<223> Pen

<220>
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<222> (9)..(9)
<223> D-Lys

<400> 96

Cys Arg Ser Asp Thr Leu Xaa Phe Xaa
1 5

<210> 97
<211> 9
<212> PRT
<213> Unknown

<220>
<223> Synthetic Construct

<220>
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<220>
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<223> N(alpha)METHYLATION

<220>
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<223> Pen

<220>
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<223> D-Phe, 2-Nal, HPhe, Bip, Phe(4-F), Tyr(OMe), Ala(3,3 biphenyl), Trp(di-hydro), dTrp (di-hydro), Phe(4-Me)

<220>
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<223> D-Lys

<400> 97

Cys Arg Ser Asp Thr Leu Xaa Xaa Xaa
1 5

<210> 98
<211> 8
<212> PRT
<213> Unknown

<220>
<223> Synthetic Construct

<220>
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<223> Disulfide bond between Cys at position 2 and Xaa at position 8

<220>

<221> MOD_RES
<222> (3)..(3)
<223> N(alpha)METHYLATION

<220>
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<222> (8)..(8)
<223> Pen

<400> 98

Ser Cys Arg Ser Asp Thr Leu Xaa
1 5

<210> 99
<211> 8
<212> PRT
<213> Unknown

<220>
<223> Synthetic Construct

<220>
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<223> Disulfide bond between Cys at position 2 and Xaa at position 8

<220>
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<222> (3)..(3)
<223> N(alpha)METHYLATION

<220>
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<222> (8)..(8)
<223> Pen

<400> 99

Asn Cys Arg Ser Asp Thr Leu Xaa
1 5

<210> 100
<211> 8
<212> PRT
<213> Unknown

<220>
<223> Synthetic Construct

<220>
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<222> (1)..(7)
<223> Disulfide bond between Cys at position 1 and Xaa at position 7

<220>
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<223> N(alpha)METHYLATION

<220>
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<222> (7)..(7)
<223> Pen

<400> 100

Cys Arg Ser Asp Thr Leu Xaa Trp
1 5

<210> 101
<211> 8
<212> PRT
<213> Unknown

<220>
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<220>
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<222> (1)..(7)
<223> Disulfide bond between Cys at position 1 and Xaa at position 7

<220>
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<222> (2)..(2)
<223> N(alpha)METHYLATION

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Pen

<220>
<221> MOD_RES
<222> (8)..(8)
<223> D-Trp, D-Phe

<400> 101

Cys Arg Ser Asp Thr Leu Xaa Xaa
1 5

<210> 102
<211> 9
<212> PRT
<213> Unknown

<220>
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<220>
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<220>
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<223> N(alpha)METHYLATION

<220>
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<223> Pen

<220>
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<222> (2)..(8)
<223> Disulfide bond between Xaa at position 2 and Xaa at position 8

<220>
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<222> (2)..(2)
<223> N(alpha)METHYLATION

<220>
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<222> (3)..(3)
<223> N(alpha)METHYLATION

<220>
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<223> Pen

<400> 102

Lys Xaa Arg Ser Asp Thr Leu Xaa Trp
1 5

<210> 103
<211> 10
<212> PRT
<213> Unknown

<220>
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<220>
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<223> N(alpha)METHYLATION

<220>
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<223> Disulfide bond between Xaa at position 2 and Xaa at position 8

<220>
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<223> N(alpha)METHYLATION

<220>
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<222> (8)..(8)
<223> Pen

<220>
<221> MOD_RES
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<223> N(alpha)METHYLATION

<400> 103

Lys Xaa Arg Ser Asp Thr Leu Xaa Trp Lys
1 5 10

<210> 104
<211> 10
<212> PRT
<213> Unknown

<220>
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<220>
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<223> D-Lys

<220>
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<223> Pen

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<223> Disulfide bond between Xaa at position 2 and Xaa at position 8

<220>
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<223> Pen

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<223> N(alpha)METHYLATION

<220>
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<223> D-Lys

<400> 104

Xaa Xaa Arg Ser Asp Thr Leu Xaa Trp Xaa
1 5 10

<210> 105
<211> 10

<212> PRT
<213> Unknown

<220>
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<220>
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<223> Pen

