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(54) Title: MU-CONOPEPTIDES

(57) Abstract: The present invention is to μ -conopeptides, derivatives or pharmaceutically acceptable salts thereof. The present invention is further directed to the use of this peptide, derivatives thereof and pharmaceutically acceptable salts thereof for the treatment of disorders associated with voltage-gated sodium channels. Thus, the μ -conopeptides or derivatives are useful as neuromuscular blocking agents, local anesthetic agents, analgesic agents and neuroprotective agents. The μ -conopeptides are also useful for treating neuromuscular disorders. The invention is further directed to nucleic acid sequences encoding the μ -conopeptides and encoding propeptides, as well as the propeptides.



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TITLE OF THE INVENTION

MU-CONOPEPTIDES

CROSS-REFERENCE TO RELATED APPLICATIONS

5 [0001] The present application claims benefit under 35 USC §119(e) to U.S. provisional patent applications Serial No. 60/219,619 filed on 21 July 2000, Serial No. 60/245,157 filed on 3 November 2000, Serial No. 60/264,319 filed on 29 January 2001 and Serial No. 60/277,270 filed on 21 March 2001. Each of these applications is incorporated herein by reference.

10 [0002] This invention was made with Government support under Grant No. PO1 GM48677 awarded by the National Institute of General Medical Sciences, National Institutes of Health, Bethesda, Maryland. The United States Government has certain rights in the invention.

BACKGROUND OF THE INVENTION

15 [0003] The present invention is to μ -conopeptides, derivatives or pharmaceutically acceptable salts thereof. The present invention is further directed to the use of this peptide, derivatives thereof and pharmaceutically acceptable salts thereof for the treatment of disorders associated with voltage-gated sodium channels. Thus, the μ -conopeptides or derivatives are useful as neuromuscular blocking agents, local anesthetic agents, analgesic agents and
20 neuroprotective agents. The μ -conopeptides are also useful for treating neuromuscular disorders. The invention is further directed to nucleic acid sequences encoding the μ -conopeptides and encoding propeptides, as well as the propeptides.

[0004] The publications and other materials used herein to illuminate the background of the invention, and in particular, cases to provide additional details respecting the practice, are
25 incorporated by reference, and for convenience are referenced in the following text by author and date and are listed alphabetically by author in the appended bibliography.

[0005] *Conus* is a genus of predatory marine gastropods (snails) which envenomate their prey. Venomous cone snails use a highly developed projectile apparatus to deliver their cocktail of toxic conotoxins into their prey. In fish-eating species such as *Conus magus* the cone detects
30 the presence of the fish using chemosensors in its siphon and when close enough extends its proboscis and fires a hollow harpoon-like tooth containing venom into the fish. This immobilizes the fish and enables the cone snail to wind it into its mouth via an attached filament. For general information on *Conus* and their venom see the website address

<http://grimwade.biochem.unimelb.edu.au/cone/referenc.html>. Prey capture is accomplished through a sophisticated arsenal of peptides which target specific ion channel and receptor subtypes. Each *Conus* species venom appears to contain a unique set of 50-200 peptides. The composition of the venom differs greatly between species and between individual snails within each species, each optimally evolved to paralyse its prey. The active components of the venom are small peptides toxins, typically 10-40 amino acid residues in length and are typically highly constrained peptides due to their high density of disulphide bonds.

[0006] The venoms consist of a large number of different peptide components that when separated exhibit a range of biological activities: when injected into mice they elicit a range of physiological responses from shaking to depression. The paralytic components of the venom that have been the focus of recent investigation are the α -, ω - and μ -conotoxins. All of these conotoxins act by preventing neuronal communication, but each targets a different aspect of the process to achieve this. The α -conotoxins target nicotinic ligand gated channels, the μ -conotoxins target the voltage-gated sodium channels and the ω -conotoxins target the voltage-gated calcium channels (Olivera et al., 1985; Olivera et al., 1990). For example a linkage has been established between α -, α A- & ϕ -conotoxins and the nicotinic ligand-gated ion channel; ω -conotoxins and the voltage-gated calcium channel; μ -conotoxins and the voltage-gated sodium channel; δ -conotoxins and the voltage-gated sodium channel; κ -conotoxins and the voltage-gated potassium channel; conantokins and the ligand-gated glutamate (NMDA) channel.

[0007] However, the structure and function of only a small minority of these peptides have been determined to date. For peptides where function has been determined, three classes of targets have been elucidated: voltage-gated ion channels; ligand-gated ion channels, and G-protein-linked receptors.

[0008] *Conus* peptides which target voltage-gated ion channels include those that delay the inactivation of sodium channels, as well as blockers specific for sodium channels, calcium channels and potassium channels. Peptides that target ligand-gated ion channels include antagonists of NMDA and serotonin receptors, as well as competitive and noncompetitive nicotinic receptor antagonists. Peptides which act on G-protein receptors include neurotensin and vasopressin receptor agonists. The unprecedented pharmaceutical selectivity of conotoxins is at least in part defined by a specific disulfide bond frameworks combined with hypervariable amino acids within disulfide loops (for a review see McIntosh et al., 1998).

[0009] There are drugs used in the treatment of pain, which are known in the literature and to the skilled artisan. See, for example, Merck Manual, 16th Ed. (1992). However, there is a demand for more active analgesic agents with diminished side effects and toxicity and which are non-addictive. The ideal analgesic would reduce the awareness of pain, produce analgesia over a wide range of pain types, act satisfactorily whether given orally or parenterally, produce minimal or no side effects, be free from tendency to produce tolerance and drug dependence.

[0010] Due to the high potency and exquisite selectivity of the conopeptides, several are in various stages of clinical development for treatment of human disorders. For example, two *Conus* peptides are being developed for the treatment of pain. The most advanced is ω -conotoxin MVIIA (ziconotide), an N-type calcium channel blocker (see Heading, C., 1999; U.S. Patent No. 5,859,186). ω -Conotoxin MVIIA, isolated from *Conus magus*, is approximately 1000 times more potent than morphine, yet does not produce the tolerance or addictive properties of opiates. ω -Conotoxin MVIIA has completed Phase III (final stages) of human clinical trials and has been approved as a therapeutic agent. ω -Conotoxin MVIIA is introduced into human patients by means of an implantable, programmable pump with a catheter threaded into the intrathecal space. Preclinical testing for use in post-surgical pain is being carried out on another *Conus* peptide, contulakin-G, isolated from *Conus geographus* (Craig et al. 1999). Contulakin-G is a 16 amino acid O-linked glycopeptide whose C-terminus resembles neurotensin. It is an agonist of neurotensin receptors, but appears significantly more potent than neurotensin in inhibiting pain in *in vivo* assays.

[0011] In view of a large number of biologically active substances in *Conus* species it is desirable to further characterize them and to identify peptides capable of treating disorders involving voltage gated ion channels, such as stroke and pain. Surprisingly, and in accordance with this invention, Applicants have discovered novel conotoxins that can be useful for the treatment of disorders involving voltage gated ion channels and could address a long felt need for a safe and effective treatment.

SUMMARY OF THE INVENTION

[0012] The present invention is to μ -conopeptides, derivatives or pharmaceutically acceptable salts thereof. The present invention is further directed to the use of this peptide, derivatives thereof and pharmaceutically acceptable salts thereof for the treatment of disorders associated with voltage-gated sodium channels. Thus, the μ -conopeptides or derivatives are

useful as neuromuscular blocking agents, local anesthetic agents, analgesic agents and neuroprotective agents. The μ -conopeptides are also useful for treating neuromuscular disorders. The invention is further directed to nucleic acid sequences encoding the μ -conopeptides and encoding propeptides, as well as the propeptides.

5 [0013] More specifically, the present invention is directed to μ -conopeptides, having the amino acid sequences set forth in Tables 1 and 2 below.

[0014] The present invention is also directed to derivatives or pharmaceutically acceptable salts of the μ -conopeptides or the derivatives. Examples of derivatives include peptides in which the Arg residues may be substituted by Lys, ornithine, homoargine, nor-Lys,
10 N-methyl-Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys or any synthetic basic amino acid; the Lys residues may be substituted by Arg, ornithine, homoargine, nor-Lys, or any synthetic basic amino acid; the Tyr residues may be substituted with meta-Tyr, ortho-Tyr, nor-Tyr, mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr, nitro-Tyr or any synthetic hydroxy containing amino acid; the Ser residues may be substituted with Thr or any synthetic hydroxylated amino
15 acid; the Thr residues may be substituted with Ser or any synthetic hydroxylated amino acid; the Phe residues may be substituted with any synthetic aromatic amino acid; the Trp residues may be substituted with Trp (D), neo-Trp, halo-Trp (D or L) or any aromatic synthetic amino acid; and the Asn, Ser, Thr or Hyp residues may be glycosylated. The halogen may be iodo, chloro, fluoro or bromo; preferably iodo for halogen substituted-Tyr and bromo for halogen-substituted
20 Trp. The Tyr residues may also be substituted with the 3-hydroxyl or 2-hydroxyl isomers (meta-Tyr or ortho-Tyr, respectively) and corresponding O-sulpho- and O-phospho-derivatives. The acidic amino acid residues may be substituted with any synthetic acidic amino acid, e.g., tetrazolyl derivatives of Gly and Ala. The aliphatic amino acids may be substituted by synthetic derivatives bearing non-natural aliphatic branched or linear side chains C_nH_{2n+2} up to and
25 including $n=8$. The Met residues may be substituted by norleucine (Nle). The Cys residues may be in D or L configuration and may optionally be substituted with homocysteine (D or L).

[0015] Examples of synthetic aromatic amino acid include, but are not limited to, nitro-Phe, 4-substituted-Phe wherein the substituent is C_1 - C_3 alkyl, carboxyl, hydroxymethyl, sulphomethyl, halo, phenyl, -CHO, -CN, -SO₃H and -NHAc. Examples of synthetic hydroxy
30 containing amino acid, include, but are not limited to, such as 4-hydroxymethyl-Phe, 4-hydroxyphenyl-Gly, 2,6-dimethyl-Tyr and 5-amino-Tyr. Examples of synthetic basic amino acids include, but are not limited to, N-1-(2-pyrazoliny)-Arg, 2-(4-piperiny)-Gly, 2-(4-

piperinyl)-Ala, 2-[3-(2S)pyrrolinyl)-Gly and 2-[3-(2S)pyrrolinyl)-Ala. These and other synthetic basic amino acids, synthetic hydroxy containing amino acids or synthetic aromatic amino acids are described in Building Block Index, Version 3.0 (1999 Catalog, pages 4-47 for hydroxy containing amino acids and aromatic amino acids and pages 66-87 for basic amino acids; see also <http://www.amino-acids.com>), incorporated herein by reference, by and available from RSP Amino Acid Analogues, Inc., Worcester, MA. Examples of synthetic acid amino acids include those derivatives bearing acidic functionality, including carboxyl, phosphate, sulfonate and synthetic tetrazolyl derivatives such as described by Ornstein et al. (1993) and in U.S. Patent No. 5,331,001, each incorporated herein by reference.

[0016] Optionally, in the μ -conopeptides of the present invention, the Asn residues may be modified to contain an N-glycan and the Ser, Thr and Hyp residues may be modified to contain an O-glycan (e.g., g-N, g-S, g-T and g-Hyp). In accordance with the present invention, a glycan shall mean any N-, S- or O-linked mono-, di-, tri-, poly- or oligosaccharide that can be attached to any hydroxy, amino or thiol group of natural or modified amino acids by synthetic or enzymatic methodologies known in the art. The monosaccharides making up the glycan can include D-allose, D-altrose, D-glucose, D-mannose, D-gulose, D-idose, D-galactose, D-talose, D-galactosamine, D-glucosamine, D-N-acetyl-glucosamine (GlcNAc), D-N-acetyl-galactosamine (GalNAc), D-fucose or D-arabinose. These saccharides may be structurally modified, e.g., with one or more O-sulfate, O-phosphate, O-acetyl or acidic groups, such as sialic acid, including combinations thereof. The glycan may also include similar polyhydroxy groups, such as D-penicillamine 2,5 and halogenated derivatives thereof or polypropylene glycol derivatives. The glycosidic linkage is beta and 1-4 or 1-3, preferably 1-3. The linkage between the glycan and the amino acid may be alpha or beta, preferably alpha and is 1-.

[0017] Core O-glycans have been described by Van de Steen et al. (1998), incorporated herein by reference. Mucin type O-linked oligosaccharides are attached to Ser or Thr (or other hydroxylated residues of the present peptides) by a GalNAc residue. The monosaccharide building blocks and the linkage attached to this first GalNAc residue define the "core glycans," of which eight have been identified. The type of glycosidic linkage (orientation and connectivities) are defined for each core glycan. Suitable glycans and glycan analogs are described further in U.S. Serial No. 09/420,797 filed 19 October 1999 and in PCT Application No. PCT/US99/24380 filed 19 October 1999 (PCT Published Application No. WO 00/23092), each incorporated herein by reference. A preferred glycan is Gal(β 1 $\rightarrow$ 3)GalNAc(α 1 $\rightarrow$).

[0018] Optionally, in the μ -conopeptides described above, pairs of Cys residues may be replaced pairwise with isoteric lactam or ester-thioether replacements, such as Ser/(Glu or Asp), Lys/(Glu or Asp), Cys/(Glu or Asp) or Cys/Ala combinations. Sequential coupling by known methods (Barnay et al., 2000; Hruby et al., 1994; Bitan et al., 1997) allows replacement of native
5 Cys bridges with lactam bridges. Thioether analogs may be readily synthesized using halo-Ala residues commercially available from RSP Amino Acid Analogues.

[0019] The present invention is further directed to derivatives of the above peptides and peptide derivatives which are acyclic permutations in which the cyclic permutants retain the native bridging pattern of native toxin. See, for example, Craik et al. (2001).

10 [0020] The present invention is further directed to a method of treating disorders associated with voltage gated ion channel disorders in a subject comprising administering to the subject an effective amount of the pharmaceutical composition comprising a therapeutically effective amount of a μ -conopeptide described herein or a pharmaceutically acceptable salt or solvate thereof. The present invention is also directed to a pharmaceutical composition
15 comprising a therapeutically effective amount of a μ -conopeptide described herein or a pharmaceutically acceptable salt or solvate thereof and a pharmaceutically acceptable carrier.

[0021] More specifically, the present invention is further directed to uses of these peptides or nucleic acids as described herein as neuromuscular blocking agents, local anesthetic agents, analgesic agents and neuroprotective agents. The μ -conopeptides are also useful for
20 treating neuromuscular disorders.

[0022] The present invention is directed to the use of μ -conopeptides as a local anesthetic for treating pain. The μ -conopeptides have long lasting anesthetic activity and are particularly useful for spinal anesthesia, either administered acutely for post-operative pain or via an intrathecal pump for severe chronic pain situations. The μ -conopeptides are also useful as
25 analgesics in chronic and neuropathic pain states, such as trigeminal neuralgia, diabetic neuropathy, post-herpetic neuralgia, neuroma pain and phantom limb pain. The μ -conopeptides are also useful for treating burn pain and as ocular anesthetics.

[0023] The present invention is directed to the use of μ -conopeptides as neuroprotectants. The μ -conopeptides are useful for the treatment and alleviation of epilepsy
30 and as a general anticonvulsant agent. The μ -conopeptides are also useful for treating neurodegenerative diseases, such as Amyotrophic Lateral Sclerosis (ALS). The μ -conopeptides are further useful as cerebroprotectants, such as for reducing neurotoxic injury associated with

conditions of hypoxia, anoxia or ischemia which typically follows stroke, cerebrovascular accident, brain or spinal cord trauma, myocardial infarct, physical trauma, drowning, suffocation, perinatal asphyxia, or hypoglycemic events.

[0024] The present invention is directed to the use of μ -conopeptides as neuromuscular blockers and for treating neuromuscular disorders. As such, the μ -conopeptides are useful for providing relaxation of muscle, for treating benign essential blepharospasm and other forms of focal dystonia and for anti-wrinkle use.

[0025] More specifically, the present invention is also directed to nucleic acids which encode μ -conopeptides of the present invention or which encodes precursor peptides for these μ -conopeptides, as well as the precursor peptide. The nucleic acid sequences encoding the precursor peptides of other μ -conopeptides of the present invention are set forth in Table 1. Table 1 also sets forth the amino acid sequences of these precursor peptides.

[0026] The present invention is further directed to the use of selectively radioiodinated or radiotritiated μ -conopeptides for characterizing pore occlusion sites on different sodium channel subtypes or for use in screening assays.

[0027] The present invention is also directed to the use of μ -conopeptides for screening small molecule libraries to identify small molecules that are selective blocking agents at specific sodium channel subtypes expressed in mammalian systems. In one embodiment, the blocking activity of a small molecule at a particular sodium channel subtype is compared to the blocking activity of a μ -conopeptide at the same sodium channel subtype. In a second embodiment, the ability of a small molecule to displace a μ -conopeptide from a sodium channel subtype is determined. In a third embodiment, the binding affinity of a small molecule for a sodium channel subtype is compared to the binding affinity of a μ -conopeptide for the same sodium channel subtype.

DETAILED DESCRIPTION OF THE PREFERRED EMBODIMENT

[0028] The present invention is to μ -conopeptides, derivatives or pharmaceutically acceptable salts thereof. The present invention is further directed to the use of this peptide, derivatives thereof and pharmaceutically acceptable salts thereof for the treatment of disorders associated with voltage-gated sodium channels. Thus, the μ -conopeptides or derivatives are useful as neuromuscular blocking agents, local anesthetic agents, analgesic agents and neuroprotective agents. The μ -conopeptides are also useful for treating neuromuscular

disorders. The invention is further directed to nucleic acid sequences encoding the μ -conopeptides and encoding propeptides, as well as the propeptides.

[0029] The present invention, in another aspect, relates to a pharmaceutical composition comprising an effective amount of an μ -conopeptides, a mutein thereof, an analog thereof, an active fragment thereof or pharmaceutically acceptable salts or solvates. Such a pharmaceutical composition has the capability of acting at voltage gated ion channels, and are thus useful for treating a disorder or disease of a living animal body, including a human, which disorder or disease is responsive to the partial or complete blockade of voltage gated ion channels of the central nervous system comprising the step of administering to such a living animal body, including a human, in need thereof a therapeutically effective amount of a pharmaceutical composition of the present invention.

[0030] The present invention is directed to the use of μ -conopeptides as neuromuscular blockers and for treating neuromuscular disorders. As such, the μ -conopeptides are useful for providing relaxation of muscle, for treating benign essential blepharospasm and other forms of focal dystonia and for anti-wrinkle use. Thus, in one aspect, the μ -conopeptides are useful as neuromuscular blocking agents in conjunction with surgery or for intubation of the trachea by conventional parenteral administration e.g., intramuscular or intravenous administration in solution. In a second aspect, the μ -conopeptides are useful as agents for treating neuromuscular disorders such as myofascial pain syndrome, chronic muscle spasm, dystonias and spasticity.

[0031] The primary factor detrimental to neurons in neurological disorders associated with deficient oxygen supply or mitochondrial dysfunction is insufficient ATP production relative to their requirement. As a large part of the energy consumed by brain cells is used for maintenance of the Na^+ gradient across the cellular membrane, reduction of energy demand by down-modulation of voltage-gated Na^+ -channels is one strategy for neuroprotection. In addition, preservation of the inward Na^+ gradient may be beneficial because it is an essential driving force for vital ion exchanges and transport mechanisms such as Ca^{2+} homeostasis and neurotransmitter uptake. Thus, the μ -conopeptides of the present invention are useful as neuroprotectants.

[0032] Thus, the pharmaceutical compositions of the present invention are useful as neuroprotectants, especially cerebroprotectants, neuromuscular blockers, analgesics (both as a local anesthetic and for general analgesia use) or adjuvants to general anesthetics. A "neurological disorder or disease" is a disorder or disease of the nervous system including, but

not limited to, global and focal ischemic and hemorrhagic stroke, head trauma, spinal cord injury, hypoxia-induced nerve cell damage as in cardiac arrest or neonatal distress or epilepsy. In addition, a "neurological disorder or disease" is a disease state and condition in which a neuroprotectant, anticonvulsant, analgesic and/or as an adjunct in general anesthesia may be indicated, useful, recommended or prescribed.

[0033] More specifically, the present invention is directed to the use of these compounds for reducing neurotoxic injury associated with conditions of hypoxia, anoxia or ischemia which typically follows stroke, cerebrovascular accident, brain or spinal cord trauma, myocardial infarct, physical trauma, drowning, suffocation, perinatal asphyxia, or hypoglycemic events.

The present invention is further directed to the use of these compounds for treating pain, including acute and chronic pain, such migraine, nociceptive and neuropathic pain.

[0034] A "neuroprotectant" is a compound capable of preventing the neuronal death associated with a neurological disorder or disease. An "analgesic" is a compound capable of relieving pain by altering perception of nociceptive stimuli without producing anesthesia or loss of consciousness. A "muscle relaxant" is a compound that reduces muscular tension. An "adjunct in general anesthesia" is a compound useful in conjunction with anesthetic agents in producing the loss of ability to perceive pain associated with the loss of consciousness.

[0035] The invention relates as well to methods useful for treatment of neurological disorders and diseases, including, but not limited to, global and focal ischemic and hemorrhagic stroke, head trauma, spinal cord injury, hypoxia-induced nerve cell damage such as in cardiac arrest or neonatal distress, epilepsy or other convulsive disorders without undesirable side effects.

[0036] Thus, in one embodiment, the invention provides a method of reducing/alleviating/ decreasing the perception of pain by a subject or for inducing analgesia in a subject comprising administering to the subject an effective amount of the pharmaceutical composition comprising a therapeutically effective amount of a μ -conopeptide described herein or a pharmaceutically acceptable salt or solvate thereof. The pain may be acute, persistent, inflammatory or neuropathic pain. The μ -conopeptides are useful as an analgesia for chronic and neuropathic pain states, such as trigeminal neuralgia, diabetic neuropathy, post-herpetic neuralgia, neuroma pain, phantom limb pain. These peptides are also useful for treating burn pain and as ocular anesthetics.

[0037] In a second embodiment, the invention provides a method of reducing/alleviating/decreasing the perception of pain by a subject or for inducing analgesia, particularly local analgesia, in a subject comprising administering to the subject an effective amount of the pharmaceutical composition comprising a therapeutically effective amount of a μ -conopeptide described herein or a pharmaceutically acceptable salt or solvate thereof. These peptides are also useful for treating burn pain and as ocular anesthetics.

[0038] In a third embodiment, the invention provides a method of treating stroke, head or spinal cord trauma or injury, anoxia, hypoxia-induced nerve cell damage, ischemia, migraine, psychosis, anxiety, schizophrenia, inflammation, movement disorder, epilepsy, any other convulsive disorder or in the prevention of the degenerative changes connected with the same in a subject comprising administering to the subject an effective amount of the pharmaceutical composition comprising a therapeutically effective amount of a μ -conopeptide described herein or a pharmaceutically acceptable salt or solvate thereof.

[0039] In a fourth embodiment, the invention provides a method for providing a neuromuscular block or for treating neuromuscular disorders, such as methods for providing relaxation of muscle, for treating benign essential blepharospasm and other forms of focal dystonia and for anti-wrinkle use. Thus, in one aspect, the μ -conopeptides are useful as neuromuscular blocking agents in conjunction with surgery or for intubation of the trachea by conventional parenteral administration e.g., intramuscular or intravenous administration in solution. In a second aspect, the μ -conopeptides are useful as agents for treating neuromuscular disorders such as myofascial pain syndrome, chronic muscle spasm, dystonias and spasticity.

[0040] The present invention is also directed to the use of μ -conopeptides for screening small molecule libraries to identify small molecules that are selective blocking agents at specific sodium channel subtypes expressed in mammalian systems. In one embodiment, the blocking activity of a small molecule at a particular sodium channel subtype is compared to the blocking activity of a μ -conopeptide at the same sodium channel subtype. In a second embodiment, the ability of a small molecule to displace a μ -conopeptide from a sodium channel subtype is determined. In a third embodiment, the binding affinity of a small molecule for a sodium channel subtype is compared to the binding affinity of a μ -conopeptide for the same sodium channel subtype.

[0041] The μ -conopeptides described herein are sufficiently small to be chemically synthesized. General chemical syntheses for preparing the foregoing ω -conotoxin peptides are

described hereinafter. Various ones of the μ -conopeptides can also be obtained by isolation and purification from specific *Conus* species using the technique described in U.S. Patent Nos. 4,447,356 (Olivera et al., 1984); 5,514,774; 5,719,264; and 5,591,821, as well as in PCT published application WO 98/03189, the disclosures of which are incorporated herein by
5 reference.

[0042] Although the μ -conopeptides of the present invention can be obtained by purification from cone snails, because the amounts of μ -conopeptides obtainable from individual snails are very small, the desired substantially pure μ -conopeptides are best practically obtained in commercially valuable amounts by chemical synthesis using solid-phase strategy. For
10 example, the yield from a single cone snail may be about 10 micrograms or less of μ -conopeptides peptide. By "substantially pure" is meant that the peptide is present in the substantial absence of other biological molecules of the same type; it is preferably present in an amount of at least about 85% purity and preferably at least about 95% purity. Chemical synthesis of biologically active μ -conopeptides peptides depends of course upon correct
15 determination of the amino acid sequence.

[0043] The μ -conopeptides can also be produced by recombinant DNA techniques well known in the art. Such techniques are described by Sambrook et al. (1989). A gene of interest (i.e., a gene that encodes a suitable μ -conopeptides) can be inserted into a cloning site of a suitable expression vector by using standard techniques. These techniques are well known to
20 those skilled in the art. The expression vector containing the gene of interest may then be used to transfect the desired cell line. Standard transfection techniques such as calcium phosphate co-precipitation, DEAE-dextran transfection or electroporation may be utilized. A wide variety of host/expression vector combinations may be used to express a gene encoding a conotoxin peptide of interest. Such combinations are well known to a skilled artisan. The peptides
25 produced in this manner are isolated, reduced if necessary, and oxidized to form the correct disulfide bonds.

[0044] One method of forming disulfide bonds in the μ -conopeptides of the present invention is the air oxidation of the linear peptides for prolonged periods under cold room temperatures or at room temperature. This procedure results in the creation of a substantial
30 amount of the bioactive, disulfide-linked peptides. The oxidized peptides are fractionated using reverse-phase high performance liquid chromatography (HPLC) or the like, to separate peptides having different linked configurations. Thereafter, either by comparing these fractions with the

elution of the native material or by using a simple assay, the particular fraction having the correct linkage for maximum biological potency is easily determined. However, because of the dilution resulting from the presence of other fractions of less biopotency, a somewhat higher dosage may be required.

5 [0045] The peptides are synthesized by a suitable method, such as by exclusively solid-phase techniques, by partial solid-phase techniques, by fragment condensation or by classical solution couplings.

[0046] In conventional solution phase peptide synthesis, the peptide chain can be prepared by a series of coupling reactions in which constituent amino acids are added to the
10 growing peptide chain in the desired sequence. Use of various coupling reagents, e.g., dicyclohexylcarbodiimide or diisopropylcarbonyldimidazole, various active esters, e.g., esters of N-hydroxyphthalimide or N-hydroxy-succinimide, and the various cleavage reagents, to carry out reaction in solution, with subsequent isolation and purification of intermediates, is well known classical peptide methodology. Classical solution synthesis is described in detail in the
15 treatise, "Methoden der Organischen Chemie (Houben-Weyl): Synthese von Peptiden," (1974). Techniques of exclusively solid-phase synthesis are set forth in the textbook, "Solid-Phase Peptide Synthesis," (Stewart and Young, 1969), and are exemplified by the disclosure of U.S. Patent 4,105,603 (Vale et al., 1978). The fragment condensation method of synthesis is exemplified in U.S. Patent 3,972,859 (1976). Other available syntheses are exemplified by U.S.
20 Patents No. 3,842,067 (1974) and 3,862,925 (1975). The synthesis of peptides containing γ -carboxyglutamic acid residues is exemplified by Rivier et al. (1987), Nishiuchi et al. (1993) and Zhou et al. (1996).

[0047] Common to such chemical syntheses is the protection of the labile side chain groups of the various amino acid moieties with suitable protecting groups which will prevent a
25 chemical reaction from occurring at that site until the group is ultimately removed. Usually also common is the protection of an α -amino group on an amino acid or a fragment while that entity reacts at the carboxyl group, followed by the selective removal of the α -amino protecting group to allow subsequent reaction to take place at that location. Accordingly, it is common that, as a step in such a synthesis, an intermediate compound is produced which includes each of the
30 amino acid residues located in its desired sequence in the peptide chain with appropriate side-chain protecting groups linked to various ones of the residues having labile side chains.

[0048] As far as the selection of a side chain amino protecting group is concerned, generally one is chosen which is not removed during deprotection of the α -amino groups during the synthesis. However, for some amino acids, e.g., His, protection is not generally necessary. In selecting a particular side chain protecting group to be used in the synthesis of the peptides, the following general rules are followed: (a) the protecting group preferably retains its protecting properties and is not split off under coupling conditions, (b) the protecting group should be stable under the reaction conditions selected for removing the α -amino protecting group at each step of the synthesis, and (c) the side chain protecting group must be removable, upon the completion of the synthesis containing the desired amino acid sequence, under reaction conditions that will not undesirably alter the peptide chain.

[0049] It should be possible to prepare many, or even all, of these peptides using recombinant DNA technology. However, when peptides are not so prepared, they are preferably prepared using the Merrifield solid-phase synthesis, although other equivalent chemical syntheses known in the art can also be used as previously mentioned. Solid-phase synthesis is commenced from the C-terminus of the peptide by coupling a protected α -amino acid to a suitable resin. Such a starting material can be prepared by attaching an α -amino-protected amino acid by an ester linkage to a chloromethylated resin or a hydroxymethyl resin, or by an amide bond to a benzhydrylamine (BHA) resin or paramethylbenzhydrylamine (MBHA) resin. Preparation of the hydroxymethyl resin is described by Bodansky et al. (1966). Chloromethylated resins are commercially available from Bio Rad Laboratories (Richmond, CA) and from Lab. Systems, Inc. The preparation of such a resin is described by Stewart and Young (1969). BHA and MBHA resin supports are commercially available, and are generally used when the desired polypeptide being synthesized has an unsubstituted amide at the C-terminus. Thus, solid resin supports may be any of those known in the art, such as one having the formulae $-O-CH_2$ -resin support, $-NH$ BHA resin support, or $-NH$ -MBHA resin support. When the unsubstituted amide is desired, use of a BHA or MBHA resin is preferred, because cleavage directly gives the amide. In case the N-methyl amide is desired, it can be generated from an N-methyl BHA resin. Should other substituted amides be desired, the teaching of U.S. Patent No. 4,569,967 (Kornreich et al., 1986) can be used, or should still other groups than the free acid be desired at the C-terminus, it may be preferable to synthesize the peptide using classical methods as set forth in the Houben-Weyl text (1974).

[0050] The C-terminal amino acid, protected by Boc or Fmoc and by a side-chain protecting group, if appropriate, can be first coupled to a chloromethylated resin according to the procedure set forth in K. Horiki et al. (1978), using KF in DMF at about 60°C for 24 hours with stirring, when a peptide having free acid at the C-terminus is to be synthesized. Following the coupling of the BOC-protected amino acid to the resin support, the α -amino protecting group is removed, as by using trifluoroacetic acid (TFA) in methylene chloride or TFA alone. The deprotection is carried out at a temperature between about 0°C and room temperature. Other standard cleaving reagents, such as HCl in dioxane, and conditions for removal of specific α -amino protecting groups may be used as described in Schroder & Lubke (1965).

[0051] After removal of the α -amino-protecting group, the remaining α -amino- and side chain-protected amino acids are coupled step-wise in the desired order to obtain the intermediate compound defined hereinbefore, or as an alternative to adding each amino acid separately in the synthesis, some of them may be coupled to one another prior to addition to the solid phase reactor. Selection of an appropriate coupling reagent is within the skill of the art. Particularly suitable as a coupling reagent is N,N'-dicyclohexylcarbodiimide (DCC, DIC, HBTU, HATU, TBTU in the presence of HoBt or HoAt).

[0052] The activating reagents used in the solid phase synthesis of the peptides are well known in the peptide art. Examples of suitable activating reagents are carbodiimides, such as N,N'-diisopropylcarbodiimide and N-ethyl-N'-(3-dimethylaminopropyl)carbodiimide. Other activating reagents and their use in peptide coupling are described by Schroder & Lubke (1965) and Kapoor (1970).

[0053] Each protected amino acid or amino acid sequence is introduced into the solid-phase reactor in about a twofold or more excess, and the coupling may be carried out in a medium of dimethylformamide (DMF):CH₂Cl₂ (1:1) or in DMF or CH₂Cl₂ alone. In cases where intermediate coupling occurs, the coupling procedure is repeated before removal of the α -amino protecting group prior to the coupling of the next amino acid. The success of the coupling reaction at each stage of the synthesis, if performed manually, is preferably monitored by the ninhydrin reaction, as described by Kaiser et al. (1970). Coupling reactions can be performed automatically, as on a Beckman 990 automatic synthesizer, using a program such as that reported in Rivier et al. (1978).

[0054] After the desired amino acid sequence has been completed, the intermediate peptide can be removed from the resin support by treatment with a reagent, such as liquid

hydrogen fluoride or TFA (if using Fmoc chemistry), which not only cleaves the peptide from the resin but also cleaves all remaining side chain protecting groups and also the α -amino protecting group at the N-terminus if it was not previously removed to obtain the peptide in the form of the free acid. If Met is present in the sequence, the Boc protecting group is preferably first removed using trifluoroacetic acid (TFA)/ethanedithiol prior to cleaving the peptide from the resin with HF to eliminate potential S-alkylation. When using hydrogen fluoride or TFA for cleaving, one or more scavengers such as anisole, cresol, dimethyl sulfide and methylethyl sulfide are included in the reaction vessel.

[0055] Cyclization of the linear peptide is preferably affected, as opposed to cyclizing the peptide while a part of the peptido-resin, to create bonds between Cys residues. To effect such a disulfide cyclizing linkage, fully protected peptide can be cleaved from a hydroxymethylated resin or a chloromethylated resin support by ammonolysis, as is well known in the art, to yield the fully protected amide intermediate, which is thereafter suitably cyclized and deprotected. Alternatively, deprotection, as well as cleavage of the peptide from the above resins or a benzhydrylamine (BHA) resin or a methylbenzhydrylamine (MBHA), can take place at 0°C with hydrofluoric acid (HF) or TFA, followed by oxidation as described above.

[0056] The peptides are also synthesized using an automatic synthesizer. Amino acids are sequentially coupled to an MBHA Rink resin (typically 100 mg of resin) beginning at the C-terminus using an Advanced Chemtech 357 Automatic Peptide Synthesizer. Couplings are carried out using 1,3-diisopropylcarbodiimide in N-methylpyrrolidinone (NMP) or by 2-(1H-benzotriazole-1-yl)-1,1,3,3-tetramethyluronium hexafluorophosphate (HBTU) and diethylisopropylethylamine (DIEA). The Fmoc protecting group is removed by treatment with a 20% solution of piperidine in dimethylformamide(DMF). Resins are subsequently washed with DMF (twice), followed by methanol and NMP.

[0057] Muteins, analogs or active fragments, of the foregoing conotoxin peptides are also contemplated here. See, e.g., Hammerland et al. (1992). Derivative muteins, analogs or active fragments of the conotoxin peptides may be synthesized according to known techniques, including conservative amino acid substitutions, such as outlined in U.S. Patent Nos. 5,545,723 (see particularly col. 2, line 50--col. 3, line 8); 5,534,615 (see particularly col. 19, line 45--col. 22, line 33); and 5,364,769 (see particularly col. 4, line 55--col. 7, line 26), each herein incorporated by reference.

[0058] The μ -conopeptides of the present invention are also useful to reduce neurotoxic injury associated with conditions of hypoxia, anoxia or ischemia which typically follows stroke, cerebrovascular accident, brain or spinal chord trauma, myocardial infarct, physical trauma, drownings, suffocation, perinatal asphyxia, or hypoglycemic events. To reduce neurotoxic injury, an ω -conopeptide should be administered in a therapeutically effective amount to the patient within 24 hours of the onset of the hypoxic, anoxic or ischemic condition in order for the μ -conopeptide to effectively minimize the CNS damage which the patient will experience.

[0059] The μ -conopeptides of the present invention are further useful in controlling pain, e.g., as analgesic agents, and the treatment of migraine, acute pain or persistent pain. They can be used prophylactically or to relieve the symptoms associated with a migraine episode, or to treat acute or persistent pain. For these uses, an μ -conopeptide is administered in a therapeutically effective amount to overcome or to ease the pain.

[0060] The μ -conopeptides of the present invention are also useful as neuromuscular blockers and for treating neuromuscular disorders. They can be used for providing relaxation of muscle, for treating benign essential blepharospasm and other forms of focal dystonia and for anti-wrinkle use. Thus, in one aspect, the μ -conopeptides are used as neuromuscular blocking agents in conjunction with surgery or for intubation of the trachea by conventional parenteral administration e.g., intramuscular or intravenous administration in solution. In a second aspect, the μ -conopeptides are used as agents for treating neuromuscular disorders such as myofascial pain syndrome, chronic muscle spasm, dystonias and spasticity. For these uses, a μ -conopeptide is administered in a therapeutically effective amount to relax muscle or provide a neuromuscular block.

[0061] Pharmaceutical compositions containing a compound of the present invention as the active ingredient can be prepared according to conventional pharmaceutical compounding techniques. See, for example, *Remington's Pharmaceutical Sciences*, 18th Ed. (1990, Mack Publishing Co., Easton, PA). Typically, an antagonistic amount of active ingredient will be admixed with a pharmaceutically acceptable carrier. The carrier may take a wide variety of forms depending on the form of preparation desired for administration, e.g., intravenous, oral, parenteral or intrathecally. For examples of delivery methods see U.S. Patent No. 5,844,077, incorporated herein by reference.

[0062] "Pharmaceutical composition" means physically discrete coherent portions suitable for medical administration. "Pharmaceutical composition in dosage unit form" means

physically discrete coherent units suitable for medical administration, each containing a daily dose or a multiple (up to four times) or a sub-multiple (down to a fortieth) of a daily dose of the active compound in association with a carrier and/or enclosed within an envelope. Whether the composition contains a daily dose, or for example, a half, a third or a quarter of a daily dose, will
5 depend on whether the pharmaceutical composition is to be administered once or, for example, twice, three times or four times a day, respectively.

[0063] The term "salt", as used herein, denotes acidic and/or basic salts, formed with inorganic or organic acids and/or bases, preferably basic salts. While pharmaceutically acceptable salts are preferred, particularly when employing the compounds of the invention as
10 medicaments, other salts find utility, for example, in processing these compounds, or where non-medicament-type uses are contemplated. Salts of these compounds may be prepared by art-recognized techniques.

[0064] Examples of such pharmaceutically acceptable salts include, but are not limited to, inorganic and organic addition salts, such as hydrochloride, sulphates, nitrates or phosphates
15 and acetates, trifluoroacetates, propionates, succinates, benzoates, citrates, tartrates, fumarates, maleates, methane-sulfonates, isothionates, theophylline acetates, salicylates, respectively, or the like. Lower alkyl quaternary ammonium salts and the like are suitable, as well.

[0065] As used herein, the term "pharmaceutically acceptable" carrier means a non-toxic, inert solid, semi-solid liquid filler, diluent, encapsulating material, formulation auxiliary of any
20 type, or simply a sterile aqueous medium, such as saline. Some examples of the materials that can serve as pharmaceutically acceptable carriers are sugars, such as lactose, glucose and sucrose, starches such as corn starch and potato starch, cellulose and its derivatives such as sodium carboxymethyl cellulose, ethyl cellulose and cellulose acetate; powdered tragacanth; malt, gelatin, talc; excipients such as cocoa butter and suppository waxes; oils such as peanut oil,
25 cottonseed oil, safflower oil, sesame oil, olive oil, corn oil and soybean oil; glycols, such as propylene glycol, polyols such as glycerin, sorbitol, mannitol and polyethylene glycol; esters such as ethyl oleate and ethyl laurate, agar; buffering agents such as magnesium hydroxide and aluminum hydroxide; alginic acid; pyrogen-free water; isotonic saline, Ringer's solution; ethyl alcohol and phosphate buffer solutions, as well as other non-toxic compatible substances used in
30 pharmaceutical formulations.

[0066] Wetting agents, emulsifiers and lubricants such as sodium lauryl sulfate and magnesium stearate, as well as coloring agents, releasing agents, coating agents, sweetening,

flavoring and perfuming agents, preservatives and antioxidants can also be present in the composition, according to the judgment of the formulator. Examples of pharmaceutically acceptable antioxidants include, but are not limited to, water soluble antioxidants such as ascorbic acid, cysteine hydrochloride, sodium bisulfite, sodium metabisulfite, sodium sulfite, and the like; oil soluble antioxidants, such as ascorbyl palmitate, butylated hydroxyanisole (BHA), butylated hydroxytoluene (BHT), lecithin, propyl gallate, alpha-tocopherol and the like; and the metal chelating agents such as citric acid, ethylenediamine tetraacetic acid (EDTA), sorbitol, tartaric acid, phosphoric acid and the like.

[0067] For oral administration, the compounds can be formulated into solid or liquid preparations such as capsules, pills, tablets, lozenges, melts, powders, suspensions or emulsions.

In preparing the compositions in oral dosage form, any of the usual pharmaceutical media may be employed, such as, for example, water, glycols, oils, alcohols, flavoring agents, preservatives, coloring agents, suspending agents, and the like in the case of oral liquid preparations (such as, for example, suspensions, elixirs and solutions); or carriers such as starches, sugars, diluents, granulating agents, lubricants, binders, disintegrating agents and the like in the case of oral solid preparations (such as, for example, powders, capsules and tablets). Because of their ease in administration, tablets and capsules represent the most advantageous oral dosage unit form, in which case solid pharmaceutical carriers are obviously employed. If desired, tablets may be sugar-coated or enteric-coated by standard techniques. The active agent can be encapsulated to make it stable to passage through the gastrointestinal tract while at the same time allowing for passage across the blood brain barrier. See for example, WO 96/11698.

[0068] For parenteral administration, the compound may be dissolved in a pharmaceutical carrier and administered as either a solution or a suspension. Illustrative of suitable carriers are water, saline, dextrose solutions, fructose solutions, ethanol, or oils of animal, vegetative or synthetic origin. The carrier may also contain other ingredients, for example, preservatives, suspending agents, solubilizing agents, buffers and the like. When the compounds are being administered intrathecally, they may also be dissolved in cerebrospinal fluid.

[0069] A variety of administration routes are available. The particular mode selected will depend of course, upon the particular drug selected, the severity of the disease state being treated and the dosage required for therapeutic efficacy. The methods of this invention, generally speaking, may be practiced using any mode of administration that is medically acceptable,

meaning any mode that produces effective levels of the active compounds without causing clinically unacceptable adverse effects. Such modes of administration include oral, rectal, sublingual, topical, nasal, transdermal or parenteral routes. The term "parenteral" includes subcutaneous, intravenous, epidural, irrigation, intramuscular, release pumps, or infusion.

5 [0070] For example, administration of the active agent according to this invention may be achieved using any suitable delivery means, including:

(a) pump (see, e.g., Luer & Hatton (1993), Zimm et al. (1984) and Ettinger et al. (1978));

(b), microencapsulation (see, e.g., U.S. Patent Nos. 4,352,883; 4,353,888; and 5,084,350);

10 (c) continuous release polymer implants (see, e.g., U.S. Patent No. 4,883,666);

(d) macroencapsulation (see, e.g., U.S. Patent Nos. 5,284,761, 5,158,881, 4,976,859 and 4,968,733 and published PCT patent applications WO92/19195, WO 95/05452);

(e) naked or unencapsulated cell grafts to the CNS (see, e.g., U.S. Patent Nos. 5,082,670 and 5,618,531);

15 (f) injection, either subcutaneously, intravenously, intra-arterially, intramuscularly, or to other suitable site; or

(g) oral administration, in capsule, liquid, tablet, pill, or prolonged release formulation.

[0071] In one embodiment of this invention, an active agent is delivered directly into the CNS, preferably to the brain ventricles, brain parenchyma, the intrathecal space or other suitable
20 CNS location, most preferably intrathecally.

[0072] Alternatively, targeting therapies may be used to deliver the active agent more specifically to certain types of cell, by the use of targeting systems such as antibodies or cell specific ligands. Targeting may be desirable for a variety of reasons, e.g. if the agent is unacceptably toxic, or if it would otherwise require too high a dosage, or if it would not
25 otherwise be able to enter the target cells.

[0073] The active agents, which are peptides, can also be administered in a cell based delivery system in which a DNA sequence encoding an active agent is introduced into cells designed for implantation in the body of the patient, especially in the spinal cord region. Suitable delivery systems are described in U.S. Patent No. 5,550,050 and published PCT
30 Application Nos. WO 92/19195, WO 94/25503, WO 95/01203, WO 95/05452, WO 96/02286, WO 96/02646, WO 96/40871, WO 96/40959 and WO 97/12635. Suitable DNA sequences can

be prepared synthetically for each active agent on the basis of the developed sequences and the known genetic code.

[0074] Exemplary methods for administering such muscle relaxant compounds (e.g., so as to achieve sterile or aseptic conditions) will be apparent to the skilled artisan. Certain methods suitable for administering compounds useful according to the present invention are set forth in Goodman and Gilman's *The Pharmacological Basis of Therapeutics*, 7th Ed. (1985). The administration to the patient can be intermittent; or at a gradual, continuous, constant or controlled rate. Administration can be to a warm-blooded animal (e.g. a mammal, such as a mouse, rat, cat, rabbit, dog, pig, cow or monkey); but advantageously is administered to a human being. Administration occurs after general anesthesia is administered. The frequency of administration normally is determined by an anesthesiologist, and typically varies from patient to patient.