<220>
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<223> Disulfide bond between Xaa at position 1 and Xaa at position 7

<220>
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<223> N(alpha)METHYLATION

<220>
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<223> Pen

<220>
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<223> D-Lys

<400> 105

Xaa Arg Ser Asp Thr Leu Xaa Trp Phe Xaa
1 5 10

<210> 106
<211> 10
<212> PRT
<213> Unknown

<220>
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<220>
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<223> Pen

<220>
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<223> Disulfide bond between Xaa at position 1 and Xaa at position 7

<220>

<221> MOD_RES
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<223> Pen

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<223> D-Lys

<220>
<221> MOD_RES
<222> (10)..(10)
<223> N(alpha)METHYLATION

<400> 106

Xaa Arg Ser Asp Thr Leu Xaa Trp Glu Xaa
1 5 10

<210> 107
<211> 10
<212> PRT
<213> Unknown

<220>
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<220>
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<220>
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<223> Pen

<220>
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<223> Disulfide bond between Xaa at postion 1 and Xaa at position 7

<220>
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<223> N(alpha)METHYLATION

<220>
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<222> (7)..(7)
<223> Pen

<220>
<221> MOD_RES
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<223> N(alpha)METHYLATION

<400> 107

Xaa Arg Ser Asp Thr Leu Xaa Trp Glu Lys
1 5 10

<210> 108
<211> 10
<212> PRT
<213> Unknown

<220>
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<220>
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<223> Pen

<220>
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<222> (1)..(7)
<223> Disulfide bond between Xaa at position 1 and Xaa at position 7

<220>
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<222> (2)..(2)
<223> N(alpha)METHYLATION

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Pen

<220>
<221> MOD_RES
<222> (10)..(10)
<223> D-Lys

<400> 108

Xaa Arg Ser Asp Thr Leu Xaa Trp Ser Xaa
1 5 10

<210> 109
<211> 10
<212> PRT
<213> Unknown

<220>
<223> Synthetic Construct

<220>
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<220>
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<222> (1)..(1)
<223> Pen

<220>
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<223> Disulfide bond between Xaa at position 1 and Xaa at position 7

<220>
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<222> (7)..(7)
<223> Pen

<220>
<221> MOD_RES
<222> (10)..(10)
<223> D-Lys

<400> 109

Xaa Arg Ser Asp Thr Leu Xaa Trp Tyr Xaa
1 5 10

<210> 110
<211> 9
<212> PRT
<213> Unknown

<220>
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<220>
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<220>
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<222> (1)..(1)
<223> Pen

<220>
<221> DISULFID
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<223> Disulfide bond between Xaa at position 1 and Xaa at position 7

<220>
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<222> (2)..(2)
<223> N(alpha)METHYLATION

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Pen

<220>
<221> MOD_RES
<222> (8)..(8)
<223> D-Trp, D-Phe

<220>
<221> MOD_RES
<222> (9)..(9)
<223> D-Lys

<400> 110

Xaa Arg Ser Asp Thr Leu Xaa Xaa Xaa
1 5

<210> 111
<211> 9
<212> PRT
<213> Unknown

<220>
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<220>
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<223> Pen

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<223> Disulfide bond between Xaa at position 1 and Xaa at position 7

<220>
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<223> N(alpha)METHYLATION

<220>
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<222> (7)..(7)
<223> Pen

<220>
<221> MOD_RES
<222> (9)..(9)
<223> N(alpha)METHYLATION

<400> 111

Xaa Arg Ser Asp Thr Leu Xaa Trp Lys
1 5

<210> 112
<211> 9
<212> PRT
<213> Unknown

<220>
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<223> ACETYLATION

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<223> Disulfide bond between Xaa at position 1 and Xaa at position 7

<220>
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<223> N(alpha)METHYLATION