[0075] The active agent is preferably administered in an therapeutically effective amount. By a "therapeutically effective amount" or simply "effective amount" of an active compound is meant a sufficient amount of the compound to treat the desired condition at a reasonable benefit/risk ratio applicable to any medical treatment. The actual amount administered, and the rate and time-course of administration, will depend on the nature and severity of the condition being treated. Prescription of treatment, e.g. decisions on dosage, timing, etc., is within the responsibility of general practitioners or specialists, and typically takes account of the disorder to be treated, the condition of the individual patient, the site of delivery, the method of administration and other factors known to practitioners. Examples of techniques and protocols can be found in *Remington's Pharmaceutical Sciences*.

[0076] Dosage may be adjusted appropriately to achieve desired drug levels, locally or systemically. Typically the active agents of the present invention exhibit their effect at a dosage range from about 0.001 mg/kg to about 250 mg/kg, preferably from about 0.01 mg/kg to about 100 mg/kg of the active ingredient, more preferably from about 0.05 mg/kg to about 75 mg/kg. A suitable dose can be administered in multiple sub-doses per day. Typically, a dose or sub-dose may contain from about 0.1 mg to about 500 mg of the active ingredient per unit dosage form. A more preferred dosage will contain from about 0.5 mg to about 100 mg of active ingredient per unit dosage form. Dosages are generally initiated at lower levels and increased until desired effects are achieved. In the event that the response in a subject is insufficient at such doses, even higher doses (or effective higher doses by a different, more localized delivery

route) may be employed to the extent that patient tolerance permits. Continuous dosing over, for example 24 hours or multiple doses per day are contemplated to achieve appropriate systemic levels of compounds.

[0077] For the treatment of pain, if the route of administration is directly to the CNS, the dosage contemplated is from about 1 ng to about 100 mg per day, preferably from about 100 ng to about 10 mg per day, more preferably from about 1 µg to about 100 µg per day. If administered peripherally, the dosage contemplated is somewhat higher, from about 100 ng to about 1000 mg per day, preferably from about 10 µg to about 100 mg per day, more preferably from about 100 µg to about 10 mg per day. If the conopeptide is delivered by continuous infusion (e.g., by pump delivery, biodegradable polymer delivery or cell-based delivery), then a lower dosage is contemplated than for bolus delivery.

[0078] Advantageously, the compositions are formulated as dosage units, each unit being adapted to supply a fixed dose of active ingredients. Tablets, coated tablets, capsules, ampoules and suppositories are examples of dosage forms according to the invention.

[0079] It is only necessary that the active ingredient constitute an effective amount, i.e., such that a suitable effective dosage will be consistent with the dosage form employed in single or multiple unit doses. The exact individual dosages, as well as daily dosages, are determined according to standard medical principles under the direction of a physician or veterinarian for use humans or animals.

[0080] The pharmaceutical compositions will generally contain from about 0.0001 to 99 wt. %, preferably about 0.001 to 50 wt. %, more preferably about 0.01 to 10 wt.% of the active ingredient by weight of the total composition. In addition to the active agent, the pharmaceutical compositions and medicaments can also contain other pharmaceutically active compounds. Examples of other pharmaceutically active compounds include, but are not limited to, analgesic agents, cytokines and therapeutic agents in all of the major areas of clinical medicine. When used with other pharmaceutically active compounds, the conopeptides of the present invention may be delivered in the form of drug cocktails. A cocktail is a mixture of any one of the compounds useful with this invention with another drug or agent. In this embodiment, a common administration vehicle (e.g., pill, tablet, implant, pump, injectable solution, etc.) would contain both the instant composition in combination supplementary potentiating agent. The individual drugs of the cocktail are each administered in therapeutically effective amounts. A therapeutically effective amount will be determined by the parameters described above; but, in

any event, is that amount which establishes a level of the drugs in the area of body where the drugs are required for a period of time which is effective in attaining the desired effects.

[0081] The practice of the present invention employs, unless otherwise indicated,
5 conventional techniques of chemistry, molecular biology, microbiology, recombinant DNA, genetics, immunology, cell biology, cell culture and transgenic biology, which are within the skill of the art. See, e.g., Maniatis *et al.*, 1982; Sambrook *et al.*, 1989; Ausubel *et al.*, 1992; Glover, 1985; Anand, 1992; Guthrie and Fink, 1991; Harlow and Lane, 1988; Jakoby and Pastan, 1979; *Nucleic Acid Hybridization* (B. D. Hames & S. J. Higgins eds. 1984);
10 *Transcription And Translation* (B. D. Hames & S. J. Higgins eds. 1984); *Culture Of Animal Cells* (R. I. Freshney, Alan R. Liss, Inc., 1987); *Immobilized Cells And Enzymes* (IRL Press, 1986); B. Perbal, *A Practical Guide To Molecular Cloning* (1984); the treatise, *Methods In Enzymology* (Academic Press, Inc., N.Y.); *Gene Transfer Vectors For Mammalian Cells* (J. H. Miller and M. P. Calos eds., 1987, Cold Spring Harbor Laboratory); *Methods In Enzymology*,
15 Vols. 154 and 155 (Wu et al. eds.), *Immunochemical Methods In Cell And Molecular Biology* (Mayer and Walker, eds., Academic Press, London, 1987); *Handbook Of Experimental Immunology*, Volumes I-IV (D. M. Weir and C. C. Blackwell, eds., 1986); Riott, *Essential Immunology*, 6th Edition, Blackwell Scientific Publications, Oxford, 1988; Hogan et al., *Manipulating the Mouse Embryo*, (Cold Spring Harbor Laboratory Press, Cold Spring Harbor,
20 N.Y., 1986).

EXAMPLES

[0082] The present invention is described by reference to the following Examples, which are offered by way of illustration and are not intended to limit the invention in any manner.
25 Standard techniques well known in the art or the techniques specifically described below were utilized.

EXAMPLE 1

Isolation of μ -Conopeptides

30 [0083] Crude venom was extracted from venom ducts (Cruz et al., 1976), and the components were purified as previously described (Cartier et al., 1996). The crude extract from venom ducts was purified by reverse phase liquid chromatography (RPLC) using a Vydac C₁₈

semi-preparative column (10 x 250 mm). Further purification of bioactive peaks was done on a Vydac C₁₈ analytical column (4.6 x 220 mm). The effluents were monitored at 220 nm. Peaks were collected, and aliquots were assayed for activity. Throughout purification, HPLC fractions were assayed by means of intracerebral ventricular (i.c.v.) injection into mice (Clark et al., 1981).

[0084] The amino acid sequence of the purified peptides were determined by standard methods. The purified peptides were reduced and alkylated prior to sequencing by automated Edman degradation on an Applied Biosystems 477A Protein Sequencer with a 120A Analyzer (DNA/Peptide Facility, University of Utah) (Martinez et al., 1995; Shon et al., 1994).

[0085] In accordance with this method, the μ -conopeptides described as "isolated" in Table 1 were obtained. These μ -conopeptides, as well as the other μ -conopeptides and the μ -conopeptide precursors set forth in Table 1 are synthesized as described in U.S. Patent No. 5,670,622.

EXAMPLE 2

Isolation of DNA Encoding μ -Conopeptides

[0086] DNA coding for μ -conopeptides was isolated and cloned in accordance with conventional techniques using general procedures well known in the art, such as described in Olivera et al. (1996). Alternatively, cDNA libraries was prepared from *Conus* venom duct using conventional techniques. DNA from single clones was amplified by conventional techniques using primers which correspond approximately to the M13 universal priming site and the M13 reverse universal priming site. Clones having a size of approximately 300-500 nucleotides were sequenced and screened for similarity in sequence to known μ -conotoxins. The DNA sequences and encoded propeptide sequences are set forth in Table 1. DNA sequences coding for the mature toxin can also be prepared on the basis of the DNA sequences set forth in Table 1. An alignment of the μ -conopeptides of the present invention is set forth in Table 2.

TABLE 1

DNA and Amino Acid Sequences of μ -Conopeptides and Precursors

Name:	Ar3.1
Species:	arenatus
Cloned:	Yes

DNA Sequence:

CAAGAAGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTCTTGACCATCTG
TATGCTTCTGTTTCCCCTTACTGCTCTTCCGCTGGATGGGGATCAACCTGCAGACCG
ACCTGCAGAGCGTATGCAGGACGACTTTATAACTGAGCATCATCCCCTGTTTGATCC
5 TGTCAAACGGTGTTGCGAGAGGCCATGCAACATAGGATGCGTACCTTGTTGTTAATG
ACCAGCTTTGTCATCGCGGCCTCATCAAGCGAATAAGTAAAACGATTGCAGT (SEQ
ID NO:1)

Translation:

10 MMSKLGVFLTICMLLFPLTALPLDGDQPADRPAERMQDDFITEHHPLFDPVKRCCERPC
NIGCVPC (SEQ ID NO:2)

Toxin Sequence:

15 Cys-Cys-Xaa1-Arg-Xaa3-Cys-Asn-Ile-Gly-Cys-Val-Xaa3-Cys-Cys-^ (SEQ ID NO:3)

Name: Ak3.1
Species: atlanticus
Cloned: Yes

DNA Sequence:

GGATCCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTGTCTGCTTCTGTTTCCAC
TTACTGCTCTTCCGCTGGATGAAGATCAACCGGTACACCGACCTGCAGAGCGTATGC
AGGACATTTTCATCTGATCAACATCTCTTCTTTGATCTCATCAAACGGTGCTGCGAGT
25 TGCCATGCGGGCCAGGCTTTTTCGCTCCCTTGTTGCTGACATCAATAACGTGTTGATG
ACCAACTTTCTCGAG (SEQ ID NO:4)

Translation:

30 GSMMSKLGVLLTICLLLFPLTALPLDEDQPVHRPAERMQDISSDQHLFFDLIKRCCELPC
GPGFCVPCC (SEQ ID NO:5)

Toxin Sequence:

35 Cys-Cys-Xaa1-Leu-Xaa3-Cys-Gly-Xaa3-Gly-Phe-Cys-Val-Xaa3-Cys-Cys-^ (SEQ ID NO:6)

Name: A3.1
Species: aurisiacus
Cloned: Yes

DNA Sequence:

40 CAAGAGGGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTG
TTTGCTTCTGTTTCCCCTTACTGCTCTTCCGATGGATGGAGATCAATCTGTAGACCGA
CCTGAAGAGCGTATGCAGGACGACATTTTCATCTGAGCAGCATCCCTTGTTTAATCAG
AAAAGAATGTGTTGCGGCGAAGGCCGGAATGCCCCAGCTATTTTCAGAAACAGTCA
45 GATTTGTCATTGTTGTTAAATGACAACGTGTCGATGACCAACTTCGTTATCACGACT
AATGAATAAGTAAAACGATTGCAGT (SEQ ID NO:7)

Translation:

MMSKLGVLLTICLLLFPLTALPMDGDQSVDRPEERMQDDISSEQHPLFNQKRMCCGEG
RKCPYSYFRNSQICHCC (SEQ ID NO:8)

5 **Toxin Sequence:**

Met-Cys-Cys-Gly-Xaa1-Gly-Arg-Lys-Cys-Xaa3-Ser-Xaa5-Phe-Arg-Asn-Ser-Gln-Ile-Cys-His-
Cys-Cys-^ (SEQ ID NO:9)

10 **Name:** A3.2
Species: aurisiacus
Cloned: Yes

DNA Sequence:

15 GGATCCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTGTTTGCTTCTGTTTCCCC
TTACTGCTCTTCCGATCGATGGAGATCAATCTGTAGACCGACCTGCAGAGCGTATGC
AGGATGACATTTTCATCTGAGCAGCATCGCTTGTTCAATCAGAAAAGAAGGTGCTGC
CGGTGGCCATGCCCCCGACAAATCGACGGTGAATATTGTGGCTGTTGCCTTGGATGA
TAACCGTGTTGATGACCAACTTTCTCGAG (SEQ ID NO:10)

20

Translation:

GSMMSKLGVLLTICLLLFPLTALPIDGDQSVDRPAERMQDDISSEQHRLFNQKRRCCRW
PCPRQIDGEYCGCCLG (SEQ ID NO:11)

25 **Toxin Sequence:**

Cys-Cys-Arg-Xaa4-Xaa3-Cys-Xaa3-Arg-Gln-Ile-Asp-Gly-Xaa1-Xaa5-Cys-Gly-Cys-Cys-Leu-#
(SEQ ID NO:12)

30 **Name:** A3.3
Species: aurisiacus
Cloned: Yes

DNA Sequence:

35 GGATCCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTGTCTACTTCTGTTTCCCC
TTACTGCTTTTCCGATGGATGGAGATCAACCTGCAGACCAACCTGCAGATCGTATGC
AGGACGACATTTTCATCTGAGCAGTATCCCTTGTTTGATAAGAGACAAAAGTGTTGCA
CTGGGAAGAAGGGGTCATGCTCCGGCAAAGCATGCAAAAATCTCAAATGTTGCTCT
GGACGATAACGTGTTGATGACCAACTTTCTCGAG (SEQ ID NO:13)

40

Translation:

GSMMSKLGVLLTICLLLFPLTAFPMMDGDQPADQPADRMQDDISSEQYPLFDKRQKCCT
GKKGSCSGKACKNLKCCSGR (SEQ ID NO:14)

45 **Toxin Sequence:**

Xaa2-Lys-Cys-Cys-Thr-Gly-Lys-Lys-Gly-Ser-Cys-Ser-Gly-Lys-Ala-Cys-Lys-Asn-Leu-Lys-
Cys-Cys-Ser-# (SEQ ID NO:15)

Name: A3.4
Species: aurisiacus
Cloned: Yes

DNA Sequence:

GGATCCATGATGTCTAAACTGGGAGTCTTGCTGACCATCTGTCTGCTTCTGTTTCCAC
TTACTGCTGTTCCGCTGGATGGAGATCAACCTCTAGACCGACACGCGGAGCGTATGC
ATGATGGCATTTCACCTAAACGCCATCCCTGGTTTGATCCCGTCAAACGGTGTTGCA
AGGTGCAATGCGAGTCTTGCACCCCTTGTTGCTAACGTGTTGATGACCAACTTTCTC
GAG (SEQ ID NO:16)

Translation:

GSMMSKLGVLLTICLLLFPLTAVPLDGDQPLDRHAERMHDGISPKRHPWFDPVKRCK
VQCESCTPCC (SEQ ID NO:17)

Toxin Sequence:

Cys-Cys-Lys-Val-Gln-Cys-Xaa1-Ser-Cys-Thr-Xaa3-Cys-Cys-[^] (SEQ ID NO:18)

Name: Bn3.1
Species: bandanus
Cloned: Yes

DNA Sequence:

GGATCCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTGTATGCTTCTGTTTCCCC
TCACTGCTCTTCCGATGGATGGAGATCAACCTGCAGACCGACCTGCAGAGCGTAGT
CAGGACGTTTCATCTGAACAGCATCCCTTGTTTGATCCCGTCAAACGGTGTTGCAAC
TGGCCATGCTCCATGGGATGCATCCCTTGTTGCTACTATTAATAACGTGTTGATGAC
CAACTTTCTCGAG (SEQ ID NO:19)

Translation:

GSMMSKLGVLLTICMLLFPLTALPMDGDQPADRPAERSQDVSSEQHPLFDPVKRCCNW
PCSMGCIPCCYY (SEQ ID NO:20)

Toxin Sequence:

Cys-Cys-Asn-Xaa4-Xaa3-Cys-Ser-Met-Gly-Cys-Ile-Xaa3-Cys-Cys-Xaa5-Xaa5-[^] (SEQ ID NO:21)

Name: Bt3.1
Species: betulinus
Cloned: Yes

DNA Sequence:

CAAGAGGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGACCTTCTG

TCTGCTTCTGTTTCCCCTGACTGCTCTTCCGCTGGATGAAGATCAACCTGCAGACCG
ACCTGCAGAGCGTATGCAGGACATTTTCATCTGAACAGCATCCCTTGTTTGATCCCGT
CAAACGGTGTTGCGAATTGCCATGCCATGGATGCGTCCCTTGTTGCTGGCCTTAATA
ACGTGTGGATGACCAACTGTGTTATCACGGCCACGTCAAGTGTCTAATGAATAAGT
5 AAAATGATTGCAGT (SEQ ID NO:22)

Translation:

MMSKLGVLLTFCLLLFPLTALPLDEDQPADRPAERMQDISSEQHPLFDPVKRCCELPCH
GCVPCWP (SEQ ID NO:23)

Toxin Sequence:

Cys-Cys-Xaa1-Leu-Xaa3-Cys-His-Gly-Cys-Val-Xaa3-Cys-Cys-Xaa4-Xaa3-^ (SEQ ID NO:24)

15 **Name:** Bt3.2
Species: betulinus
Cloned: Yes

DNA Sequence:

20 CAAGAGGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGACCTTCTG
TCTGCTTCTGTTTCCCCTGACTGCTCTTCCGCTGGATGAAGATCAACCTGCAGACCG
ACATGCAGAGCGTATGCAGGACATTTACCTGAACAGCATCCCTCGTTTGATCCCGT
CAAACGGTGTTGCGGGCTGCCATGCAATGGATGCGTCCCTTGTTGCTGGCCTTCATA
ACGTGTGGACGACCAACTTTGTTATCACGGCCACGTCAAGTGTCTGATGAATAAGTA
25 AAACGATTGCAGT (SEQ ID NO:25)

Translation:

MMSKLGVLLTFCLLLFPLTALPLDEDQPADRHAERMQDISPEQHPSFDPVKRCCGLPCN
GCVPCWPS (SEQ ID NO:26)

Toxin Sequence:

Cys-Cys-Gly-Leu-Xaa3-Cys-Asn-Gly-Cys-Val-Xaa3-Cys-Cys-Xaa4-Xaa3-Ser-^ (SEQ ID
NO:27)

35 -----
Name: Bt3.3
Species: betulinus
Cloned: Yes

DNA Sequence:

40 CAAGAGGGATCGATAGCAGTTCATGATGTTTAAACTGGGAGTCTTGTTGACCATCTA
TATGCTTCTGTTTCCCTTTACTGCTCTTCCGCTGGATGGAGATCAACCTGCAGACCAA
CCTCTAGAGCGCATGCAGTATGACATGTTACGTGCAGTGAATCCCTGGTTTGATCCC
45 GTCAAAAGGTGCTGCTCGAGGAACTGCGCAGTATGCATCCCTTGTTGCCCGAATTGG
CCAGCTTGATTATCGCGGCCAAGAGTCTAATGAATAAGTAAAACGATTGCAGT (SEQ
ID NO:28)

Translation:

MMFKLGVLLTIYMLLPFTALPLDGDQPADQPLERMQYDMLRAVNPWFDPVKRCCSR
NCAVCIPCCPNWPA (SEQ ID NO:29)

5

Toxin Sequence:

Cys-Cys-Ser-Arg-Asn-Cys-Ala-Val-Cys-Ile-Xaa3-Cys-Cys-Xaa3-Asn-Xaa4-Xaa3-Ala-^ (SEQ
ID NO:30)

10

Name: Bu3.1
Species: bullatus
Cloned: Yes

15 **DNA Sequence:**

CAAGAAGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTG
TCTGCTTCTGTTTCCCCTTTTTGCTCTTCCGCAGGATGGAGATCAACCTGCAGACCGA
CCTGCAGAGCGTATGCAGGACGACATTTTCATCTGAGCAGAATTCCTTGCTTGAGAA
GAGAGTTACTGACAGGTGCTGCAAAGGGAAGAGGGAATGCGGCAGATGGTGCAGA
20 GATCACTCGCGTTGTTGCGGTCGACGATAAGCTGTTGATGACCAGCTTTGTTATCAC
GGCTACATCAAGTGTCTAGTGAATAAGTAAAATGATTGCAGT (SEQ ID NO:31)

Translation:

MMSKLGVLLTICLLLFLPLFALPQDGDQPADRPAERMQDDISSEQNSLLEKRVTDRCKG
25 KRECGRWCRDHSRCCGRR (SEQ ID NO:32)

Toxin Sequence:

Val-Thr-Asp-Arg-Cys-Cys-Lys-Gly-Lys-Arg-Xaa1-Cys-Gly-Arg-Xaa4-Cys-Arg-Asp-His-Ser-
Arg-Cys-Cys-# (SEQ ID NO:33)

30

Name: Bu3.1A
Species: bullatus
Cloned: Yes

35

DNA Sequence:

CAAGAGGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTG
TCTGCTTCTGTTTCCCCTTTTTGCTCTTCCGCAGGATGGAGATCAACCTGCAGACCGA
CCTGCAGAGCGTATGCAGGATGACATTTTCATCTGAGCAGAATCCCTTGCTTGAGAA
40 GAGAGTTGGTGACAGGTGCTGCAAAGGGAAGAGGGGGTGCAGGAGATGGTGCAGA
GATCACTCACGTTGTTGCGGTCGACGATAACGTGTTGATGACCAGCTTTGTTATCAC
GGCTACATCAAGTGTCTTAGTGATTAAGTAAAACGATTGCAGT (SEQ ID NO:34)

Translation:

MMSKLGVLLTICLLLFLPLFALRQDGDQPADRPAERMQDDISSEQNPLLEKRVGDRCK
45 GKRGCGRWCRDHSRCCGRR (SEQ ID NO:35)

Toxin Sequence:

Val-Gly-Asp-Arg-Cys-Cys-Lys-Gly-Lys-Arg-Gly-Cys-Gly-Arg-Xaa4-Cys-Arg-Asp-His-Ser-Arg-Cys-Cys-# (SEQ ID NO:36)

5

Name: Bu3.2
Species: bullatus
Cloned: Yes

10 **DNA Sequence:**

CAAGAAGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTG
TCTGCTTCTGTTTCCCCTTTTTGCTCTTCCGCAGGATGGAGATCAACCTGCAGACCGA
CCTGCAGAGCGTATGCAGGACGACATTTTCATCTGAGCAGAATCCCTTGCTTGAGAA
GAGAGTTGGTGAAAGGTGCTGCAAAAACGGGAAGAGGGGGTGCGGCAGATGGTGC
15 AGAGATCACTCACGTTGTTGCGGTTCGACGATAACGTGTTGATGACCGAGGCTTTCGT
TATCACGGCTACATCAAGTGTCTAGTGAATAAGTAAAACGATTGCAGT (SEQ ID
NO:37)

Translation:

20 MMSKLGVLITICLLLFPLFALPQDGDQPADRPAERMQDDISSEQNPLLEKRVGERCCKN
GKRGCGRWCRDHSRCCGRR (SEQ ID NO:38)

Toxin Sequence:

25 Val-Gly-Xaa1-Arg-Cys-Cys-Lys-Asn-Gly-Lys-Arg-Gly-Cys-Gly-Arg-Xaa4-Cys-Arg-Asp-His-
Ser-Arg-Cys-Cys-# (SEQ ID NO:39)

Name: Bu3.3
Species: bullatus
30 **Cloned:** Yes

DNA Sequence:

CAAGAGGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTG
TCTGCTTCTGTTTCCCCTTTTTGCTCTTCCGCAGGACGGAGATCAACCTGCAGACCG
35 ACCTGCAGAGCGTATGCAGGACGACCTTTCATCTGAGCAGCATCCCTTGTTTGAGAA
GAGAATTGTTGACAGGTGCTGCAACAAAGGGAACGGGAAGAGGGGGTGACGAGCA
TGGTGCAGAGATCACTCACGTTGTTGCGGTTCGACGATGAACTGTTGATGACCGAGG
CTTTGGTTATCACGGCTACATCAAGTGTCTAGTGAATAAGTAAAACGATTGCAGT
(SEQ ID NO:40)

40

Translation:

MMSKLGVLITICLLLFPLFALPQDGDQPADRPAERMQDDLSEQHPLFEKRIVDRCCNK
GNGKRGCGRWCRDHSRCCGRR (SEQ ID NO:41)

45 **Toxin Sequence:**

Ile-Val-Asp-Arg-Cys-Cys-Asn-Lys-Gly-Asn-Gly-Lys-Arg-Gly-Cys-Ser-Arg-Xaa4-Cys-Arg-Asp-His-Ser-Arg-Cys-Cys-# (SEQ ID NO:42)

Name: Bu3.4
Species: bullatus
Cloned: Yes

DNA Sequence:

CAAGAAGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTG
TCTGCTTCTGTTTCCCCTTTTTGCTCTTCCGCAGGATGGAGATCAACCTGCAGACCGA
CCTGCTGAGCGTATGCAGGACGACATTTTCATCTGAGCGGAATCCCTTGTTTGAGAAG
AGCGTTGGTTTATATTGCTGCCGACCCAAACCCAAACGGGCAGATGATGTGCGACAG
ATGGTGCGAAAAAACTCACGTTGTTGCGGTCGACGATAATGTGTTGATGACCAGC
TTTGTATCAAGGCTACATCAAGTATCTAGTGAATAAGTAAAACGATTGCAGT (SEQ
ID NO:43)

Translation:

MMSKLGVLLTICLLLFPLFALPQDGDQPADRPAERMQDDISSERNPLFEKSVGLYCCRP
KPNGQMMCDRWCEKNSRCCGRR (SEQ ID NO:44)

Toxin Sequence:

Val-Gly-Leu-Xaa5-Cys-Cys-Arg-Xaa3-Lys-Xaa3-Asn-Gly-Gln-Met-Met-Cys-Asp-Arg-Xaa4-
Cys-Xaa1-Lys-Asn-Ser-Arg-Cys-Cys-# (SEQ ID NO:45)

Name: Bu3.5
Species: bullatus
Cloned: Yes

DNA Sequence:

CAAGAAGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTTTTGTTGACCATCTG
TCTGCTTCTGTTTCCCCTTACTGCTCTTCCGATGGATGGAGATCAATCTGTAGACCGA
CCTGCAGAACGTATGCAGGACGACCTTTTCATCTGAGCAGCATCCCTTGTTTGTTTCAG
AAAAGAAGGTGTTGCGGCGAAGGCTTGACATGCCCCAGATATTGGAAAAACAGTCA
GATTTGTGCTTGTTGTTAAATGACAACGTGTCGATGACCAACTTCGGTATCACGACT
ACGCCAAGTGTCTAATGAATAAGTAAAACGATTGCAGT (SEQ ID NO:46)

Translation:

MMSKLGVLLTICLLLFPLTALPMDGDQSVDRPAERMQDDLSEQHPLFVQKRRCCGEG
LTCPRYWKNSQICACC (SEQ ID NO:47)

Toxin Sequence:

Arg-Cys-Cys-Gly-Xaa1-Gly-Leu-Thr-Cys-Xaa3-Arg-Xaa5-Xaa4-Lys-Asn-Ser-Gln-Ile-Cys-Ala-
Cys-Cys-^ (SEQ ID NO:48)

Name: Bu3.5A
Species: bullatus
Cloned: Yes

5 **DNA Sequence:**

CAAGAGGGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTG
TCTGCTTCTGTTTCCCCTTTTTGCTCTTCCGCAGGATGGAGATCAACCTGCAGACCGA
CCTGCTGAGCGTATGCAGGACGACATTTTCATCTGAGCAGGATCCCTTGTTTGTTCAG
AAAAGAAGGTGTTGCGGCGAAGGCTTGACATGCCCCAGATATTGGAAAAACAGTCA
10 GATTTGTGCTTGTTGTTAAATGACAACGTGTGATGACCAACTTCGGTATCACGACTA
CGCCAAGTGTCTAATGAATAAGTAAAACGATTGCAGT (SEQ ID NO:49)

Translation:

MMSKLGVLLTICLLLFPLFALPQDGDQPADRPAERMQDDISSEQDPLFVQKRRCCGEGL
15 TCPRYWKNSQICACC (SEQ ID NO:50)

Toxin Sequence:

Arg-Cys-Cys-Gly-Xaa1-Gly-Leu-Thr-Cys-Xaa3-Arg-Xaa5-Xaa4-Lys-Asn-Ser-Gln-Ile-Cys-Ala-
Cys-Cys-^ (SEQ ID NO:51)

20
Name: Cp3.1
Species: capitaneus
Cloned: Yes

25 **DNA Sequence:**

GGATCCATGATGTCTAAACTGGGAGTCTTGGTGACCATCTGCCTGCTTCTGTTTCCC
CTTGCTGCTTTTCCACTGGATGGAAATCAACCTGCAGACCACCCTGCAAAGCGTACG
CAAGATGACAGTTCAGCTGCCCTGATCAATACCTGGATTGATCATTCCCATTCTTGC
30 TGCAGGGACTGCGGTGAAGATTGTGTTGGTTGTTGCCGGTAACGTGTTGATGACCAA
CTTTCTCGAG (SEQ ID NO:52)

Translation:

GSMMSKLGVLVTICLLLFPLAAFPLDGNQPADHPAKRTQDDSSAALINTWIDHSHSCCR
35 DCGEDCVGCCR (SEQ ID NO:53)

Toxin Sequence:

Ser-Cys-Cys-Arg-Asp-Cys-Gly-Xaa1-Asp-Cys-Val-Gly-Cys-Cys-Arg-^ (SEQ ID NO:54)

40
Name: Ca3.1
Species: characteristicus
Cloned: Yes

45 **DNA Sequence:**

CAAGAGGGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTG
TCTGCTTCTGTTTCCCCTTACTGCTCTTCCAATGGATGGAGATCAACCTGCAGACCA

ACCTGCAGATCGTATGCAGGACGACATTTTCATCTGAGCAGTATCCCTTGTTTGATAT
GAGAAAAAGGTGTTGCGGCCCCGGCGGTTTCATGCCCCGTATATTTTCAGAGACAATT
TTATTTGTGGTTGTTGTTAAATGACAACGTGTCGATGACCAACTTCATTATCACGAC
TACGCCAAGTGTCTAATGAATAAGTAAAATGATTGCAGT (SEQ ID NO:55)

5

Translation:

MMSKLGVLLTICLLLFPLTALPMDGDQPADQPADRMQDDISSEQYPLFDMRKRC CGPG
GSCP VYFRDNFICGCC (SEQ ID NO:56)

10 **Toxin Sequence:**

Cys-Cys-Gly-Xaa3-Gly-Gly-Ser-Cys-Xaa3-Val-Xaa5-Phe-Arg-Asp-Asn-Phe-Ile-Cys-Gly-Cys-
Cys-^ (SEQ ID NO:57)

15 **Name:** Ca3.2
Species: characteristic
Cloned: Yes

DNA Sequence:

20 CAAGAGGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTG
TCTGCTTCTGTTTCCCCTTACTGCTCTTCCGATGGATGGAGATGAACCTGCAAACCG
ACCTGTGCGAGCGTATGCAGGACAACATTTTCATCTGAGCAGTATCCCTTGTTTGAGAA
GAGACGAGATTGTTGCACTCCGCCGAAGAAATGCAAAGACCGACAATGCAAACCCC
AGAGATGTTGCGCTGGACGATAACGTGTTGATGACCAACTTTATCACGGCTACGTCA
25 AGTGTTTAGTGAATAAGTAAAATGATTGCAGT (SEQ ID NO:58)

Translation:

MMSKLGVLLTICLLLFPLTALPMDGDEPANRPVERMQDNISSEQYPLFEKRRDCCTPPK
KCKDRQCKPQRCCAGR (SEQ ID NO:59)

30

Toxin Sequence:

Arg-Asp-Cys-Cys-Thr-Xaa3-Xaa3-Lys-Lys-Cys-Lys-Asp-Arg-Gln-Cys-Lys-Xaa3-Gln-Arg-
Cys-Cys-Ala-# (SEQ ID NO:60)

35

Name: Ca3.3
Species: characteristic
Cloned: Yes

40 **DNA Sequence:**

CAAGAGGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTG
TCTGCTTCTGTTTCCCCTTACTGCTCTTCCACTGGATGGAGATCAACCTGCAGATCAA
TCTGCAGAGCGACCTGCAGAGCGTACGCAGGACGACATTCAGCAGCATCCGTTATA
TGATCCGAAAAGAAGGTGTTGCCGTTATCCATGCCCCGACAGCTGCCACGGATCTTG
45 CTGCTATAAGTGATAACATGTTGATGGCCAGCTTTGTTATCACGGCCACGTCAAGTG
TCTTAATGAATAAGTAAAACGATTGCAGT (SEQ ID NO:61)

Translation:

MMSKLGVLLTICLLLFPLTALPLDGDQPADQSAERPAERTQDDIQQHPLYDPKRRCCRY
PCPDSCHGSCCYK (SEQ ID NO:62)

5 **Toxin Sequence:**

Arg-Cys-Cys-Arg-Xaa5-Xaa3-Cys-Xaa3-Asp-Ser-Cys-His-Gly-Ser-Cys-Cys-Xaa5-Lys-^ (SEQ
ID NO:63)

10 **Name:** Ca3.4
Species: characteristic
Cloned: Yes

DNA Sequence:

15 CAAGAGGGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGCCTTGTTGACCATCT
GTCTACTTCTGTTTTCCCTTACTGCTGTTCCGCTGGATGGAGATCAACATGCAGACC
AACCTGCACAGCGTCTGCAGGACCGCATTCCAACCTGAAGATCATCCCTTATTTGATC
CCAACAAACGGTGTTGCCCGCCGGTGGCATGCAACATGGGATGCAAGCCTTGTTGT
GGATGACCAGCTTTGTTATCGCGGTCTTCATGAAGTGTCTTAATGAATAAGTAAAAT
20 GATTGCAGT (SEQ ID NO:64)

Translation:

MMSKLGALLTICLLLFSLTAVPLDGDQHADQPAQRLQDRIPTEHDHPLFDPNKRCCPPVA
CNMGCKPCCG (SEQ ID NO:65)

25

Toxin Sequence:

Cys-Cys-Xaa3-Xaa3-Val-Ala-Cys-Asn-Met-Gly-Cys-Lys-Xaa3-Cys-Cys-# (SEQ ID NO:66)

30 **Name:** Ca3.5
Species: characteristic
Cloned: Yes

DNA Sequence:

35 CAAGAGGGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGCCTTGTTGACCATCT
GTCTACTTCTGTTTTCCCTAACTGCTGTTCCGCTGGATGGAGATCAACATGCAGACC
AACCTGCAGAGCGTCTGCATGACCGCCTTCCAACCTGAAAATCATCCCTTATATGATC
CCGTCAAACGGTGTTGCGATGATTGGAATGCGACTATTCTTGCTGGCCTTGCTGTA
TGTTTGGATAACCTTTGTTATCGCGGCCTCATCAAGTGTCTAATGAATAAGTAAAAC
40 GATTGCAGT (SEQ ID NO:67)

Translation:

MMSKLGALLTICLLLFSLTAVPLDGDQHADQPAERLHDRLPTENHPLYDPVKRCCDDSE
CDYSCWPCCMFG (SEQ ID NO:68)

45

Toxin Sequence:

Cys-Cys-Asp-Asp-Ser-Xaa1-Cys-Asp-Xaa5-Ser-Cys-Xaa4-Xaa3-Cys-Cys-Met-Phe-# (SEQ ID

NO:69)

Name: Ca3.6
Species: caracteristicus
Cloned: Yes

DNA Sequence:

GGATCCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTGTCTGCTTCTGTTTCCCC
TTACTGCTGTTCCGCTGGATGGAGATCAACCTGCAGACCGACCTGCAGAGCGTAAG
CAGGACGTTTCATCTGAACAGCATCCCTTCTTTGATCCCGTCAAACGGTGTTGCCGC
CGGTGTTACATGGGATGCATCCCTTGTTGCTTTTAACGTGTTGATGACCAACTTTCTC
GAG (SEQ ID NO:70)

Translation:

GSMMSKLGVLITICLLLFPLTAVPLDGDQPADRPAERKQDVSSEQHPFFDPVKRCCRRC
YMGCI PCCF (SEQ ID NO:71)

Toxin Sequence:

Cys-Cys-Arg-Arg-Cys-Xaa5-Met-Gly-Cys-Ile-Xaa3-Cys-Cys-Phe-^ (SEQ ID NO:72)

Name: Cr3.1
Species: circumcisuus
Cloned: Yes

DNA Sequence:

CAAGAAGGATCGATAGCAGTTCATGATGTCTAAACTGGGGGTATTGTTGACCATCT
GTCTGCTTCTGTTTCCCCTTACTGCTCTTCCAATGGATGGAGATCAACCTGCAGACC
AACCTGCAGATCGTATGCAGGACGACATTTTCATCTGAGCAGTATCCCTTGTTTGATA
AGAGACGAAAGTGTTGCGGCAAAGACGGGCCATGCCCCAAATATTTCAAAGACAAT
TTTATTTGTGGTTGTTGTTAAATGACAACGTGTCGATGACCAACTTCGTTATCACGAT
TCGCCAAGTGTCTTAATGAATAAGTAAAATGATTGCAGT (SEQ ID NO:73)

Translation:

MMSKLGVLITICLLLFPLTALPMDGDQPADQPADRMQDDISSEQYPLFDKRRKCCGKD
GPCPKYFKDNFICGCC (SEQ ID NO:74)

Toxin Sequence:

Arg-Lys-Cys-Cys-Gly-Lys-Asp-Gly-Xaa3-Cys-Xaa3-Lys-Xaa5-Phe-Lys-Asp-Asn-Phe-Ile-Cys-
Gly-Cys-Cys-^ (SEQ ID NO:75)

Name: Da3.1
Species: dalli
Cloned: Yes

DNA Sequence:

CAAGAGGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGCCTTGTTGACCATCT
GTCTACTTCTGTTTTCCCTAACTGCTGTTCCGCTGGATGGAGATCAACATGCAGACC
AACCTGCAGAGCGTCTGCAGGACCGCCTTCCAACCTGAAAATCATCCCTTATATGATC
5 CCGTCAAACGGTGTGCGATGATTCGGAATGCGACTATTCTTGCTGGCCTTGCTGTA
TTTTATCATAACCTTTGTTATCGCGGCCTCATCAAGTGTCAAATGAATAAGTAAAAT
GATTGCAGT (SEQ ID NO:76)

Translation:

10 MMSKLGALLTICLLLFSLTAVPLDGDQHADQPAERLQDRLPTENHPLYDPVKRCCDDSE
CDYSCWPCCILS (SEQ ID NO:77)

Toxin Sequence:

15 Cys-Cys-Asp-Asp-Ser-Xaa1-Cys-Asp-Xaa5-Ser-Cys-Xaa4-Xaa3-Cys-Cys-Ile-Leu-Ser-^ (SEQ
ID NO:78)

Name: Da3.2

Species: dalli

20 **Cloned:** Yes

DNA Sequence:

CAAGAGGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGACCATTTG
TCTACTTCTGTTTTCCCTTACTGCTGTTCCACTGGATGGAGATCAGCCTGCAGACCG
25 ACCTGCAGAGCGTATGCAGGACGGCATTTCATCTGAACATCATCCATTTTTTTGATTC
CGTCAAAAAGAAACAACAGTGTGCCCCGCCGGTGGCATGCAACATGGGATGCGAGC
CTTGTTGTGGATGACCAGCTTTGTTATCGCGGCTCATGAAGTGTCTAATGAATAAG
TAAACGATTGCAGT (SEQ ID NO:79)

Translation:

30 MMSKLGVLLTICLLLFPLTAVPLDGDQPADRPAERMQDGISSEHHPFFDSVKKKQQCCP
PVACNMGCEPCCG (SEQ ID NO:80)

Toxin Sequence:

35 Xaa2-Gln-Cys-Cys-Xaa3-Xaa3-Val-Ala-Cys-Asn-Met-Gly-Cys-Xaa1-Xaa3-Cys-Cys-# (SEQ
ID NO:81)

Name: Da3.3

40 **Species:** dalli

Cloned: Yes

DNA Sequence:

CAAGAAGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGATCATATG
45 TCTATTTCTGTTTTCCCTTACTGCTGTTCACTCAATGGAGATCAGCCTGCAGACCAA
TCTGCAGAGCGTATGCAGGACAAAATTCATCTGAACATCATCCCTTTTTTGATCCC
GTCAAACGTTGTTGCAACGCGGGGTTTTGCCGCTTCGGATGCACGCCTTGTTGTTGG

TGACCAGCTTTGTTATCGCGGCCTCATCAAGTGTCTAATGAATAAGTAAAATGATTG
CAGT (SEQ ID NO:82)

Translation:

5 MMSKLGVLIIICLFLFPLTAVQLNGDQPADQSAERMQDKISSEHHPFFDPVKRCCNAGF
CRFGCTPCCW (SEQ ID NO:83)

Toxin Sequence:

10 Cys-Cys-Asn-Ala-Gly-Phe-Cys-Arg-Phe-Gly-Cys-Thr-Xaa3-Cys-Cys-Xaa4-^ (SEQ ID NO:84)

Name: Di3.1
Species: distans
Cloned: Yes

DNA Sequence:

15 CAAGAGGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGCTGACCATCTT
TCTGCTTCTGTTTCCCCTTACTGCTGTTCCGCTGGATGGAGATCAACCCGCAGACGG
ACTTGCAGAGCGCATGCAGGACGACAGTTCAGCTGCACTGATTAGAGACTGGCTTC
20 TTCAAACCCGACAGTGTGTGTGCATCCATGCCCATGCACGCCTTGCTGTAGATGAC
CAGCTTTGTCATCGCGGCTACGTCAAGTATCTAATGAATAAGTAAGTAAAACGATTG
CAGT (SEQ ID NO:85)

Translation:

25 MMSKLGVLITIFLLLFLPTAVPLDGDQPADGLAERMQDDSSAALIRDWLLQTRQCCVH
PCPCTPCCR (SEQ ID NO:86)

Toxin Sequence:

30 Xaa2-Cys-Cys-Val-His-Xaa3-Cys-Xaa3-Cys-Thr-Xaa3-Cys-Cys-Arg-^ (SEQ ID NO:87)

Name: E3.1
Species: ermineus
Cloned: Yes

DNA Sequence:

35 ACCTCAAGAGGGATCGATCGCAGTTCATGATGTCTAAACTGGGAGCCTTGTTGACC
ATCTGTCTGCTTCTGTTTCCCATTAAGTCTTCTGATGGATGGAGATCAGCCTGCAG
ACCGACCTGCAGAGCGTACGGAGGATGACATTTTCATCTGACTACATTCCCTGTTGCA
40 GTTGGCCATGCCCCCGATACTCCAACGGTAAACTTGTTTGTGTTTGTGCTTGGATG
ATAATGTGTTGATGACCAACTTTGTTATCACGGCTACGTCAAGTGTCTACTGAATAA
GTAAATGATTGCAGTA (SEQ ID NO:88)

Translation:

45 MMSKLGALLTICLLLPITALLLMDGDQPADRPAERTEDDISSDYIPCCSWPCPRYSNGKL
VCFCLG (SEQ ID NO:89)

Toxin Sequence:

Cys-Cys-Ser-Xaa4-Xaa3-Cys-Xaa3-Arg-Xaa5-Ser-Asn-Gly-Lys-Leu-Val-Cys-Phe-Cys-Cys-Leu-# (SEQ ID NO:90)

5

Name: Ge3.2
Species: generalis
Cloned: Yes

10 **DNA Sequence:**

GGATCCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTGTCTGGTTCTGTTTCCCC
TTACTGCTCTTCCACTGGATGGAGAACAACCTGTAGACCGACATGCCGAGCATATGC
AGGATGACAATTCAGCTGCACAGAACCCCTGGGTTATTGCCATCAGACAGTGTTGC
ACGTTCTGCAACTTTGGATGCCAACCTTGTTGCCTCACCTGATAACGTGTTGATGAC
15 CAACTTTCTCGAG (SEQ ID NO:91)

Translation:

GSMMSKLGVLLTICLVLFPLTALPLDGEQPVDRHAEHMQDDNSAAQNPWVIAIRQCCT
FCNFGCQPCCLT (SEQ ID NO:92)

20

Toxin Sequence:

Xaa2-Cys-Cys-Thr-Phe-Cys-Asn-Phe-Gly-Cys-Gln-Xaa3-Cys-Cys-Leu-Thr-^ (SEQ ID NO:93)

25

Name: Ge3.3
Species: generalis
Cloned: Yes

DNA Sequence:

30 GGATCCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTGTCTGGTTCTGTTTCCCC
TTACTGCTCTTCCACTGGATGGAGAACAACCTGTAGACCGACATGCCGAGCATATGC
AGGATGACAATTCAGCTGCACAGAACCCCTGGGTTATTGCCATCAGACAGTGTTGC
ACGTTCTGCAACTTTGGATGCCAGCCTTGTTGCGTCCCCTGATAACGTGTTGATGAC
CAACTTTCTCGAG (SEQ ID NO:94)

35

Translation:

GSMMSKLGVLLTICLVLFPLTALPLDGEQPVDRHAEHMQDDNSAAQNPWVIAIRQCCT
FCNFGCQPCCVP (SEQ ID NO:95)

40 **Toxin Sequence:**

Xaa2-Cys-Cys-Thr-Phe-Cys-Asn-Phe-Gly-Cys-Gln-Xaa3-Cys-Cys-Val-Xaa3-^ (SEQ ID NO:96)

45

Name: μ -GIIIA
Species: geographus
Cloned: Yes

DNA Sequence:

GTCGACTCTAGAGGATCCGACAACAAAGAGTCAACCCCACTGCCACGTCAAGAGCG
AAGCGCCACAGCTAAGACAAGAGGGATCGATAGCAGTTCATGATGTCTAAACTGGG
5 AGTCTTGTTGACCATCTGTCTGCTTCTGTTTCCCCTTACTGCTCTTCCGATGGATGGA
GATGAACCTGCAAACCGACCTGTCGAGCGTATGCAGGACAACATTTTCATCTGAGCA
GTATCCCTTGTTTGAGAAGAGACGAGATTGTTGCACTCCGCCGAAGAAATGCAAAG
ACCGACAATGCAAACCCAGAGATGTTGCGCTGGACGATAACGTGTTGATGACCAA
CTTTATCACGGCTACGTCAAGTGTTTAGTGAATAAGTAAAATGATTGCAGTCTTGCT
10 CAGATTTGCTTTTGTGTTTTGGTCTAAAGATCAATGACCAAACCGTTGTTTTGATGCG
GATTGTCATATATTTCTCGATTCCAATCCAACACTAGATGATTTAATCACGATAGAT
TAATTTTCTATCAATGCCTTGATTTTTCGTCTGTCATATCAGTTTTGTTTATATTTATT
TTTTCGTCACTGTCTACACAAACGCATGCATGCACGCATGCACGCACACACGCACGC
ACGCTCGCACAAACATGCGCGCGCACGCACACACACACACACACACAAACACA
15 CACACAAGCAATCACACAATTATTGACATTATTTATTTATTCATTGATGTATTTGTTA
TTCGTTTGCTTGTTTTTAGAATAGTTTGAGGCCGTCTTTTTGGATTTATTTGAACTGC
TTTATTGTATACGAGTACTTCGTGCTTTGAAACACTGCTGAAAATAAAACAAACACT
GACGTAGC (SEQ ID NO:97)

Translation:

MMSKLGVLLTICLLLFPLTALPMDGDEPANRPVERMQDNISSEQYPLFEKRRDCCTPPK
KCKDRQCKPQRCCAGR (SEQ ID NO:98)

Toxin Sequence:

25 Arg-Asp-Cys-Cys-Thr-Xaa3-Xaa3-Lys-Lys-Cys-Lys-Asp-Arg-Gln-Cys-Lys-Xaa3-Gln-Arg-
Cys-Cys-Ala-# (SEQ ID NO:99)

Name: μ -GIIIB

30 **Species:** geographus

Isolated: Yes

Cloned: Yes

DNA Sequence:

GGCCAGACGACAACAAAGAGTCAACCCCACTGCCACGTCAAGAGCGAAGCGCCAC
AGCTAAGACAAGAGGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTT
GACCATCTGTCTGCTTCTGTTTCCCCTTACTGCTCTTCCGATGGATGGAGATGAACCT
GCAAACCGACCTGTCGAGCGTATGCAGGACAACATTTTCATCTGAGCAGTATCCCTTG
TTTGAGAAGAGACGAGATTGTTGCACTCCGCCGAGGAAATGCAAAGACCGACGATG
40 CAAACCCATGAAATGTTGCGCTGGACGATAACGTGTTGATGACCAACTTTATCACG
GCTAGCTCAGTGTTTAGTGAATAAGTAAAATGATTGCAGTCTTGCTCAGATTGCTTT
TGTGTTTTGGTCTAAGATCAATGACCAAACCGTTGTTTTGATGCGGATTGTCATATA
TTTCTCGATTCCAATCCAACACTAGATGATTTAATCACGATAGATTAATTTTCTATCA
ATGCCTTGATTTTTTCGTCTGTCATATCAGTTTTGTTTATATTTATTTTTTCGTCACTGT
45 CTACACAAACGCATGCATGCACGCATGCACGCACACACGCACGCACGCTCGCACAA
ACATGCGCGCGCACGCACACACACACACACACAAACACACACACGAAGCAATC
ACACAATTAGTTGACATTATTTATTTATTCATTGATGTATTTGTTATTCGTTTGCTTGT

TTTTAGAATAGTTTGAGGCCGTCTTTTTGGATTTATTTGAACTGCTTTATTGTATACG
AGTACTTCGTGCTTTGAAACACTGCTGAAAATAAAACAAACACTGACGTAGCAAAA
AAAAAAA (SEQ ID NO:100)

5 **Translation:**

MMSKLGVLLTICLLLFPLTALPMDGDEPANRPVERMQDNISSEQYPLFEKRRDCCTPPR
KCKDRRCKPMKCCAGR (SEQ ID NO:101)

Toxin Sequence:

10 Arg-Asp-Cys-Cys-Thr-Xaa3-Xaa3-Arg-Lys-Cys-Lys-Asp-Arg-Arg-Cys-Lys-Xaa3-Met-Lys-
Cys-Cys-Ala-# (SEQ ID NO:102)

Name: μ -GIIC

15 **Species:** geographus

Isolated: Yes

Toxin Sequence:

20 Arg-Asp-Cys-Cys-Thr-Xaa3-Xaa3-Lys-Lys-Cys-Lys-Asp-Arg-Arg-Cys-Lys-Xaa3-Leu-Lys-
Cys-Cys-Ala-# (SEQ ID NO:103)

Name: Gm3.1

25 **Species:** gloriamaris

Cloned: Yes

DNA Sequence:

CTCACTATAGGAATTCGAGCTCGGTACACGGGATCGATAGCAGTTCATGATGTCTAA
30 ACTGGGAGCCTTGTTGACCATCTGTCTACTTCTGTTTTCCCTAACTGCTGTTCCGCTG
GATGGAGATCAACATGCAGACCAACCTGCAGAGCGTCTGCATGACCGCCTTCCAAC
TGAAAATCATCCCTTATATGATCCCGTCAAACGGTGTTGCGATGATTCCGAATGCGA
CTATTCTTGCTGGCCTTGCTGTATGTTTGGATAACCTTTGTTATCGCGGCCTCGATAA
GTGTCTAATGAATAAGTAAAACGATTGCAGTAGGC (SEQ ID NO:104)

35

Translation:

MMSKLGALLTICLLLFSLTAVPLDGDQHADQPAERLHDRLPTENHPLYDPVKRCCDDSE
CDYSCWPCCMFG (SEQ ID NO:105)

40 **Toxin Sequence:**

Cys-Cys-Asp-Asp-Ser-Xaa1-Cys-Asp-Xaa5-Ser-Cys-Xaa4-Xaa3-Cys-Cys-Met-Phe-# (SEQ ID
NO:106)

45 **Name:** Gm3.2

Species: gloriamaris

Cloned: Yes

DNA Sequence:

5 GTTCATGATGTCTAAACTGGGAGTCTTGTTGATCATCTGTCTACTTCTGTTTCCCCTT
ACTGCTGTTCCGCTGGATGGAGATCAACCTGCAGACCGATATGCAGAGCGTATGCA
GGACGACATTTTCATCTGAACATCATCCCATGTTTGATGCCGTCAGAGGGTGTTGCCA
TCTGTTGGCATGCCGCTTCGGATGCTCGCCTTGTTGTTGGTGATCAGCTTTGTTATCG
CGGCCTCATCAAGTGACTCTAATGCAAA (SEQ ID NO:107)

Translation:

10 MMSKLGVLIIICLLLFPLTAVPLDGDQPADRYAERMQDDISSEHHPMFDAVRGCCHLLA
CRFGCSPCCW (SEQ ID NO:108)

Toxin Sequence:

15 Gly-Cys-Cys-His-Leu-Leu-Ala-Cys-Arg-Phe-Gly-Cys-Ser-Xaa3-Cys-Cys-Xaa4-^ (SEQ ID
NO:109)

Name: Gm3.3

Species: gloriamaris

20 **Cloned:** Yes

DNA Sequence:

25 GAGACGACAAGGAACAGTCAACCCACAGCCACGCCAAGAGCAGACAGCCACAGC
TACGTGAAGAAGGGTGGAGAGAGGTTTCGTGATGTTGAAAATGGGAGTGGTGCTATT
CATCTTCCTGGTACTGTTTCCCCTGGCAACGCTCCAGCTGGATGCAGATCAACCTGT
AGAACGATATGCGGAGAACAAACAGCTCCTCAACCCAGATGAAAGGAGGGAAATC
ATATTGCATGCTCTGGGGACGCGATGCTGTTCTTGGGATGTGTGCGACCAACCCGAGT
TGTACTTGCTGCGGCGGTTAGCGCCGAACATCCATGGCGCTGTGCTGGGCGGTTTTA
TCCAACAACGACAGCGTTTGTTGATTTTCATGTATCATTGCGCCACAGTCTCTTGCTA
30 AGAATGACGAACATGATTGCACTCTGGTTCAGATTTTCGTGTTCTTTTCTGACAATAA
ATGACAAAACCTCCAAAAAA (SEQ ID NO:110)

Translation:

35 MLKMGVVLFIPLVLFPLATLQLDADQPVERYAENKQLLNPDERREIILHALGTRCCSWD
VCDHPSTCCGG (SEQ ID NO:111)

Toxin Sequence:

Cys-Cys-Ser-Xaa4-Asp-Val-Cys-Asp-His-Xaa3-Ser-Cys-Thr-Cys-Cys-Gly-# (SEQ ID NO:112)

40

Name: La3.1

Species: laterculatus

Cloned: Yes

45 **DNA Sequence:**

CGACCTCAAGAAGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGA
CCATCTGTCTGCTTCTGTTTCCCCTTACTGCTCTCCGATGGATGGAGATCAACCTGC

AGACCGACCTGCAGAGCGTATGCAGGACGTTTCATCTGAACAGCATCCCTTGTATG
ATCCCGTCAAACGGTGTTGCGACTGGCCATGCAGCGGATGCATCCCTTGTTGCTAAT
AGTAACAACGTGTTGATAACCAACTTTCTTACCACGACTACGTCAAGTGTCTAATGA
ATAAGTAAAATGATTGCAGT (SEQ ID NO:113)

5

Translation:

MMSKLGVLLTICLLLFPLTALPMDGDQPADRPAERMQDVSSEQHPLYDPVKRCCDWPC
SGCIPCC (SEQ ID NO:114)

10

Toxin Sequence:

Cys-Cys-Asp-Xaa4-Xaa3-Cys-Ser-Gly-Cys-Ile-Xaa3-Cys-Cys-^ (SEQ ID NO:115)

Name: La3.2

15

Species: laterculatus

Cloned: Yes

DNA Sequence:

20

CGACCTCAAGAAGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTGTA
CCATCTGTCTGCTTCTGTTTCCCCTTACTGCTCTGGATGGAGATCAACCTGCAGACC
GACTTGCAGAGCGTATGCAGGACGACATTTTCATCTGAGCAGCATCCCTTTGAAAAG
AGACGAGACTGTTGCACACCTCCGAAGAAATGCAGAGACCGACAATGCAAACCTGC
ACGTTGTTGCGGAGGATAACGTGTTGATGACCAACTTTGTTATCACGGCTACGTCAA
GTGTCTAGTGAATAAGTAAAACGATTGCAGT (SEQ ID NO:116)

25

Translation:

MMSKLGVLLTICLLLFPLTALDGDQPADRLAERMQDDISSEQHPFEKRRDCCTPPKKCR
DRQCKPARCCGG (SEQ ID NO:117)

30

Toxin Sequence:

Arg-Asp-Cys-Cys-Thr-Xaa3-Xaa3-Lys-Lys-Cys-Arg-Asp-Arg-Gln-Cys-Lys-Xaa3-Ala-Arg-
Cys-Cys-Gly-# (SEQ ID NO:118)

35

Name: La3.3

Species: laterculatus

Cloned: Yes

DNA Sequence:

40

GGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTGACCATCTGTCTGC
TTCTGTTTCCCCTTACTGCTCTTCCGATGGATGGAGATCAACTTGCACGCCGATCTGC
AGAGCGTATGCAGGACAACATTTTCATCTGAGCAGCATCACCTCTTTGAAAAGAGAC
GACCACCATGTTGCACCTATGACGGGAGTTGCCTAAAAGAATCATGCATGCGTAAA
GCTTGTTGCGGATGATAACGTGTTGATGACCAACTTTGTTATCACGGCTACTCAAGT
GTCTAATGAATAAGTAAAATGATTGCAGTA (SEQ ID NO:119)

45

Translation:

MMSKLGVLLTICLLLFPLTALPMDGDQLARRSAERMQDNISSEQHHLFEKRRPPCCTYD
GSCLKESCMRKACCG (SEQ ID NO:120)

Toxin Sequence:

- 5 Arg-Xaa3-Xaa3-Cys-Cys-Thr-Xaa5-Asp-Gly-Ser-Cys-Leu-Lys-Xaa1-Ser-Cys-Met-Arg-Lys-
Ala-Cys-Cys-# (SEQ ID NO:121)

Name: La3.3A

10 **Species:** laterculatus

Cloned: Yes

DNA Sequence:

- 15 GGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGACCACCTGTCTGC
TTCTGTTTCCCCTTACTGCTCTTCCGATGGATGGAGATCAACTTGCACGCCGACCTG
CAGAGCGTATGCAGGACAACATTTTCATCTGAGCAGCATCCCTTCTTTGAAAGGAGA
CGACCACCATGTTGCACCTATGACGGGAGTTGCCTAAAAGAATCATGCAAGCGTAA
AGCTTGTTGCGGATAATAACGTGTTGATGACCAACTTTGTTATCACGGCTACTCAAG
TGTCTAATGAATAAGTAAAATGATTGCAGTA (SEQ ID NO:122)

20

Translation:

MMSKLGVLLTTCLLLFPLTALPMDGDQLARRPAERMQDNISSEQHPPFFERRRPPCCTYD
GSCLKESCKRKACCG (SEQ ID NO:123)

25 **Toxin Sequence:**

Arg-Xaa3-Xaa3-Cys-Cys-Thr-Xaa5-Asp-Gly-Ser-Cys-Leu-Lys-Xaa1-Ser-Cys-Lys-Arg-Lys-
Ala-Cys-Cys-# (SEQ ID NO:124)

30 **Name:** Lp3.1

Species: leopardus

Cloned: Yes

DNA Sequence:

- 35 GGATCCATGATGTCTAAACTGGGAGTCTTGTTGACCGTCTGTCTGCTTCTGTTTCCCC
T TACTGCTCTTTCGGCTGGTTGGAGATCAACCTGCAGAGCGACCTGCAAAGCGTACGC
AGGACGACATTCCAGATGGACAGCATCCGTTAAATGATAGGCAGATAAACTGTTGC
CCGTGGCCATGCCCTAGTACATGCCGCCATCAATGCTGCCATTAATGATAACGTGTT
GATGACCAACTTTCTCGAG (SEQ ID NO:125)

40

Translation:

GSMMSKLGVLLTVCLLLFPLTALRLVGDQPAERPAKRTQDDIPDGQHPLNDRQINCCP
WPCPSTCRHQCCH (SEQ ID NO:126)

45 **Toxin Sequence:**

Xaa2-Ile-Asn-Cys-Cys-Xaa3-Xaa4-Xaa3-Cys-Xaa3-Ser-Thr-Cys-Arg-His-Gln-Cys-Cys-His-
(SEQ ID NO:127)

Name: Lv3.1
Species: lividus
Cloned: Yes

DNA Sequence:

GGATCCATGATGTCTAAACTGGGAGTCTTGTTGACCGTCTGTCTGCTTCTGTTTCCCC
TTACTGCTCTTCGGCTGGTTAGAGATCAACCTGCAGAGCGACCTGCAAAGCGTACGC
10 AGGACGACATTCCAAATGGACAGGATCCGTTAATTGATAGGCAGATAAATTGTTGC
CCTTGGCCATGCCCTGATTCATGCCACTATCAATGCTGCCACTGATAACGTGTTGAT
GACCAACTTTCTCGAG (SEQ ID NO:128)

Translation:

15 GSMMSKLGVLLTVCLLLFPLTALRLVRDQPAERPAKRTQDDIPNGQDPLIDRQINCCPW
PCPDSCHYQCCH (SEQ ID NO:129)

Toxin Sequence:

20 Xaa2-Ile-Asn-Cys-Cys-Xaa3-Xaa4-Xaa3-Cys-Xaa3-Asp-Ser-Cys-His-Xaa5-Gln-Cys-Cys-His-[^]
(SEQ ID NO:130)

Name: L3.1
Species: lynceus
Cloned: Yes

DNA Sequence:

AAGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTGTCTG
CTTCTGTTTCCCCTTACTGCTCTTCCGATGGATGGAGATCAATCTGCAGACCGACTTG
30 CAGAGCGTATGCAGGACAACATTTTCATCTGAGCAGCATCCCTTCTTTGAAAAGAGA
GGACGAGACTGTTGCACACCTCCGAGGAAATGCAGAGACCGAGCCTGCAAACCTCA
ACGTTGTTGCGGAGGATAAGCTGTTGATGACCAACTTTGTTATACGGC (SEQ ID
NO:131)

Translation:

35 MMSKLGVLLTICLLLFPLTALPMDGDQSADRLAERMQDNISSEQHPFFEKRGRDCCTPP
RKCRDRACKPQRCCGG (SEQ ID NO:132)

Toxin Sequence:

40 Gly-Arg-Asp-Cys-Cys-Thr-Xaa3-Xaa3-Arg-Lys-Cys-Arg-Asp-Arg-Ala-Cys-Lys-Xaa3-Gln-
Arg-Cys-Cys-Gly-# (SEQ ID NO:133)

Name: M3.1
Species: magus
Cloned: Yes

DNA Sequence:

CAAGAGGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTG
TCTGCTTCTGTTTCCCCTTACTGCTCTTCCGATGGATGGAGATGAACCTGCAAACCG
ACCTGTGCGAGCGTATGCAGGACAACATTTTCATCTGAGCAGTATCCCTTGTTTGAGAA
5 GAGACGAGATTGTTGCACTCCGCCGAAGAAATGCAAAGACCGACAATGCAAACCCC
AGAGATGTTGCGCTGGACGATAACGTGTTGATGACCAACTTTATCACGGCTACGTCA
AGTGTTTAGTGAATAAGTAAAATGATTGCAGTCTTGCTCAGATTTGCTTTTGTGTTTT
GGTCTAAAGATCAATGACCAAACCGTTGTTTTGATGCGGATTGTCATATATTTCTCG
ATTCCAATCCAACACTAGATGATTTAATCACGATAGATTAATTTTCTATCAATGCCT
10 TGATTTTTTCGTCTGTCATATCAGTTTTGTTTATATTTATTTTTTCGTCACTGTCTACAC
AAACGCATGCATGCACGCATGCACGCACACACGCACGCACGCTCGCACAAACATGC
GCGCGCACGCACACACACACACACACACAAACACACACACGAAGCAATCACAC
AATTAGTTGACATTATTTATTTATTCATTGATGTATTTGTTATTCGTTTGCTTGTTTT
AGAATAGTTTGAGGCCGTCTTTTTGGATTTATTTGAACTGCTTTATTGTATACGAGTA
15 CTTCGTGCGGGGAAACACTGCTGAAAATAAAACAAACACTGACGTAGCAAAAAAA
AAAAA (SEQ ID NO:134)

Translation:

MMSKLGVLLTICLLLFPLTALPMDGDEPANRPVERMQDNISSEQYPLFEKRRDCCTPPK
20 KCKDRQCKPQRCCAGR (SEQ ID NO:135)

Toxin Sequence:

Arg-Asp-Cys-Cys-Thr-Xaa3-Xaa3-Lys-Lys-Cys-Lys-Asp-Arg-Gln-Cys-Lys-Xaa3-Gln-Arg-
Cys-Cys-Ala-# (SEQ ID NO:136)
25

Name: M3.2
Species: magus
Cloned: Yes
30

DNA Sequence:

CAAGAGGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTG
TCTGCTTCTGTTTCCCCTTACTGCTCTTCCAATGGATGGAGATCAACCTGCAGACCA
ACCTGCAGATCGTATGCAGGACGACATTTTCATCTGAGCAGTATCCCTTGTTTGATAT
35 GAGAAAAAGGTGTTGCGGCCCGCGGTTTCATGCCCCGTATATTTTCAGAGACAATT
TTATTTGTGGTTGTTGTAAATGACAACGTGTCGATGACCAACTTCATTATCACGAC
TACGCCAAGTGTCTAATGAATAAAATAAAATGATTGCAGTCTCGCTCAGATTTGCTTT
TGTATTTTGGTCTAAAGATCAATGACCAAACCGTTGTTTTGGTGTGGATTTTCATATA
TTTCTCGAGTCCTATCCAACACTAGATGATTTAATCACGATAGATCTGATTTTTTTAT
40 CAAAGGCTTGGTTTTTCGTCTGTACATCAGTTTTGTTTATATTTAATTTTTTCGTCACT
GATTACACACACGCATGAACGCACAGAGTACTAACACATACACACACACACACACA
CACACACACACACACACACACACACACACACACACACGCGCGCGCGCGCGCG
CCATCTAGTAGCGCCGCGACGACACACAC (SEQ ID NO:137)

Translation:

MMSKLGVLLTICLLLFPLTALPMDGDQPADQPADRMQDDISSEQYPLFDMRKRC CGPG
45 GSCP VYFRDNFICGCC (SEQ ID NO:138)

Toxin Sequence:

Cys-Cys-Gly-Xaa3-Gly-Gly-Ser-Cys-Xaa3-Val-Xaa5-Phe-Arg-Asp-Asn-Phe-Ile-Cys-Gly-Cys-Cys-^ (SEQ ID NO:139)

Name: M3.3
Species: magus
Cloned: Yes

DNA Sequence:

CAAGAGGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTG
TTTGCTTCTGTTTCCCCTTACTGCTCTTCCGAGGGATGGAGATCAATCTGTAGACCGA
CCTGCAGAGCGTATGCAGGACGACATTTTCATCTGAGCTGCATCCCTTGTC AATCAGA
AAAAGAATGTGTTGCGGCGAGAGTGCGCCATGCCCCAGCTATTTTCAGAAACAGTCA
GATTTGTCAATTGTTGTTAAATGACAACGTGTCGATGACCACCTTCGTTATCACGACT
AATGATAAGTAAAATGATTGCAGTCTCGCTCAGATTTGCTTTTGTATTTTGGTCTAA
AGATCAATGACCAAACCGTTGTTTTGATGTGGATTTTCATATATTTCTCGAGTCCTAT
CCAACACTAGATGATTTAATCACGATAGATCTGATTTTTTTTATCAAAGCCTTGGTTTT
TCGTCTGTCACATCAGTTTTGTTTATATTTAATTTTTTCGTCACTGATTACACACACGC
ATGAACGCACAGACGTACTAACACATACACACACACACACACACACACACACACAC
ACACACACACACACACACAC (SEQ ID NO:140)

Translation:

MMSKLGVLLTICLLLFPLTALPRDGDQSVDRPAERMQDDISSE LHPLSIRKRMCCGESAP
CPSYFRNSQICHCC (SEQ ID NO:141)

Toxin Sequence:

Met-Cys-Cys-Gly-Xaa1-Ser-Ala-Xaa3-Cys-Xaa3-Ser-Xaa5-Phe-Arg-Asn-Ser-Gln-Ile-Cys-His-Cys-Cys-^ (SEQ ID NO:142)

Name: M3.4
Species: magus
Cloned: Yes

DNA Sequence:

CAAGAGGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTG
TCTGCTTCTGTTTCCCCTTACTGCTCTTCCAATGGATGGAGATCAACCTGCAGACCA
ACCTGCAGATCGTATGCAGGACGACATTTTCATCTGAGCAGTATCCCTTGTTTGATAA
GAGACAAAAGTGTTGCGGCCCCGCGGTTTCATGCCCCGTATATTTACAGACAATTT
TATTTGTGGTTGTTGTTAAATGACAACGTGTCGATGACCAACTTCATTATCACGACT
ACGCCAAGTGTCTAATGAATAAAATAAAATGATTGCAGTCTCGCTCAGATTTGCTTTT
GTATTTGGTCTAAAGATCAATGACCAAACCGTTGTTTTGGTGCTGGATTTTCATATA
TTTCTCGATTCCATCCAACACTAGATGATTTAATCACGATAGATCTGATTTTTTTAT
CAATGCCTTAATTTTTTGCTCTGTCATATCAGTTTTGTTTATAT (SEQ ID NO:143)