<220>
<221> MOD_RES
<222> (4)..(4)
<223> D-Asp

<220>
<221> MOD_RES
<222> (9)..(9)
<223> D-Lys

<400> 112

Xaa Arg Ser Xaa Thr Leu Xaa Trp Xaa
1 5

<210> 113
<211> 9
<212> PRT
<213> Unknown

<220>
<223> Synthetic Construct

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<223> Pen

<220>
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<222> (2)..(8)
<223> Disulfide bond between Xaa at position 2 and Xaa at position 8

<220>
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<223> N(alpha)METHYLATION

<220>
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<223> Pen

<400> 113

Pro Xaa Arg Ser Asp Thr Leu Xaa Trp
1 5

<210> 114
<211> 9
<212> PRT
<213> Unknown

<220>
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<220>
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<223> Disulfide bond between Xaa at position 2 and Xaa at position 8

<220>
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<223> N(alpha)METHYLATION

<220>
<221> MOD_RES
<222> (8)..(8)
<223> Pen

<400> 114

Leu Xaa Arg Ser Asp Thr Leu Xaa Trp
1 5

<210> 115
<211> 9
<212> PRT
<213> Unknown

<220>
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<223> Pen

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<222> (2)..(8)
<223> Disulfide bond between Xaa at position 2 and Xaa at position 8

<220>
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<223> N(alpha)METHYLATION

<220>
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<223> Pen

<400> 115

His Xaa Arg Ser Asp Thr Leu Xaa Trp
1 5

<210> 116
<211> 9
<212> PRT
<213> Unknown

<220>
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<223> Pen

<220>
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<222> (2)..(8)
<223> Disulfide bond between Xaa at position 2 and Xaa at position 8

<220>
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<223> N(alpha)METHYLATION

<220>
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<222> (8)..(8)
<223> Pen

<400> 116

Glu Xaa Arg Ser Asp Thr Leu Xaa Trp
1 5

<210> 117
<211> 9
<212> PRT
<213> Unknown

<220>
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<223> Pen

<220>
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<223> Disulfide bond between Xaa at position 2 and Xaa at position 8

<220>
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<222> (3)..(3)
<223> N(alpha)METHYLATION

<220>
<221> MOD_RES
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<223> Pen

<400> 117

Arg Xaa Arg Ser Asp Thr Leu Xaa Trp
1 5

<210> 118
<211> 9
<212> PRT
<213> Unknown

<220>
<223> Synthetic Construct

<220>
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<223> Pen

<220>
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<222> (2)..(8)
<223> Disulfide bond between Xaa at position 2 and Xaa at position 8

<220>
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<223> N(alpha)METHYLATION

<220>
<221> MOD_RES
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<223> Pen

<400> 118

Ser Xaa Arg Ser Asp Thr Leu Xaa Trp
1 5

<210> 119
<211> 9
<212> PRT
<213> Unknown

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

<220>
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<222> (2)..(8)
<223> Disulfide bond between Xaa at position 2 and Xaa at position 8

<220>
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<222> (3)..(3)
<223> N(alpha)METHYLATION

<220>
<221> MOD_RES
<222> (8)..(8)
<223> Pen

<400> 119

Phe Xaa Arg Ser Asp Thr Leu Xaa Trp
1 5

<210> 120
<211> 10
<212> PRT
<213> Unknown

<220>
<223> Synthetic Construct

<220>
<221> MOD_RES
<222> (1)..(1)
<223> ACETYLATION

<220>
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<222> (1)..(1)
<223> Pen

<220>
<221> DISULFID
<222> (1)..(7)
<223> Disulfide bond between Xaa at position 1 and Xaa at position 7

<220>
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<222> (2)..(2)
<223> N(alpha)METHYLATION

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Pen

<220>
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<222> (8)..(8)
<223> D-Phe, D-Trp, 2-Nal, 3-3-diPhe, Beta-HTrp, Phe(4-CF3), 1-Nal, 2-Nal, Phe(2,4-Cl2), Phe(3,4-Cl2), D-1-Nal, D-2-Nal, HPhe, D-HPhe, 2,2-Indane, 1,1-Indane

<220>
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<222> (10)..(10)
<223> D-Lys