Translation:

MMSKLGVLLTICLLLFPLTALPMDGDQPADQPADRMQDDISSEQYPLFDKRQKCCGPG
GSCP VYFTDNFICGCC (SEQ ID NO:144)

5 **Toxin Sequence:**

Xaa2-Lys-Cys-Cys-Gly-Xaa3-Gly-Gly-Ser-Cys-Xaa3-Val-Xaa5-Phe-Thr-Asp-Asn-Phe-Ile-Cys-
Gly-Cys-Cys-^ (SEQ ID NO:145)

10 **Name:** M3.5
Species: magus
Cloned: Yes

DNA Sequence:

15 CAAGAGGGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTG
TCTGCTTCTGTTTCCCCTTACTGCTCTTCCAATGGATGGAGATCAACCTGCAGACCA
ACCTGCAGATCGTATGCAGGACGACATTTTCATCTGAGCAGTATCCCTTGTTTGATAA
GAGACAAAAGTGTTGCGGCCCCGCGGTTTCATGCCCCGTATATTTTCAGAGACAATTT
TATTTGTGGTTGTTGTTAAATGACAACGTGTCGATGACCATCTTCATTATCACGACT
20 ACGCCAAGTGTCTAATGAATAAAATAAAATGATTGCAGTCTCGCTCAGATTTGCTTTT
GTATTTTGGTCTAAAGATCAATGACCAAACCGTTGTTTTGGTGTGGATTTTCATATAT
TTCTCGATTCTATCCAACACTAGATGATTTAATCACGATAGATCTGATTTTTT (SEQ
ID NO:146)

25 **Translation:**

MMSKLGVLLTICLLLFPLTALPMDGDQPADQPADRMQDDISSEQYPLFDKRQKCCGPG
GSCP VYFRDNFICGCC (SEQ ID NO:147)

Toxin Sequence:

30 Xaa2-Lys-Cys-Cys-Gly-Xaa3-Gly-Gly-Ser-Cys-Xaa3-Val-Xaa5-Phe-Arg-Asp-Asn-Phe-Ile-
Cys-Gly-Cys-Cys-^ (SEQ ID NO:148)

Name: U001
35 **Species:** magus
Isolated: No

Toxin Sequence:

40 Xaa2-Lys-Cys-Cys-Ser-Gly-Gly-Ser-Cys-Xaa3-Leu-Xaa5-Phe-Arg-Asp-Arg-Leu-Ile-Cys-Xaa3-
Cys-Cys-^ (SEQ ID NO:149)

Name: Comatose/Death
Species: marmoreus
45 **Isolated:** Yes

Toxin Sequence:

Ser-Lys-Gln-Cys-Cys-His-Leu-Ala-Ala-Cys-Arg-Phe-Gly-Cys-Thr-Xaa3-Cys-Cys-Asn-^ (SEQ ID NO:150)

5 **Name:** Mr3.1
 Species: marmoreus
 Cloned: Yes

DNA Sequence:

10 CAAGAAGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTG
 TCTGCTTCTGTTTCCCGTTACTGCTCTTCCGATGGATGGTGATCAACCTGCAGACCGA
 CTTGTAGAGCGTATGCAGGACAACATTTTCATCTGAGCAGCATCCCTTCTTTGAAAAG
 AGAAGAGGAGGCTGTTGCACACCTCCGAGGAAATGCAAAGACCGAGCCTGCAAAC
 CTGCACGTTGCTGCGGCCAGGATAACGTGTTGATGACCAACTTTGTTATCACGGCT
15 ACGTCAAGTGTCTAGTGAATAAGTAAAACGATTGCAG (SEQ ID NO:151)

Translation:

MMSKLGVLLTICLLLFVPTALPMDGDQPADRLVERMQDNISSEQHPFFEKRRGGCCTPP
RKCKDRACKPARCCGPG (SEQ ID NO:152)

Toxin Sequence:

Arg-Gly-Gly-Cys-Cys-Thr-Xaa3-Xaa3-Arg-Lys-Cys-Lys-Asp-Arg-Ala-Cys-Lys-Xaa3-Ala-Arg-
Cys-Cys-Gly-Xaa3-# (SEQ ID NO:153)

25 **Name:** Mr3.2
 Species: marmoreus
 Cloned: Yes

DNA Sequence:

30 GAGCTCGGTACCCCGACCTCAAGAGGGATCGATAGCAGTTCATGATGTCTAAACTG
 GGAATCTTGTTGACCATCTGTCTACTTCTATTTCCCTTACTGCTGTTCCGCTGGATG
 GAGATCAACCTGCAGACCGACCTGCAGAGCGTATGCAGGACGACATTTTCATCTGAA
 CATCATCCCTTTTTTGATCCCGTCAAACGGTGTTGCAGGTTATCATGCGGCCTGGGA
35 TGCCACCCTTGTTGTGGATGACCAGCTTTGTTATCGCGGCCTCATCAAGTGTCTAAT
 GAATAAGTAAAA (SEQ ID NO:154)

Translation:

40 MMSKLGILLTICLLLFPLTAVPLDGDQPADRPAERMQDDISSEHHPPFFDPVKRCCRLSCG
 LGCHPCCG (SEQ ID NO:155)

Toxin Sequence:

Cys-Cys-Arg-Leu-Ser-Cys-Gly-Leu-Gly-Cys-His-Xaa3-Cys-Cys-# (SEQ ID NO:156)

45 **Name:** Mr3.3
 Species: marmoreus

Cloned: Yes

DNA Sequence:

5 GGCCTACACCAAGCTTGCATGCCTGCAGGTCGACTCTAGAGGATCCCCGATCGATA
GCAGTTCATGATGTCTAGACTGGGAGTCTTGTTGACCATCTGTCTACTTCTGTTTCCC
CTTACTGCTGTTCCGCTGGATGGAGATCAACCTGCGGACCGACCTGCAGAGCGCCTG
CAGGACGACATTTTCATCTGAACATCATCCCCATTTTGATTCCGGCAGAGAGTGTTGC
GGTTCGTTTCGCATGCCGCTTTGGATGCGTGCTTGTGTATGACCAGCTTTGTTAT
CACGGCCTCATCGAGTGTCTAATGAATAAGTAAAACGATTGCAGTAGGCGGGTACC
10 GAGCTCGAATTCC (SEQ ID NO:157)

Translation:

15 MMSRLGVLLTICLLLFPLTAVPLDGDQPADRPAERLQDDISSEHHPHFDSGRECCGSFAC
RFGCVPCCV (SEQ ID NO:158)

Toxin Sequence:

Xaa1-Cys-Cys-Gly-Ser-Phe-Ala-Cys-Arg-Phe-Gly-Cys-Val-Xaa3-Cys-Cys-Val-^ (SEQ ID
NO:159)

20 **Name:** Mr3.4
Species: marmoreus
Cloned: Yes

25 **DNA Sequence:**

CGACCTCAAGAGGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGA
CCATCTGTCTACTTCTATTTCCCCTTACTGCTGTTCCGCTGGATGGAGACCAACCTGC
AGACCGACCTGCAGAGCGTATGCAGGACGACATTTTCATCTGAACGTCATCCTTTTTT
TGATCGCAGCAAACAGTGTTGCCATCTGCCGGCATGCCGCTTCGGATGTACGCCTTG
30 TTGTTGGTGATCAGCTTTGTTATCGCGTCCTCATCAAGTGTCTAATGAATAAGTAAA
ATGATTGCAG (SEQ ID NO:160)

Translation:

35 MMSKLGVLLTICLLLFPLTAVPLDGDQPADRPAERMQDDISSERHPFFDRSKQCCHLPA
CRFGCTPCCW (SEQ ID NO:161)

Toxin Sequence:

Ser-Lys-Gln-Cys-Cys-His-Leu-Xaa3-Ala-Cys-Arg-Phe-Gly-Cys-Thr-Xaa3-Cys-Cys-Xaa4-^
(SEQ ID NO:162)

40 **Name:** Mr3.5
Species: marmoreus
Cloned: Yes

45 **DNA Sequence:**

GGATCCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTGTCTGCTTCTGTTTCCCC

TTACTGCTCTTCCGCTGGATGGAGATCAACCTGCAGACCAACGTGCAGAGCGTACG
CAGGCCGAGAAGCATTTCCTTGCCTGATCCGAGAATGGGCTGTTGCCCGTTTCCATGC
AAAACCAGTTGCACTACTTTGTGTTGCGGGTGATGATAACGTGTTGATGACCAACTT
TCTCGAG (SEQ ID NO:163)

5

Translation:

GSMMSKLGVLLTICLLLFPLTALPLDGDQPADQRAERTQAEKHSLPDPRMGCCPFPCKT
SCTTLCCG (SEQ ID NO:164)

10 **Toxin Sequence:**

Met-Gly-Cys-Cys-Xaa3-Phe-Xaa3-Cys-Lys-Thr-Ser-Cys-Thr-Thr-Leu-Cys-Cys-# (SEQ ID
NO:165)

15 **Name:** U014
Species: marmoreus
Isolated: Yes

Toxin Sequence:

20 Cys-Cys-His-Xaa4-Asn-Xaa4-Cys-Asp-His-Leu-Cys-Ser-Cys-Cys-Gly-Ser-^ (SEQ ID NO:166)

Name: U017
Species: marmoreus
25 **Cloned:** Yes

DNA Sequence:

GCCAAGCTTGCATGCCTGCAGGATGACTCTAGAGGATCCCCACCTCAAGAGGGATC
GATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTGTCTACTTCTGTT
30 TGCCCTTACTGCTGTTCCGCTGGATGGAGATCAACCTGCAGACCGACCTGCAGAACG
TATGCAGGACGACATTTTCATCTGAACGTCATCCCATGTTTGATGCCGTCAGAGATTG
TTGCCCGTTGCCGGCATGCCCTTTGGATGCAACCCTTGTTGTGGATGACCAGCTTT
GTTATCGGGACCTCATCAAGTGTCTAATGAATAAGTAAAAAACGATTCGAGTGGGT
ACCGAGCTCGAATTCC (SEQ ID NO:167)

35

Translation:

MMSKLGVLLTICLLLFALTAVPLDGDQPADRPAERMQDDISSERHPMFDAVRDCCPLP
ACPFGCNPCCG (SEQ ID NO:168)

40 **Toxin Sequence:**

Asp-Cys-Cys-Xaa3-Leu-Xaa3-Ala-Cys-Xaa3-Phe-Gly-Cys-Asn-Xaa3-Cys-Cys-# (SEQ ID
NO:169)

45 **Name:** U019
Species: marmoreus
Isolated: Yes

Toxin Sequence:

Cys-Cys-Ala-Xaa3-Ser-Ala-Cys-Arg-Leu-Gly-Cys-Arg-Xaa3-Cys-Cys-Arg-^ (SEQ ID NO:170)

5

Name: U020
Species: marmoreus
Isolated: Yes

10 **Toxin Sequence:**

Cys-Cys-Ala-Xaa3-Ser-Ala-Cys-Arg-Leu-Gly-Cys-Arg-Xaa3-Cys-Cys-Arg-^ (SEQ ID NO:171)

15 **Name:** U022
Species: marmoreus
Isolated: Yes

Toxin Sequence:

Cys-Cys-Ala-Xaa3-Ser-Ala-Cys-Arg-Leu-Gly-Cys-Arg-Xaa3-Cys-Cys-Arg-^ (SEQ ID NO:172)

20

Name: U024
Species: marmoreus
Isolated: Yes

25

Toxin Sequence:

Gly-Cys-Cys-Gly-Ser-Phe-Ala-Cys-Arg-Phe-Gly-Cys-Val-Xaa3-Cys-Cys-Val-^ (SEQ ID NO:173)

30

Name: Nb3.1
Species: nobilis
Cloned: Yes

35 **DNA Sequence:**

GGATCCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTGTCTACTTCTGTTTCCCC
TTACTGCTCTTCCGCTGGATGAAGATCAACCGGTACACCGACCTGCAGAGCGTATGC
AGGACATTTTCATCTGATCAACATCTCTTCTTTGATCTCATCAAACGGTGCTGCGAGT
TGCCATGCGGGCCAGGCTTTTGCGTCCCTTGTTGCTGACATCAATAACGTGTTGATG
40 ACCAACTTCTCGAG (SEQ ID NO:174)

Translation:

GSMMSKLGVLLTICLLLFPLTALPLDEDQPVHRPAERMQDISSDQHLFFDLIKRCCELPC
GPGFCVPCC (SEQ ID NO:175)

45

Toxin Sequence:

Cys-Cys-Xaa1-Leu-Xaa3-Cys-Gly-Xaa3-Gly-Phe-Cys-Val-Xaa3-Cys-Cys-^ (SEQ ID NO:176)

Name: Nb3.2
Species: nobilis
Cloned: Yes

DNA Sequence:

GGATCCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTGTCTACTTCTGTTTCCCC
TTACTGCTTTTCCGATGGATGGAGATCAACCTGCAGACCAACCTGCAGATCGTATGC
10 AGGACGACATTTTCATCTGAGCAGTATCCCTTGTTTGATAAGAGACAAAAGTGTTGCA
CTGGGAAGAAGGGGTCATGCTCCGGCAAAGCATGCAAAAATCTCAAATGTTGCTCT
GGACGATAACGTGTTGATGACCAACTTTCTCGAG (SEQ ID NO:177)

Translation:

15 GSMMSKLGVLLTICLLLFPLTAFPMGDQPADQPADRMQDDISSEQYPLFDKRQKCCT
GKKGSCSGKACKNLKCCSGR (SEQ ID NO:178)

Toxin Sequence:

Xaa2-Lys-Cys-Cys-Thr-Gly-Lys-Lys-Gly-Ser-Cys-Ser-Gly-Lys-Ala-Cys-Lys-Asn-Leu-Lys-
20 Cys-Cys-Ser-# (SEQ ID NO:179)

Name: Pu3.1
Species: pulicarius
Cloned: Yes

DNA Sequence:

GGATCCATGATGTCTAAACTGGGAGTTTTGTTGACCATCTGTCTGCTTCTGTTTCCCC
TTACTGCTGTTCCGCTGGATGGAGATCAACCTGCAGACCGACCTGCAGAGCGTATGC
30 AGGACATTGCAACTGAACAGCATCCCTTCTTTGATCCCGTCAAACGGTGTTGCAACA
GCTGTTACATGGGATGCATCCCTTGTTGCTTCTAGTAATAACGTGTTGATGACCAAC
TTTCTCGAG (SEQ ID NO:180)

Translation:

35 GSMMSKLGVLLTICLLLFPLTAVPLDGDQPADRPAERMQDIATEQHPFFDPVKRCCNSC
YMGCI PCCF (SEQ ID NO:181)

Toxin Sequence:

Cys-Cys-Asn-Ser-Cys-Xaa5-Met-Gly-Cys-Ile-Xaa3-Cys-Cys-Phe-^ (SEQ ID NO:182)

Name: Qc3.1
Species: quercinus
Cloned: Yes

DNA Sequence:

GGATCCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTGTCTGCTTCTGTTTCCCC

TTACAGCTCTTCAGCTGGATGGAGATCAACCTGCAGACCGACCTGCAGAGCGTACG
CAGGACATTGCATCTGAACAGTATCGAAAGTTTGATCAGAGACAGAGGTGTTGCCA
GTGGCCATGCCCCGGTAGTTGCAGATGCTGCCGTACTGGTTAACGTGTTGATGACCA
ACTTTCTCGAG (SEQ ID NO:183)

5

Translation:

GSMMSKLGVLLTICLLLFPLTALQLDGDQPADRPAERTQDLASEQYRKFDQRQRCCQW
PCPGSCRCRTG (SEQ ID NO:184)

10 **Toxin Sequence:**

Xaa2-Arg-Cys-Cys-Gln-Xaa4-Xaa3-Cys-Xaa3-Gly-Ser-Cys-Arg-Cys-Cys-Arg-Thr-# (SEQ ID NO:185)

15 **Name:** QcIIIA
Species: quercinus
Isolated: Yes

Toxin Sequence:

20 Cys-Cys-Ser-Gln-Asp-Cys-Leu-Val-Cys-Ile-Xaa3-Cys-Cys-Xaa3-Asn-# (SEQ ID NO:186)

Name: QcIIIB
Species: quercinus
25 **Isolated:** Yes

Toxin Sequence:

Cys-Cys-Ser-Arg-His-Cys-Xaa4-Val-Cys-Ile-Xaa3-Cys-Cys-Xaa3-Asn-? (SEQ ID NO:187)

30

Name: R3.1
Species: radiatus
Isolated: Yes
Cloned: Yes

35

DNA Sequence:

TCAAGAAGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGACCATCT
GTCTGCTTCTGTTTCCCCTTACTGCTCTTCCGATGGATGGAGATCAACCTGTAGACCG
ACTTGCAGAGCGTATGCAGGACAACATTTTCATCTGAGCAGCATACCTTCTTTGAAAA
40 GAGACTACCATCGTGTTGCTCCCTTAACTTGCGGCTTTGCCCAGTACCAGCATGCAA
ACGTAACCCTTGTTGCACAGGATAACGTGTTGATGACCAACTTTGTTATCACGGCTA
CGTCAAGTGTCTAGTGAATAAGTAAACGATTGCAGT (SEQ ID NO:188)

Translation:

45 MMSKLGVLLTICLLLFPLTALPMDGDQPVDRLAERMQDNISSEQHTFFEKRLPSCCSLN
LRLCPVPACKRNPCCCTG (SEQ ID NO:189)

Toxin Sequence:

Leu-Xaa3-Ser-Cys-Cys-Ser-Leu-Asn-Leu-Arg-Leu-Cys-Xaa3-Val-Xaa3-Ala-Cys-Lys-Arg-Asn-Xaa3-Cys-Cys-Thr-# (SEQ ID NO:190)

5

Name: R3.2
Species: radiatus
Cloned: Yes

10 **DNA Sequence:**

AGGTCGACTCTAGAGGATCCCCAAGGATCGATAGCAGTTCATGATGTCTAAACTGG
GAGTCTTGTGACCATCTGTCTGCTTCTGTTTCCCCTTACTGCTCTTCCGATGGATGG
AGATCAACCTGCAGACCGACTTGCAGAGCGTATGCAGGACGACATTTTCATCTGAGC
AGCATCCCTTCTTTAAAAAGAGACAACAAAGATGTTGCACCGTTAAGAGGATTTGT
15 CCAGTACCAGCATGCAGAAGTAAACCTTGTTGCAAATCATAACGTATTGATGACCA
ACTTTGTTATCACGGCTACGTCAAGTGTCTAGTGAATAAGTAAAATGATTGCAG
(SEQ ID NO:191)

Translation:

20 MMSKLGVLLTICLLLFPLTALPMDGDQPADRLAERMQDDISSEQHPFFKKRQQRCCTV
KRICPVPACRSKPCKS (SEQ ID NO:192)

Toxin Sequence:

25 Xaa2-Gln-Arg-Cys-Cys-Thr-Val-Lys-Arg-Ile-Cys-Xaa3-Val-Xaa3-Ala-Cys-Arg-Ser-Lys-Xaa3-
Cys-Cys-Lys-Ser-^ (SEQ ID NO:193)

30 **Name:** R3.3
Species: radiatus
Cloned: Yes

DNA Sequence:

ACCTCAAGAAGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTGACC
ATCTGTCTGCTTCTGTTTCCCGTTACTGCTCTTCCGATGGATGGTGATCAACCTGCAG
35 ACCGACTTGTAGAGCGTATGCAGGACAACATTTTCATCTGAGCAGCATCCCTTCTTTG
AAAAGAGAAGAGAGGAGGCTGTTGCACACCTCCGAGGAAATGCAAAGACCGAGCCTG
CAAACCTGCACGTTGCTGCGGCCAGGATAACGTGTTGATGACCAACTTTGTTATCA
CGGCTACGTCAAGTGTCTAGTGAATAAGTAAAACGATTGCAGT (SEQ ID NO:194)

40 **Translation:**

MMSKLGVLLTICLLFPVTALPMDGDQPADRLVERMQDNISSEQHPFFEKRRGGCCTPP
RKCKDRACKPARCCGPG (SEQ ID NO:195)

Toxin Sequence:

45 Arg-Gly-Gly-Cys-Cys-Thr-Xaa3-Xaa3-Arg-Lys-Cys-Lys-Asp-Arg-Ala-Cys-Lys-Xaa3-Ala-Arg-
Cys-Cys-Gly-Xaa3-# (SEQ ID NO:196)

Name: Ra3.1
Species: rattus
Cloned: Yes

DNA Sequence:

GGATCCATGATGTCTAAACTGGGAGTCTTGGTGACCATCTGCCTGCTTCTGTTCCCT
CTTGCTGCTTTTCCACTGGATGGAGATCAACCTGCAGACCACCCTGCAAAGCGTACG
CAAGATGACAGTTCAGCTGCCCTGATCAATGCCTGGCTTGATGAATCCCAGACTTGC
TGCAGTAACTGCGGTGAAGATTGTGATGGTTGTTGCCAGTAACGTGTTGATGACCAA
CTTTCTCGAG (SEQ ID NO:197)

Translation:

GSMMSKLGVLVTICLLLFPLAAFPLDGDQPADHPAKRTQDDSSAALINAWLDESQTCCS
NCGEDCDGCCQ (SEQ ID NO:198)

Toxin Sequence:

Xaa2-Thr-Cys-Cys-Ser-Asn-Cys-Gly-Xaa1-Asp-Cys-Asp-Gly-Cys-Cys-Gln-^ (SEQ ID
NO:199)

Name: Sm3.1
Species: stercusmuscarum
Cloned: Yes

DNA Sequence:

GACCTCAAGAGGGATCGATAGCAGTTCGTGATGTCTAAACTGGGAGTCTTGTTGAC
CATCTGTCTGCTTCTGTTTCCTCTTACTGCTCTTCCGATGGATGGAGATCAACCTGCA
GACCAACCTGCAGATCGTATGCAGGACGACATTTTCATCTGAGCAGTATCCCTTGTTT
GATAAGAGACAAAAGTGTGCACTGGGAAGAAGGGGTCATGCTCCGGCAAAGCAT
GCAAAAATCTCAAATGTTGCTCTGGACGATAACGTGTTGATGACCAACTTTGTTATC
ACGGCTACGTCAAGTGTCTAATGAATAAGTAAAACGATTGCAGT (SEQ ID NO:200)

Translation:

MSKLGVLVTICLLLFPLTALPMDGDQPADQPADRMQDDISSEQYPLFDKRQKCCTGKK
GSCSGKACKNLKCCSGR (SEQ ID NO:201)

Toxin Sequence:

Xaa2-Lys-Cys-Cys-Thr-Gly-Lys-Lys-Gly-Ser-Cys-Ser-Gly-Lys-Ala-Cys-Lys-Asn-Leu-Lys-
Cys-Cys-Ser-# (SEQ ID NO:202)

Name: U034
Species: stercusmuscarum
Isolated: Yes
Cloned: Yes

DNA Sequence:

GATCGATAGCAGTTCGTGATGTCTAAACTGGGAGTCTTGTTGACCATCTGTCTGCTT
CTGTTTCCCCTTACTGCTCTTCCGATGGATGGAGATCAACCTGCAGACCAACCTGCA
5 GATCGTATGCAGAACGACATTTTCATCTGAGCAGTATCCCTTGTTTGATAAGAGACAA
AAGTGTGCGGCCCCGGCGCGTCATGCCCCAGATATTTCAAAGACAATTTTATTTGT
GGTTGTTGTTAAATGACAACGTGTGCGATGACCAACTTCGTTATCACGACTTCGCCAA
GTGTCTAATGAATAAGTAAAACGATTGCAGT (SEQ ID NO:203)

10 **Translation:**

MSKLGVLLTICLLLFPLTALPMDGDQPADQPADRMQNDISSEQYPLFDKRQKCCGPGAS
CPRYFKDNFICGCC (SEQ ID NO:204)

Toxin Sequence:

15 Xaa2-Lys-Cys-Cys-Gly-Xaa3-Gly-Ala-Ser-Cys-Xaa3-Arg-Xaa5-Phe-Lys-Asp-Asn-Phe-Ile-
Cys-Gly-Cys-Cys-^ (SEQ ID NO:205)

Name: S3.1

20 **Species:** striatus

Cloned: Yes

DNA Sequence:

CGACCTTTCAAGAGGGATCGATAGCAGTTCGCGATGTCTAAACTGGGGGTATTGTTG
25 ACCATCTGTCTGCTTCTGTTTCCCCTTACTGCTCTTCCGATGGATGAAGATCAACCTG
CAGACCAACTTGAAGATCGTATGCAGGACGACATTTTCATCTGAGCAGTATCCCTCGT
TTGTTAGGAGACAAAAGTGTTGCGGCGAAGGCTCGTCATGCCCCAAATATTTCAA
AACAATTTTATTTGTGGTTGTTGTTAAATGACAACGTGTGCGATGACCAACTTCGTTA
TCACGACTACGCCAAGTGTCTTGTCTAATGATAATAAAATGATTCC (SEQ ID NO:206)

30

Translation:

MSKLGVLLTICLLLFPLTALPMDEDQPADQLEDQMDDISSEQYPSFVRRQKCCGEGSS
CPKYFKNNFICGCC (SEQ ID NO:207)

35 **Toxin Sequence:**

Xaa2-Lys-Cys-Cys-Gly-Xaa1-Gly-Ser-Ser-Cys-Xaa3-Lys-Xaa5-Phe-Lys-Asn-Asn-Phe-Ile-Cys-
Gly-Cys-Cys-^ (SEQ ID NO:208)

40 **Name:** S3.2

Species: striatus

Cloned: Yes

DNA Sequence:

45 GGATCCATGATGTCTAAACTGGGAGTCTTGTTGACCGTCTGTCTGCTTCTGTTTCCCC
TACTGCTCTTCCGCTGGATGGAGATCAACCTGCAGACCGACCTGCAGAGCGTATGC
AGGACGACATTTTCATCTGACGAGCATCCCTTGTTTGATAAGAGACAAAACCTGTTGCA

ATGGGGGATGCTCCAGCAAATGGTGCAGAGATCACGCACGTTGTTGCGGTCGATGA
TAACGTGTTGATGACCAACTTTCTCGAG (SEQ ID NO:209)

Translation:

5 GSMMSKLGVLLTVCLLLFPLTALPLDGDQPADRPAERMQDDISSDEHPLFDKRQNCCN
GGCSSKWCRDHARCCGR (SEQ ID NO:210)

Toxin Sequence:

10 Xaa2-Asn-Cys-Cys-Asn-Gly-Gly-Cys-Ser-Ser-Lys-Xaa4-Cys-Arg-Asp-His-Ala-Arg-Cys-Cys-#
(SEQ ID NO:211)

Name: Ts3.1

Species: tessulatus

15 **Cloned:** Yes

DNA Sequence:

GGATCCATGATGTCTAAACTGGGAGTCTTGTTGACCATGTGTCTGCTTCTGTTTCCCC
TTACTGCTGTTCCGCTGGATGGAGATCAACCTGCAGACCGACCTGCAGAGCGTAGG
20 CAGGACATTGCAACTGACGATCATCCTTTGTTTGATCCCGTCAAACGGTGCTGCCAC
AAATGCTATATGGGATGCATCCCTTGTTGCATTAGTAACGTGTTGATGACCAACTT
TCTCGAG (SEQ ID NO:212)

Translation:

25 GSMMSKLGVLLTMCLLLFPLTAVPLDGDQPADRPAERRQDIATDDHPLFDPVKRCCHK
CYMGCIPCCI (SEQ ID NO:213)

Toxin Sequence:

30 Cys-Cys-His-Lys-Cys-Xaa5-Met-Gly-Cys-Ile-Xaa3-Cys-Cys-Ile-^ (SEQ ID NO:214)

Name: Ts3.2

Species: tessulatus

35 **Cloned:** Yes

DNA Sequence:

GGATCCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTGTGTGCTTCTGTTTCCCC
TTACTGCTGTTCCGCTGGATGGAGATCAACCTGCAGACCAACCTGCAGAGCGTACG
CAGAACGAGCAGCATCCCTTGATGATCAGAAAAGAAAGTGTTGCCGGCCGCCATG
40 CGCCATGAGCTGCGGCATGGCTAGGTGTTGCTATTAATGATAACGTGTTGATGACCA
ACTTTCTCGAG (SEQ ID NO:215)

Translation:

45 GSMMSKLGVLLTICVLLFPLTAVPLDGDQPADQPAERTQNEQHPLYDQKRKCCRPPCA
MSCGMARCCY (SEQ ID NO:216)

Toxin Sequence:

Lys-Cys-Cys-Arg-Xaa3-Xaa3-Cys-Ala-Met-Ser-Cys-Gly-Met-Ala-Arg-Cys-Cys-Xaa5-^ (SEQ ID NO:217)

5 **Name:** Circling
 Species: textile
 Isolated: Yes
 Cloned: Yes

10 **DNA Sequence:**

GAGTCAACCCACTGTCACGCCAAGAGCGGACGCCACAGCTAAGGCAAGAAGGATC
GATAGCAGTTCATGATGTCTAAACTGGGAGCCTTGTTGACCATCTGTCTACTTCTGT
TTTCCCTTACTGCTGTTCCGCTGGATGGAGATCAACATGCAGACCAACCTGCACAGC
GTCTGCAGGACCGCATTCCAACCTGAAGATCATCCCTTATTTGATCCCAACAAACGGT
15 GTTGCCCGCCGGTGGCATGCAACATGGGATGCAAGCCTTGTTGTGGATGACCAGCTT
TGTATCGCGGTCTCATGAAGTGTCTAATGAATAAGTAAAACGATTGCAGTTTCGTT
CAGATTTGCTGTTGTATTTTGGTCTAAAGATTAATGACCAAACCTGTTCTTTTGATCCG
GATTTTCACGTATTTCTCGATTCCCTATTCAACACTAGATAAGTTAATCACGACAGAT
CTGATTTTCCATCAATGCCTTGCTTTTGGTCTGTCATATAAATCTTGTTTATATTTAA
20 TTTCTCGTCACTTTCAACACGCACACACACACACACACACACGCGCGCGC (SEQ ID
NO:218)

Translation:

MMSKLGALLTICLLLFSLTAVPLDGDQHADQPAQRLQDRIPTEHDHPLFDPNKRCCPPVA
25 CNMGCKPCCG (SEQ ID NO:219)

Toxin Sequence:

Cys-Cys-Xaa3-Xaa3-Val-Ala-Cys-Asn-Met-Gly-Cys-Lys-Xaa3-Cys-Cys-Gly-^ (SEQ ID
NO:220)

30

Name: Scratcher I
Species: textile
Cloned: Yes

35

DNA Sequence:

GGATCCAGACGACAAAGAAGAGTCAACCCACTGCCACGTCAAGAGCAGAGCCCAC
AGCTAAGACAAGAAGGATCGATAGCAGTTCATGATGTTTAAACTGGGAGTCTTGTT
GACCATCTGTCTCCTTCTGTTTTCCCTTAATGCTGTTCCGTTGGATGGAGATCAACCT
40 GCAGACCAACCTGCAGAGCGTCTGCTGGACGACATTTCAATTTGAAAATAATCCCTTT
TATGATCCCGCCAAACGGTGTGTCAGGACTTGCTTCGGTTGCACACCTTGTTGTGGA
TGACCAGCCTCATCAAGTGTCTAACGAATAAGTAAAGCGATTGCAGTCTCGTTTCAG
ATTTACTTTTGTATTCTGGTCTAAAGATTAATGACCAAACCTCTTCTTTTGATCCGGAT
GTACATATATTTCTCGATTCCCTATCCAACGCTAGATAAGCTAATCACGACAGATCTG
45 ATTTTCTGTCAATGCCTTGCTTTTGGTCTCTCATATCACTCTTGTTTATATTTAATTT
CTCGTCACTATATATATATACACACACACACACACGGAATCCGATTGTCCAGTA
CCGTTCTTGGGATCGAGGTATTGCTGCGATGGCTTATTCTGTACTCTTTTCTTCTGCG

CTTGATAGTGATGTCTTCTACTCCCATCTGTGCTACCCCTGGCTTGATCTTTGATAGG
CGTGTGCCCTTCACTGGTTATAAACCCCTCTGATCCTACTCTCTGGACGCCTCGGGG
GCCCAACCTCCAAATAAAGCGACATCCAATGAAAAA (SEQ ID NO:221)

5 **Translation:**

MMFKLGVLLTICLLLFSLNAVPLDGDQPADQPAERLLDDISFENNPFYDPAKRCCRTCF
GCTPCCG (SEQ ID NO:222)

Toxin Sequence:

10 Cys-Cys-Arg-Thr-Cys-Phe-Gly-Cys-Thr-Xaa3-Cys-Cys-# (SEQ ID NO:223)

Name: Tx3.1

Species: textile

15 **Cloned:** Yes

DNA Sequence:

GGAACAGTCAACCCACAGCCACGCCAAGAGCAGACAGCCACAGCTACGTGAAGA
AGGGTGGAGAGAGGTTTCATGATGTTGAAAATGGGAGTGGTGCTATTCATCTTTCTGG
20 TACTGTTTCCCCTGGCAACGCTCCAGCTGGATGCAGATCAACCTGTAGAACGATATG
CGGAGAACAAACAGCTCCTCAACCCAGATGAAAGGAGGGGAAATCCTATTGCCTGCT
CTGAGGAAGTTCTGCTGTGATTCTGAATTGGTGCCACATTTTCGGATTGTGAGTGCTGC
TACGGTTAGCGCCGAACATCCATGGCACTGTGCTGGGCGGTTTCATCCCAACAACG
ACAGCGTTTGTGATTTTCATGTATCATTGCGCCACAGTCTCTTGTCTAAGAATGACG
25 AACATGATTGCACTCTGGTTCAGATTTCGTGTTCTTTTCTGACAATAAATGACAAAcC
TCC (SEQ ID NO:224)

Translation:

MMLKMGVVLFIFLVLFPLATLQLDADQPVERYAENKQLLNPDERREILLPALRKFCDS
30 NWCHISDCECCYG (SEQ ID NO:225)

Toxin Sequence:

Phe-Cys-Cys-Asp-Ser-Asn-Xaa4-Cys-His-Ile-Ser-Asp-Cys-Xaa1-Cys-Cys-Xaa5-# (SEQ ID
NO:226)

35

Name: U031

Species: textile

Isolated: Yes

40 **Cloned:** Yes

DNA Sequence:

CAAGGAACAGTCAACCCACAGCCACGCCAAGAGCAGACAGCCACAGCTACGTGA
AGAAGGGTGGAGAGAGGTTTCGTGATGTTGAAAATGGGAGTGGTGCTATTCATCTTC
45 CTGGTACTGTTTCCCCTGGCAACGCTCCAGCTGGATGCAGATCAACCTGTAGAACGA
TATGCGGAGAACAAACAGCTCCTCAGCCCAGATGAAAGGAGGGGAAATCATATTGCA
TGCTCTGGGGACGCGATGCTGTTCTTGGGATGTGTGCGACCACCCGAGTTGTA

CTGCGGTTAGCGCCGAACATCCATGGCGCTGTGCTGGGCGGTTTTATCCCAACAACG
ACAGCGTTTGTGATTTCATGTATCATTGCGCCACGTCTCTTGTCTAAGAATGACG
AACATGATTGCACTCTGGTTCAGATTTCGTGTTCTTTTCTGACAATAAATGACAAAA
CNCC (SEQ ID NO:227)

5

Translation:

MLKMGVVLFIPLVLFPLATLQLDADQPVERYAENKQLLSPDERREILHALGTRCCSWD
VCDHPSTCCG (SEQ ID NO:228)

10 **Toxin Sequence:**

Cys-Cys-Ser-Xaa4-Asp-Val-Cys-Asp-His-Xaa3-Ser-Cys-Thr-Cys-Cys-# (SEQ ID NO:229)

Name: U032

15 **Species:** textile

Isolated: Yes

Cloned: Yes

DNA Sequence:

20 GGATCCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTGTCTGCTTCTGTTTCCCC
TTACTGCTCTTCCGCTGGATGGAGATCAACCCGCAGACCAAGCTGCAGAGCGTATG
CAGGCCGAGCAGCATCCCTTGTTTGATCAGAAAAGACGGTGCTGCAAGTTTCCATG
CCCCGATAGTTGCAGATATTTGTGTTGCGGGTGATGATAACGTGTTGATGACCAACT
TTCTCGAG (SEQ ID NO:230)

25

Translation:

GSMMSKLGVLLTICLLLFPLTALPLDGDQPADQAAERMQAEQHPLFDQKRRCKFPCP
DSCRYLCCG (SEQ ID NO:231)

30 **Toxin Sequence:**

Arg-Cys-Cys-Lys-Phe-Xaa3-Cys-Xaa3-Asp-Ser-Cys-Arg-Xaa5-Leu-Cys-Cys-# (SEQ ID
NO:232)

35 **Name:** T3.1

Species: tulipa

Cloned: Yes

DNA Sequence:

40 CGACCTCAAGAGGGATCGATAGCAGTTCATGTCTAAACTGGGAGTCTTGTTGACAA
TCTGTCTGCTTCTGTTTCCCCTTACTGCTCTGCCGATGGATGGAGATGAACCTGCAG
ACCGACCTGCAGAGCGTATGCAGGACAACATTTTCATCTGAGCAGCATCCCTTGTTTG
AGGAGAGACACGGATGTTGCAAGGGGCCCCGAAGGATGCTCCTCCAGAGAATGCAG
ACCCAACATTGTTGCGGTGACGATAACGTGTTGAGGGCCAACCTTTGTTATCACGG
45 CTACGTCAAGTGTTTAGTGAATAAGTAAAATGATTGCAG (SEQ ID NO:233)

Translation:

MSKLGVLLTICLLLFPLTALPMDGDEPADRPAERMQDNISSEQHPLFEERHGCCCKGPEG
CSSRECRPQHCCGRR (SEQ ID NO:234)

Toxin Sequence:

5 His-Gly-Cys-Cys-Lys-Gly-Xaa3-Xaa1-Gly-Cys-Ser-Ser-Arg-Xaa1-Cys-Arg-Xaa3-Gln-His-
Cys-Cys-# (SEQ ID NO:235)

Name: Fi3.1

10 **Species:** figulinus

Cloned: Yes

DNA Sequence:

15 CAAGAAGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGCTGACCATCT
GTCTGCTTCTGATTCCCCTTACTGCTCTTTCGCTGGATGGAGATCAACCTGCAGACC
GACCTGCAGAGCGTATGCAGGATGGAATTTTCATCTGAACAGCATCCCATGTTTGATC
CCGTCAGACGGTGTGCCCCGTGGCCATGCAACATAGGATGCGTACCTTGTTGTTGAT
GACCAGTTTTGTTATCGCGGCCTCATCAAATGTCTAATGAATAAGTAAAACGATTGC
AGT (SEQ ID NO:236)

20

Translation:

MMSKLGVLLTICLLLIPLTALS LDGDQPADRPAERMQDGISSEQHPMFDPVRRCCPWPC
NIGCVPC (SEQ ID NO:237)

25 **Toxin Sequence:**

Cys-Cys-Xaa3-Xaa4-Xaa3-Cys-Asn-Ile-Gly-Cys-Val-Xaa3-Cys-Cys-^ (SEQ ID NO:238)

Name: Fi3.2

30 **Species:** figulinus

Cloned: Yes

DNA Sequence:

35 CAAGAGGGATCGATAGCAGTTCATGATGTTTAAACTGGGAGTCCTGTTGACCATCTG
TATGCTTCTGTTTCCCTTTACTGCTCTTCCGCTGGATGGAGAGCAACCTGCAGACCA
ACCTGCAGAGCGCATGCAGTATGACATGTTACGTGCAATGAATCCCTGGTTTGATCC
CGTCAAAAGGTGCTGCTCGAAGAACTGCGCAGTATGCATCCCTTGTTGCCCGTAACT
GACCAGCTTGATTATCGCGGCCAAGGCTCTAATGAATAAGTAAAACGATTGCAGT
(SEQ ID NO:239)

40

Translation:

MMFKLGVLLTICMLLFPFTALPLDGEQPADQPAERMQYDMLRAMNPWFDPVKRCCSK
NCAVCIPCCP (SEQ ID NO:240)

45 **Toxin Sequence:**

Cys-Cys-Ser-Lys-Asn-Cys-Ala-Val-Cys-Ile-Xaa3-Cys-Cys-Xaa3-^ (SEQ ID NO:241)

Name: Fi3.3
Species: figulinus
Cloned: Yes

DNA Sequence:

CAAGAGGGATCGATAGCAGTTCATGATGTCTAAACTGAGAGTCTTGTTGACCTTATG
TCTGCTTCTGTTTCCCCTTACTGCTCTTCCGCTGAATGAAGATCAACCTGCAGAGCGT
ATGCAGGACGACAATTCATCTGAGCAGCACCCCTTGTATGACCACAAACGAAAGTG
TTGCCGGTGGCCATGCCCCGCAAGATGCGGCTCTTGTTGCCTGTAATAACGTGTTGG
CCAACCTTTGTTATCACGGCCACGTCAAATGTTTAATGAATAAGTAAAACGATTGCAG
T (SEQ ID NO:242)

Translation:

MMSKLRVLLTLCLLLFPLTALPLNEDQPAERMQDDNSSEQHPLYDHKRKCCRWPCPAR
CGSCCL (SEQ ID NO:243)

Toxin Sequence:

Cys-Cys-Arg-Xaa4-Xaa3-Cys-Xaa3-Ala-Arg-Cys-Gly-Ser-Cys-Cys-Leu-^ (SEQ ID NO:244)

Name: Fi3.4
Species: figulinus
Cloned: Yes

DNA Sequence:

CAAGAGGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGACCTTATG
TCTGCTTCTGTTTCCCCTGACTGCTCTTCCGCTGGATGAAGATCAAGCTGCAGACCG
ACCTGCAGAGCGTATGCAGGGCATGTCATCTGAACAGCATCCCTTCTTTGATCCCGT
CAAACGGTGTGCGAGTTGTCACGCTGCCTTGGATGCGTCCCTTGTTGCACATCTTA
ATAACGTGTGGATGACCAACTGTGTTATCACGGCCACGTCAAGTGTCTAATGAATA
AGTAAAATGATTGCAGT (SEQ ID NO:245)

Translation:

MMSKLGVLLTLCLLLFPLTALPLDEDQAADRPAERMQGMSSSEQHPFFDPVKRCCELSR
CLGCVPCCTS (SEQ ID NO:246)

Toxin Sequence:

Cys-Cys-Xaa1-Leu-Ser-Arg-Cys-Leu-Gly-Cys-Val-Xaa3-Cys-Cys-Thr-Ser-^ (SEQ ID NO:247)

Name: Fi3.5
Species: figulinus
Cloned: Yes

DNA Sequence:

CAAGAGGGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGACCTTATG
TCTGCTTCTGTTTCCCCTGACTGCTCTTCCGCTGGATGAAGATCAACCTGCAGACCG
ACCTGCAGAGCGTATGCAGGGCATGTCATCTGAACAGCATCCCTTCTTTGATCCCGT
CAAACGGTGTGCGAGTTGTCAAAATGCCATGGATGCGTCCCTTGTTGCATACCTTA
5 ATAACGTGCGGATGACCAACTGTGTTATCACGGCCACGTCAAGTGTCTAATGAATA
AGTAAATGATTGCAGT (SEQ ID NO:248)

Translation:

MMSKLGVLLTLCLLLFPLTALPLDEDQPADRPAERMQGMSSSEQHPFFDPVKRCCELSK
10 CHGCVPCIP (SEQ ID NO:249)

Toxin Sequence:

Cys-Cys-Xaa1-Leu-Ser-Lys-Cys-His-Gly-Cys-Val-Xaa3-Cys-Cys-Ile-Xaa3-^ (SEQ ID NO:250)

15
Name: Qc3.2
Species: quercinus
Cloned: Yes

DNA Sequence:

CAAGAGGGGATCGATAGCAGTTCATGATGTCTAAACTCGGAGTCTTGTTGACCATCTG
TCTGGTTCTGTTTCCCCTTACAGCTCTTCAGCTGGATGGAGATCAACCTGCAGACCG
ACCTGCAGAGCGTACGCAGGACATTTATCTGAACAGTATCGAAAGTTTGATCAGA
GACAGAGGTGTTGCCGGTGGCCATGCCCCGGTAGTTGCAGATGCTGCCGTTATCGTT
25 AACGTGTTGGTGACCAGCTTTGTTATCACGACCACGCCAAGTGTCTAACGAATAAGT
AAAATGATTGCAGT (SEQ ID NO:251)

Translation:

MMSKLGVLLTICLVLFPLTALQLDGDQPADRPAERTQDISSEQYRKFDQRQRCCRWP
30 GSCRCCRYR (SEQ ID NO:252)

Toxin Sequence:

Xaa2-Arg-Cys-Cys-Arg-Xaa4-Xaa3-Cys-Xaa3-Gly-Ser-Cys-Arg-Cys-Cys-Arg-Xaa5-Arg-^
(SEQ ID NO:253)

35
Name: Qc3.3
Species: quercinus
Cloned: Yes

DNA Sequence:

CAAGAGGGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTG
TCTGCTTCTGTTTCCCCTTACTGCTCTTCCACTGGATGGAGATCAACCTGCAGATCAA
TCTGCAGAGCGACCTGCAGAGCGTACGCAGGACGACATTCAGCAGCATCCGTTATA
45 TGATCCGAAAAGAAGGTGTTGCCGTTATCCATGCCCCGACAGCTGCCACGGATCTTG
CTGCTATAAGTGATAACATGTTGATGGCCAGCTTTGTTATCACGGCCACGTCAAGTG
TCTAATGAATAAGTAAACGATTGCAGT (SEQ ID NO:254)