<220>
<221> MOD_RES
<222> (10)..(10)
<223> N(alpha)METHYLATION

<400> 120

Xaa Arg Ser Asp Thr Leu Xaa Xaa Glu Xaa
1 5 10

<210> 121
<211> 10
<212> PRT
<213> Unknown

<220>
<223> Synthetic Construct

<220>
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<223> Pen

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<222> (1)..(7)
<223> Disulfide bond between Xaa at position 1 and Xaa at position 7

<220>
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<222> (2)..(2)
<223> N(alpha)METHYLATION

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<221> MOD_RES
<222> (7)..(7)
<223> Pen

<220>
<221> MOD_RES
<222> (10)..(10)
<223> D-Lys

<400> 121

Xaa Arg Ser Asp Thr Leu Xaa Trp Leu Xaa
1 5 10

<210> 122
<211> 10
<212> PRT
<213> Unknown

<220>
<223> Synthetic Construct

<220>
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<223> Pen

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<223> Disulfide bond between Xaa at position 1 and Xaa at position 7

<220>
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<223> N(alpha)METHYLATION

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<222> (7)..(7)
<223> Pen

<220>
<221> MOD_RES
<222> (10)..(10)
<223> D-Lys

<400> 122

Xaa Arg Ser Asp Thr Leu Xaa Trp His Xaa
1 5 10

<210> 123
<211> 10
<212> PRT
<213> Unknown

<220>
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<220>
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<220>
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<222> (7)..(7)
<223> Pen

<220>
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<223> D-Lys

<400> 123

Xaa Arg Ser Asp Thr Leu Xaa Trp Arg Xaa
1 5 10

<210> 124
<211> 10
<212> PRT
<213> Unknown

<220>

<223> Synthetic Construct

<220>
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<222> (7)..(7)
<223> Pen

<220>
<221> MOD_RES
<222> (10)..(10)
<223> D-Lys

<400> 124

Xaa Arg Ser Asp Thr Leu Xaa Trp Trp Xaa
1 5 10

<210> 125
<211> 10
<212> PRT
<213> Unknown

<220>
<223> Synthetic Construct

<220>
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<223> Disulfide bond between Xaa at position 1 and Xaa at position 7

<220>
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<223> N(alpha)METHYLATION

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Pen

<220>
<221> MOD_RES
<222> (10)..(10)
<223> D-Lys

<400> 125

Xaa Arg Ser Asp Thr Leu Xaa Trp Pro Xaa
1 5 10

<210> 126
<211> 10
<212> PRT
<213> Unknown

<220>
<223> Synthetic Construct

<220>
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<223> ACETYLATION

<220>
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<223> Pen

<220>
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<223> Disulfide bond between Xaa at position 1 and Xaa at position 7

<220>
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<223> N(alpha)METHYLATION

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Pen

<220>
<221> MOD_RES
<222> (10)..(10)
<223> D-Lys

<400> 126

Xaa Arg Ser Asp Thr Leu Xaa Trp Asn Xaa
1 5 10

<210> 127
<211> 9
<212> PRT
<213> Unknown

<220>
<223> Synthetic Construct

<220>
<221> MOD_RES
<222> (1)..(1)
<223> ACETYLATION

<220>
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<222> (1)..(1)
<223> Pen

<220>
<221> DISULFID
<222> (1)..(7)
<223> Disulfide bond between Xaa at position 1 and Xaa at position 7

<220>
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<222> (2)..(2)
<223> N(alpha)METHYLATION

<220>
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<222> (7)..(7)
<223> Pen

<220>
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<222> (8)..(8)
<223> D-Phe

<220>
<221> MOD_RES
<222> (9)..(9)
<223> D-Lys

<400> 127

Xaa Arg Thr Asp Thr Leu Xaa Xaa Xaa
1 5

<210> 128
<211> 9
<212> PRT
<213> Unknown

<220>
<223> Synthetic Construct

<220>
<221> MOD_RES
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<223> ACETYLATION

<220>
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<222> (1)..(1)
<223> Pen

<220>
<221> DISULFID
<222> (1)..(7)
<223> Disulfide bond between Xaa at position 1 and Xaa at position 7

<220>

<221> MOD_RES
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<223> N(alpha)METHYLATION

<220>
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<222> (7)..(7)
<223> Pen

<220>
<221> MOD_RES
<222> (8)..(8)
<223> D-Phe

<220>
<221> MOD_RES
<222> (9)..(9)
<223> D-Lys

<400> 128

Xaa Arg Ile Asp Thr Leu Xaa Xaa Xaa
1 5

<210> 129
<211> 9
<212> PRT
<213> Unknown

<220>
<223> Synthetic Construct

<220>
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<223> ACETYLATION

<220>
<221> DISULFID
<222> (1)..(7)
<223> Disulfide bond between Cys at position 1 and Cys at position 7

<220>
<221> MOD_RES
<222> (2)..(2)
<223> N(alpha)METHYLATION

<220>
<221> MOD_RES
<222> (8)..(8)
<223> D-Phe

<220>
<221> MOD_RES
<222> (9)..(9)
<223> D-Lys

<400> 129

Cys Arg Ser Asp Ile Leu Cys Xaa Xaa
1 5

<210> 130
<211> 9
<212> PRT

<213> Unknown

<220>
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<220>
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<222> (1)..(7)
<223> Disulfide bond between Cys at position 1 and Cys at position 7

<220>
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<223> N(alpha)METHYLATION

<220>
<221> MOD_RES
<222> (8)..(8)
<223> D-Phe

<220>
<221> MOD_RES
<222> (9)..(9)
<223> D-Lys

<400> 130

Cys Arg Ser Asp Val Leu Cys Xaa Xaa
1 5

<210> 131
<211> 9
<212> PRT
<213> Unknown

<220>
<223> Synthetic Construct

<220>
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<223> ACETYLATION

<220>
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<222> (1)..(7)
<223> Disulfide bond between Cys at position 1 and Cys at position 7

<220>
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<222> (2)..(2)
<223> N(alpha)METHYLATION

<220>
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<222> (6)..(6)
<223> HLeu, cyclobutyl-Ala, HCha, Nle

<220>
<221> MOD_RES

<222> (9)..(9)
<223> D-Lys

<400> 131

Cys Arg Ser Asp Thr Xaa Cys Trp Xaa
1 5

<210> 132
<211> 9
<212> PRT
<213> Unknown

<220>
<223> Synthetic Construct

<220>
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<223> ACETYLATION

<220>
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<222> (1)..(7)
<223> Disulfide bond between Cys at position 1 and Cys at position 7

<220>
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<222> (2)..(2)
<223> N(alpha)METHYLATION

<220>
<221> MOD_RES
<222> (9)..(9)
<223> D-Lys

<400> 132

Cys Arg Ser Asp Thr Leu Cys Trp Xaa
1 5

<210> 133
<211> 10
<212> PRT
<213> Unknown

<220>
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<220>
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<223> ACETYLATION

<220>
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<222> (1)..(1)
<223> Pen

<220>
<221> DISULFID
<222> (1)..(7)
<223> Disulfide bond between Xaa at position 1 and Xaa at position 7

<220>
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<222> (2)..(2)
<223> N(alpha)METHYLATION

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Pen

<220>
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<223> D-Asp, D-Glu, Beta-HGlu, 1-Nal, 2-Nal, Bip, Beta-HPhe, Beta-Glu

<220>
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<222> (10)..(10)
<223> D-Lys

<400> 133

Xaa Arg Ser Asp Thr Leu Xaa Trp Xaa Xaa
1 5 10

<210> 134
<211> 10
<212> PRT
<213> Unknown

<220>
<223> Synthetic Construct

<220>
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<220>
<221> MOD_RES
<222> (1)..(1)
<223> Pen

<220>
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<222> (1)..(7)
<223> Disulfide bond between Xaa at position 1 and Xaa at position 7

<220>
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<222> (2)..(2)
<223> N(alpha)METHYLATION

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Pen

<220>
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<222> (8)..(8)
<223> D-Phe, D-Trp, 1-Nal, 2-Nal, Phe(4-CF3), HPhe

<220>
<221> MOD_RES
<222> (8)..(8)

<223> D-Phe, D-Trp, 1-Nal, 2-Nal, Phe(4-CF3), HPhe

<220>
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<222> (9)..(9)
<223> D-Glu, D-Tyr

<220>
<221> MOD_RES
<222> (10)..(10)
<223> D-Lys

<400> 134

Xaa Arg Ser Asp Thr Leu Xaa Xaa Xaa Xaa
1 5 10

<210> 135
<211> 10
<212> PRT
<213> Unknown

<220>
<223> Synthetic Construct

<220>
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<220>
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<223> Pen

<220>
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<222> (1)..(7)
<223> Disulfide bond between Xaa at position 1 and Xaa at position 7

<220>
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<222> (2)..(2)
<223> N(alpha)METHYLATION

<220>
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<223> Pen

<220>
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<222> (9)..(9)
<223> D-Glu

<220>
<221> MOD_RES
<222> (10)..(10)
<223> D-Lys

<400> 135

Xaa Arg Ser Asp Thr Leu Xaa Phe Xaa Xaa
1 5 10

<210> 136
<211> 9
<212> PRT
<213> Unknown

<220>
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<220>
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<223> Pen

<220>
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<222> (1)..(7)
<223> Disulfide bond between Xaa at position 1 and Xaa at position 7

<220>
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<222> (2)..(2)
<223> N(alpha)METHYLATION

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Pen

<220>
<221> MOD_RES
<222> (9)..(9)
<223> D-Lys

<400> 136

Xaa Lys Ser Asp Thr Leu Xaa Trp Xaa
1 5

<210> 137
<211> 10
<212> PRT
<213> Unknown

<220>
<223> Synthetic Construct

<220>
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<223> ACETYLATION

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Pen

<220>
<221> DISULFID
<222> (1)..(7)
<223> Disulfide bond between Xaa at position 1 and Xaa at position 7

<220>
<221> MOD_RES
<222> (2)..(2)
<223> N(alpha)METHYLATION

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Pen

<220>
<221> MOD_RES
<222> (10)..(10)
<223> N(alpha)METHYLATION

<400> 137

Xaa Arg Ser Asp Thr Leu Xaa Trp Tyr Lys
1 5 10

<210> 138
<211> 9
<212> PRT
<213> Unknown

<220>
<223> Synthetic Construct

<220>
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<223> ACETYLATION

<220>
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<222> (1)..(1)
<223> Pen

<220>
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<222> (1)..(7)
<223> Disulfide bond between Xaa at position 1 and Xaa at position 7

<220>
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<222> (2)..(2)
<223> N(alpha)METHYLATION

<220>
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<222> (6)..(6)
<223> Nle

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Pen

<220>
<221> MOD_RES
<222> (9)..(9)
<223> D-Lys

<400> 138

Xaa Arg Ser Asp Thr Xaa Xaa Trp Xaa
1 5

<210> 139
<211> 10
<212> PRT
<213> Unknown

<220>
<223> Synthetic Construct

<220>
<221> MOD_RES
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<223> ACETYLATION

<220>
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<222> (1)..(1)
<223> Pen

<220>
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<222> (1)..(7)
<223> Disulfide bond between Xaa at position 1 and Xaa at position 7

<220>
<221> MOD_RES
<222> (2)..(2)
<223> N(alpha)METHYLATION

<220>
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<222> (6)..(6)
<223> Nle

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Pen

<220>
<221> MOD_RES
<222> (10)..(10)
<223> D-Lys

<400> 139

Xaa Arg Ser Asp Thr Xaa Xaa Trp Glu Xaa
1 5 10

<210> 140
<211> 8
<212> PRT
<213> Unknown

<220>
<223> Synthetic Construct

<220>
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<222> (1)..(1)
<223> Pen

<220>
<221> DISULFID
<222> (1)..(7)
<223> Disulfide bond between Xaa at position 1 and Xaa at position 7

<220>
<221> MOD_RES
<222> (2)..(2)
<223> N(alpha)METHYLATION

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Pen

<220>
<221> MOD_RES
<222> (8)..(8)
<223> D-Phe

<400> 140

Xaa Arg Ser Asp Thr Leu Xaa Xaa
1 5

<210> 141
<211> 8
<212> PRT
<213> Unknown

<220>
<223> Synthetic Construct

<220>
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<220>
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<222> (1)..(7)
<223> Disulfide bond between Xaa at position 1 and Xaa at position 7

<220>
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<222> (2)..(2)
<223> N(alpha)METHYLATION

<220>
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<222> (7)..(7)
<223> Pen

<400> 141

Xaa Arg Ser Asp Thr Leu Xaa Trp
1 5

<210> 142
<211> 10
<212> PRT
<213> Unknown

<220>
<223> Synthetic Construct

<220>
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<223> ACETYLATION

<220>
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<222> (1)..(1)
<223> Pen

<220>
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<222> (1)..(7)
<223> Disulfide bond between Xaa at position 1 and Xaa at position 7

<220>
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<222> (2)..(2)
<223> N(alpha)METHYLATION

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Pen

<220>
<221> MOD_RES
<222> (10)..(10)
<223> D-Lys

<400> 142

Xaa Arg Ser Asp Thr Leu Xaa Trp Asp Xaa
1 5 10

<210> 143
<211> 10
<212> PRT
<213> Unknown

<220>
<223> Synthetic Construct

<220>
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<223> ACETYLATION

<220>
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<222> (1)..(1)
<223> Pen

<220>
<221> DISULFID
<222> (1)..(7)
<223> Disulfide bond between Xaa at position 1 and Xaa at position 7

<220>
<221> MOD_RES
<222> (2)..(2)
<223> N(alpha)METHYLATION

<220>

<221> MOD_RES
<222> (7)..(7)
<223> Pen

<220>
<221> MOD_RES
<222> (10)..(10)
<223> D-Lys

<400> 143

Xaa Arg Ser Asp Thr Leu Xaa His Glu Xaa
1 5 10

<210> 144
<211> 10
<212> PRT
<213> Unknown

<220>
<223> Synthetic Construct

<220>
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<222> (1)..(1)
<223> ACETYLATION

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Pen

<220>
<221> DISULFID
<222> (1)..(7)
<223> Disulfide bond between Xaa at position 1 and Xaa at position 7

<220>
<221> MOD_RES
<222> (2)..(2)
<223> N(alpha)METHYLATION

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Pen

<220>
<221> MOD_RES
<222> (10)..(10)
<223> D-Lys

<400> 144

Xaa Arg Ser Asp Thr Leu Xaa His Tyr Xaa
1 5 10

<210> 145
<211> 10
<212> PRT
<213> Unknown

<220>
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<220>
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<223> ACETYLATION

<220>
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<222> (1)..(1)
<223> Pen

<220>
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<222> (1)..(7)
<223> Disulfide bond between Xaa at position 1 and Xaa at position 7

<220>
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<222> (2)..(2)
<223> N(alpha)METHYLATION

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Pen

<220>
<221> MOD_RES
<222> (10)..(10)
<223> D-Lys

<400> 145

Xaa Arg Ser Asp Thr Leu Xaa Tyr Glu Xaa
1 5 10

<210> 146
<211> 10
<212> PRT
<213> Unknown

<220>
<223> Synthetic Construct

<220>
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<222> (1)..(1)
<223> ACETYLATION

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Pen

<220>
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<222> (1)..(7)
<223> Disulfide bond between Xaa at position 1 and Xaa at position 7

<220>
<221> MOD_RES
<222> (2)..(2)
<223> N(alpha)METHYLATION

<220>
<221> MOD_RES

<222> (7)..(7)
<223> Pen

<220>
<221> MOD_RES
<222> (8)..(8)
<223> 2-Nal

<220>
<221> MOD_RES
<222> (10)..(10)
<223> D-Lys

<400> 146

Xaa Arg Ser Asp Thr Leu Xaa Xaa Tyr Xaa
1 5 10