Translation:

MMSKLGVLLTICLLLFPLTALPLDGDQPADQSAERPAERTQDDIQQHPLYDPKRRCCRY
PCPDSCHGSCCYK (SEQ ID NO:255)

5

Toxin Sequence:

Arg-Cys-Cys-Arg-Xaa5-Xaa3-Cys-Xaa3-Asp-Ser-Cys-His-Gly-Ser-Cys-Cys-Xaa5-Lys-^ (SEQ
ID NO:256)

10

Name: Wi3.1
Species: wittigi
Cloned: Yes

15 **DNA Sequence:**

GGATCCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTGTCTGCTTCTGTTTCCCA
T TACTGCTCTTCCGGTGGGTGGAGATCAGCCTGCAGACCGACTTGCAGAGCGTATGC
AGGACGACACTTCATCTGAGCAGCATCCCTTTGAAAAGAGACTACCATCATGTTGC
GACTTTGAGAGGCTTTGCGTAGTACCAGCATGCATACGTCATCAGTGTGACAGGA
20 TAACGTGTTGATGACCAACTTTCTCGAG (SEQ ID NO:257)

Translation:

MMSKLGVLLTICLLLFIPITALPVGGDQPADRLAERMQDDTSSEQHPFEKRLPSCCDFERL
CVVPACIRHQCTG (SEQ ID NO:258)

25

Toxin Sequence:

Leu-Xaa3-Ser-Cys-Cys-Asp-Phe-Xaa1-Arg-Leu-Cys-Val-Val-Xaa3-Ala-Cys-Ile-Arg-His-Gln-
Cys-Cys-Thr-# (SEQ ID NO:259)

30

Name: bt3a
Species: betulinus
Isolated: Yes

35 **Toxin Sequence:**

Cys-Cys-Lys-Gln-Ser-Cys-Thr-Thr-Cys-Met-Xaa3-Cys-Cys-Xaa4-^ (SEQ ID NO:260)

40

Name: T3.2
Species: tulipa
Cloned: Yes

DNA Sequence:

45 GGATCCATGATGTCTAAACTGGGAGTCTTGTTGACAATCTGTCTGCTTCTGTTTCCCC
T TACTGCTCTGCCGATGGATGGAGATGAACCTGCAGACCGACCTGCAGAGCGTATG
CAGGACAACATTTTCATCTGAGCAGCATCCCTTGTTTGAGGAGAGACACGGATGTTG

CGAGGGGGCCGAAGGGATGCTCCTCCAGAGAATGCAGACCCCAACATTGTTGCGGTC
GACGATAACGTGTTGATGACCAACTNTCTCGAG (SEQ ID NO:261)

Translation:

5 MMSKLGVLLTICLLLFPLTALPMDGDEPADRPAERMQDNISSEQHPLFEERHGCCEGPK
GCSSRECRPQHCCGRR (SEQ ID NO:262)

Toxin Sequence:

10 His-Gly-Cys-Cys-Xaa1-Gly-Xaa3-Lys-Gly-Cys-Ser-Ser-Arg-Xaa1-Cys-Arg-Xaa3-Gln-His-
Cys-Cys-# (SEQ ID NO:263)

Name: A3.5

Species: aurisiacus

15 **Cloned:** Yes

DNA Sequence:

GGATCCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTGTCTACTTCTGTTTCCCC
TTACTGCTTTTCCGATGGATGGAGATCAACCTGCAGACCAACCTGCAGATCGTATGC
20 AGGACGACATTTTCATCTGAGCAGTATCCCTTGTTTGATAAGAGACAAAAGTGTTGCA
CTGGGAGGAAGGGGTCATGCTCCGGCAAAGCATGCAAAAATCTCAAATGTTGCTCT
GGACGATAACGTGTTGATGACCAACTTTCTCGAN (SEQ ID NO:264)

Translation:

25 MMSKLGVLLTICLLLFPLTAFPMGDGQPADQPADRMQDDISSEQYPLFDKRQKCCTGR
KGSCSGKACKNLKCCSGR (SEQ ID NO:265)

Toxin Sequence:

30 Xaa2-Lys-Cys-Cys-Thr-Gly-Arg-Lys-Gly-Ser-Cys-Ser-Gly-Lys-Ala-Cys-Lys-Asn-Leu-Lys-
Cys-Cys-Ser-# (SEQ ID NO:266)

Name: Bt3.5

Species: betulinus

35 **Cloned:** Yes

DNA Sequence:

GGATCCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTGTCTGCTTCTGTTTCCCC
TTACTGCTGTTCCGTTGGATGGAGATCAACCTGCAGACCAACCTGCAGAGCGTATGC
40 AGAACGAGCAGCATCCCTCGTTTGATCAGAAAAGAAGGTGCTGCCGGTGGCCATGC
CCCAGTATATGCGGCATGGCTAGGTGTTGCTTCGTCATGATAACGTGTTGATGACCA
ACTTTCTCGAG (SEQ ID NO:267)

Translation:

45 MMSKLGVLLTICLLLFPLTAVPLDGDQPADQPAERMQNEQHPSFDQKRRCCRWPCCPSIC
GMARCCFVMITC (SEQ ID NO:268)

Toxin Sequence:

Arg-Cys-Cys-Arg-Xaa4-Xaa3-Cys-Xaa3-Ser-Ile-Cys-Gly-Met-Ala-Arg-Cys-Cys-Phe-Val-Met-Ile-Thr-Cys-^ (SEQ ID NO:269)

Name: Bt3.6
Species: betulinus
Cloned: Yes

DNA Sequence:

GGATCCATGATGTCTAAACTGGGAGTCTTGTTGATCATCTGTCTGCTTCTGTTTCCCC
TTACTGCTGTTCCGCTGGATGGAGATCAGCCTGCAGAGCGTACGCAGATCGAGCAG
CATCCCTTGTTTGACCAGAAAAGAAGGTGTTGCCGGTGGCCATGCCCCAGTAGATG
CGGCATGGCTAGGTGTTGCTTCGTCATGATAACGTGTTGATGANCGACCTCTCNAG
(SEQ ID NO:270)

Translation:

MMSKLGVLLIICLLLFPLTAVPLDGDQPAERTQIEQHPLFDQKRRCRWPCPSRCGMAR
CCFVMITC (SEQ ID NO:271)

Toxin Sequence:

Arg-Cys-Cys-Arg-Xaa4-Xaa3-Cys-Xaa3-Ser-Arg-Cys-Gly-Met-Ala-Arg-Cys-Cys-Phe-Val-Met-Ile-Thr-Cys-^ (SEQ ID NO:272)

Name: Pr3.1
Species: parius
Cloned: Yes

DNA Sequence:

GGATCCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTGTCTGCTTCTGTTTCCCC
TTACTGCTCTTCCGATGGATGGTGATCAACCTGCAGACCGACTTGTAGAGCGTATGC
AGGACAACATTTTCATCTGAGCAGCATCCCTTCTTTGAAAAGAGAAGAGGAGGCTGT
TGCACACCTCCGAAGAAATGCAAAGACCGAGCCTGCAAACCTGCACGTTGCTGCGG
CCCAGGATAACGTGTTGATGACCAACTTTCTCGCC (SEQ ID NO:273)

Translation:

MMSKLGVLLTICLLLFPLTALPMDGDQPADRLVERMQDNISSEQHPFFEKRRGGCCTPP
KKCKDRACKPARCCGPG (SEQ ID NO:274)

Toxin Sequence:

Arg-Gly-Gly-Cys-Cys-Thr-Xaa3-Xaa3-Lys-Lys-Cys-Lys-Asp-Arg-Ala-Cys-Lys-Xaa3-Ala-Arg-Cys-Cys-Gly-Xaa3-# (SEQ ID NO:275)

Name: Pr3.2
Species: parius
Cloned: Yes

5 **DNA Sequence:**

GGATCCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTGTCTGCTTCTGTTTCCCC
TTACTGCTCTTCCGATGGATGGTGATCAACCTGCAGACCGACTTGTAGAGCGTATGC
AGGACAACATTTTCATCTGAGCAGCATCCCTTCTTTGAAAAGAGAAGAGGCTGTTGC
ACACCTCCGAGGAAATGCAAAGACCGAGCCTGCAAACCTGCACGTTGTTGCGGCCC
10 AGGATAACGTGTTGATGACCAACTTTCTCGAG (SEQ ID NO:276)

Translation:

MMSKLGVLLTICLLLFPLTALPMDGDQPADRLVERMQDNISSEQHPFFEKRRGCCTPPR
KCKDRACKPARCCGPG (SEQ ID NO:277)

15 **Toxin Sequence:**

Arg-Gly-Cys-Cys-Thr-Xaa3-Xaa3-Arg-Lys-Cys-Lys-Asp-Arg-Ala-Cys-Lys-Xaa3-Ala-Arg-
Cys-Cys-Gly-Xaa3-# (SEQ ID NO:278)

20 **Name:** Ct3.1
Species: coronatus
Cloned: Yes

25 **DNA Sequence:**

GGATCCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTGTCTGCTTCTGTTTCCAA
TTACTGCCCTTCCGCTGGATGAAGATCAACCTGCAGACCGACCTGCAGAGCGTATGC
AGGACATTGCAACTGAACAGCATCCCTTGTTTGATCCCGTCAAACGGTGCTGCGATT
GGCCATGCATCCCAGGATGCACCCCTTGTTGCTTGCCTTGATAACGTGTTGATGACC
30 AACTTTCTCGAG (SEQ ID NO:279)

Translation:

MMSKLGVLLTICLLLFPTALPLDEDQPADRPAERMQDIATEQHPLFDPVKRCCDWPCIP
GCTPCCLP (SEQ ID NO:280)

35 **Toxin Sequence:**

Cys-Cys-Asp-Xaa4-Xaa3-Cys-Ile-Xaa3-Gly-Cys-Thr-Xaa3-Cys-Cys-Leu-Xaa3-^ (SEQ ID
NO:281)

40 **Name:** Ms3.1
Species: musicus
Cloned: Yes

45 **DNA Sequence:**

GGATCCATGATGTCTAAACTGGGAGTCCTGTTGACCATCTGTCTGCTTCTGTTTCCTC
TTTCTGCTCTTCCGATGGATGAAGATCAACTTGCAGACCTACCTGCAGAGCGTATGC

GGGACACTGCAACTGTAGATCATCCCTCCTATGATCCTGACAAAGCGTGCTGCGAG
CAGAGCTGTACAACATGCTTTCCGTGCTGCTAGCCTTGAACACAGTAACGTGTTGAT
GACCAACTTTCTCGAG (SEQ ID NO:282)

5 **Translation:**

MMSKLGVLITICLLLFPLSALPMDEDQLADLPAERMRTATVDHPSYDPDKACCEQSC
TTCFPCC (SEQ ID NO:283)

Toxin Sequence:

10 Ala-Cys-Cys-Xaa1-Gln-Ser-Cys-Thr-Thr-Cys-Phe-Xaa3-Cys-Cys-^ (SEQ ID NO:284)

Name: bt3b

Species: betulinus

15 **Isolated:** Yes

Toxin Sequence:

Ala-Cys-Cys-Xaa1-Gln-Ser-Cys-Thr-Thr-Cys-Met-Xaa3-Cys-Cys-^ (SEQ ID NO:285)

20

Name: bt3c

Species: betulinus

Isolated: Yes

25

Toxin Sequence:

Cys-Cys-Xaa1-Gln-Ser-Cys-Thr-Thr-Cys-Met-Xaa3-Cys-Cys-Xaa4-? (SEQ ID NO:286)

30 **Name:** Pn3.2

Species: pennaceus

Cloned: Yes

DNA Sequence:

35 GGATCCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTGTCTGCTTCTGTTTCCCC
TTACTGCTCTTCCGCTGGATGGAGATCAACCTGCATACCAAGCTGCAGAGCGTATGC
AGGCCGAGCATCATCCCTTGTTTGATCAGAAAAGACGGTGCTGCAAGTTTCCATGCC
CCGATAGTTGCAAATATTTGTGTTGCGGGTGATGATAACATGTTGATGACCAACTTT
CTTGAG (SEQ ID NO:287)

40

Translation:

MMSKLGVLITICLLLFPLTALPLDGDQPAYQAAERMQAHHPLFDQKRRCKKFPCPDS
CKYLCCG (SEQ ID NO:288)

45 **Toxin Sequence:**

Arg-Cys-Cys-Lys-Phe-Xaa3-Cys-Xaa3-Asp-Ser-Cys-Lys-Xaa5-Leu-Cys-Cys-# (SEQ ID
NO:289)

Name: Pu3.2
Species: pulicarius
Cloned: Yes

DNA Sequence:

GGATCCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTGTCTGCTTCTGTTTCCCC
TTACTGCTCTTCCGATGGATGGTGATCAACTTGCAGACCGACTTGTAGAGCGTATGC
10 AGGACAACATTTTCATCTGAGCAGCATCCCTTCTTTGATCCCGTCAAACGGTGTTGCG
TCAGCTGTTACATGGGATGCATCCCTTGTTGCTTCTAGTAATAACGTGTTGATGACC
AACTTTCTCGAG (SEQ ID NO:290)

Translation:

15 MMSKLGVLLTICLLLFPLTALPMDGDQLADRLVERMQDNISSEQHPFFDPVKRCCVSCY
MGCIPCCF (SEQ ID NO:291)

Toxin Sequence:

Cys-Cys-Val-Ser-Cys-Xaa5-Met-Gly-Cys-Ile-Xaa3-Cys-Cys-Phe-[^] (SEQ ID NO:292)

Name: Pu3.3
Species: pulicarius
Cloned: Yes

DNA Sequence:

GGATCCATGATGTCTAAACTGGGAGTCTTGTTGACCGTCTGTCTGCTTCTGTGTCCCC
TTACTGCTCTTCCACTGGATGAAGATCAACTTGCAGACCGACCTGCAGAGCGTATGC
AGGATGACACTTCAGCTGCACAGATTTTCGGGTTTGATCCCGTCAAACGGTGCTGCA
30 AATTGCTATGCTACTCGGGATGCACTCCTTGTTGCCATATTTGATAACGTGTTGATG
ACCAACTTTCTCGAG (SEQ ID NO:293)

Translation:

35 MMSKLGVLLTVCLLLCPLTALPLDEDQLADRPAERMQDDTSAAQIFGFDPVKRCCKLL
CYSGCTPCCHI (SEQ ID NO:294)

Toxin Sequence:

Cys-Cys-Lys-Leu-Leu-Cys-Xaa5-Ser-Gly-Cys-Thr-Xaa3-Cys-Cys-His-Ile-[^] (SEQ ID NO:295)

Name: Ra3.2
Species: rattus
Cloned: Yes

DNA Sequence:

GGATCCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTGTCTGCTTGTGTTTCCGC
TTACTGCTCTTCCGATGGATGGTGATCAACCTGCAGACCGACTTGTAGAGCGTATAC

AGGACAACATTTTCATCTGAGCAGCATCCCTTCTTTGAAAAGAGAAGAGGCTGTTGC
GCACCTCCGAGGAAATGCAAAGACCGAGCCTGCAAACCTGCACGTTGCTGCGGCCC
AGGATAACGTGTTGATGACCAACTTTCTCGAG (SEQ ID NO:296)

5 **Translation:**

MMSKLGVLLTICLLVFPLTALPMDGDQPADRLVERIQDNISSEQHPFFEKRRGCCAPPRK
CKDRACKPARCCGPG (SEQ ID NO:297)

Toxin Sequence:

10 Arg-Gly-Cys-Cys-Ala-Xaa3-Xaa3-Arg-Lys-Cys-Lys-Asp-Arg-Ala-Cys-Lys-Xaa3-Ala-Arg-
Cys-Cys-Gly-Xaa3-# (SEQ ID NO:298)

Name: Sm3.3

15 **Species:** stercusmuscarum

Cloned: Yes

DNA Sequence:

GGATCCATGATGTCTAAACTGGGAGTCTTGTTGACAATCTGTCTGCTTCTGTTTCCCC
20 TTATTGCTCTTCCGCTGGATGGAGATCAACCTGCAGACCGACCTGCAGAGCGTATGC
AGGACGACATTTTCATCTGAGAAGCATCCCTTGTTTGATAAGAGACAACGGTGTTC
AATGGGCGGAGGGGATGCTCCAGCAGATGGTGCAGAGATCACTCACGTTGTTGCGG
TCGACGATAACGTGTTGATGACCAACTTTCTCGAG (SEQ ID NO:299)

25 **Translation:**

MMSKLGVLLTICLLLFLIALPLDGDQPADRPAERMQDDISSEKHPLFDKRQRCCNGRR
GCSSRWCRDHSRCCGRR (SEQ ID NO:300)

Toxin Sequence:

30 Xaa2-Arg-Cys-Cys-Asn-Gly-Arg-Arg-Gly-Cys-Ser-Ser-Arg-Xaa4-Cys-Arg-Asp-His-Ser-Arg-
Cys-Cys-# (SEQ ID NO:301)

Name: Eb3.1

35 **Species:** ebraeus

Cloned: Yes

DNA Sequence:

GGATCCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTGTCTGCTTCTGTTTCCCC
40 TTAGTGCTCTTCCACTGGATGAAGGTCAACCTGCAGACCTACCTGCAGAGCGTATGC
AGGACATTGCAACTGAACAGCATCCCTTGTTTGATCCTGTCAAACGGTGTTCGAGC
AGCCATGCTACATGGGATGCATCCCTTGTTGCTTCTAATAATAACGTGTTGATGACC
AACTTTCTCGAG (SEQ ID NO:302)

45 **Translation:**

MMSKLGVLLTICLLLFLPLTALPLDEGQPADLPAERMQDIATEQHPLFDPVKRCCEQPCY
MGCIPCCF (SEQ ID NO:303)

Toxin Sequence:

Cys-Cys-Xaa1-Gln-Xaa3-Cys-Xaa5-Met-Gly-Cys-Ile-Xaa3-Cys-Cys-Phe-^ (SEQ ID NO:304)

5

Name: Eb3.2
Species: ebraeus
Cloned: Yes

10 **DNA Sequence:**

GGATCCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTGTCTGCTTCTGTTTCCCC
TTACTGCTCTTCCACTGGATGAAGATCAACCTGCAGACCTACCTGCAGAGCGTATGC
AGGACATTGCAACTGAACAGCATCCCTTGTTTGATCCTGTCAAACGGTGCTGCGCGC
AGCCATGCTACATGGGATGCATCCCTTGTTGCTTCTAATAATAACGTGTTGATGACC
15 AACTTTCTCGAG (SEQ ID NO:305)

Translation:

MMSKLGVLLTICLLLFPLTALPLDEDQPADLPAERMQDIATEQHPLFDPVKRCCAQPCY
MGCI PCCF (SEQ ID NO:306)

20

Toxin Sequence:

Cys-Cys-Ala-Gln-Xaa3-Cys-Xaa5-Met-Gly-Cys-Ile-Xaa3-Cys-Cys-Phe-^ (SEQ ID NO:307)

25

Name: Fd3.2
Species: flavidus
Cloned: Yes

DNA Sequence:

30 GGATCCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTGTCTGCTTCTGTTTCCCC
TTACTGCTGTTCCGTTGGATGGAGATCAACCTGCAGACCAGCCTGCAGAGCGTATGC
AGAACGAGCAGCATCCCTTGTTTGATCAGAAAAGAAGGTGCTGCCGGTGGCCATGC
CCCAGTATATGCGGCATGGCTAGGTGTTGCTCGTCATGATAACGTGTTGATGACCAA
CTTTCTCGAG (SEQ ID NO:308)

35

Translation:

MMSKLGVLLTICLLLFPLTAVPLDGDQPADQPAERMQNEQHPLFDQKRRCCRWP C PSIC
GMARCCSS (SEQ ID NO:309)

40

Toxin Sequence:

Arg-Cys-Cys-Arg-Xaa4-Xaa3-Cys-Xaa3-Ser-Ile-Cys-Gly-Met-Ala-Arg-Cys-Cys-Ser-Ser-^
(SEQ ID NO:310)

45

Name: Mf3.1
Species: miliaris
Cloned: Yes

DNA Sequence:

GGATCCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTGTCTGCTTCTGTTTCCAA
TTACTGCCCTTCCACTGGATGAAGATCAACCTGCAGACCGACCTGCAGAGCGTATGC
5 AGGACATTGCAACTGAACAGCATCCCTTGTTTGATCCCGTCAAACGGTGTTGCGATT
GGCCATGCAGCGCAGGATGCTACCCTTGTTGCTTCCCTTAATAACGTGTTGATGACC
AACTNANGNAAAAAAAA (SEQ ID NO:311)

Translation:

10 MMSKLGVLLTICLLLPITALPLDEDQPADRP AERMQDIATEQHPLFDPVKRCCDWPCS
AGCYPCCFP (SEQ ID NO:312)

Toxin Sequence:

15 Cys-Cys-Asp-Xaa4-Xaa3-Cys-Ser-Ala-Gly-Cys-Xaa5-Xaa3-Cys-Cys-Phe-Xaa3-^ (SEQ ID
NO:313)

Name: Mf3.2
Species: miliaris
20 **Cloned:** Yes
Notes:

DNA Sequence:

GGATCCATGATGTCTAAACTGGGAGTGGTGCCATTCGTCTTTCTGGTCCTGTTTCCCC
25 TGGCAACACTCCAACCTGGATGCAGATCAACCTGCAGACCGACCTGCGCGTAAAAAG
GGCATTGCAACTAAACGGCATCCCTTGCTCTGATCCTGTCAGAGGGTGTTGCCCTCCA
ATGTGCACACCATGCTTCCCTTGCTGTTTTTCGTTAATAACGTGTTGATGNATGATGN
AN (SEQ ID NO:314)

Translation:

30 MMSKLGVPFVFLVLFPLATLQLDADQPADRPARKKGIATKRHPLSDPVRGCCPPMCTPCFPCC
FR (SEQ ID NO:315)

Toxin Sequence:

35 Gly-Cys-Cys-Xaa3-Xaa3-Met-Cys-Thr-Xaa3-Cys-Phe-Xaa3-Cys-Cys-Phe-Arg-^ (SEQ ID
NO:316)

Name: Af3.1
40 **Species:** ammiralis
Cloned: Yes

DNA Sequence:

CAAGAGGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTG
45 TCTGCTTCTGTTTCCCCTTACTGCTCTTCCGCTGGATGGAGATCAACCTGCAGACCA
AGCTGCAGAGCGTATGCAGGCCGAGCAGCATCCCTTGTTTGATCAGAAAAGACGGT
GTTGCAGGTTTCCATGCCCCGATACTTGCAGACATTTGTGTTGCGGGTGATGATAAC

GTGCTGATGACCCACTTTGTCATCACGGCTACGTCAAGTGTCTAATGAATAAGTAAA
ATGATTGCAGT (SEQ ID NO:317)

Translation:

5 MMSKLGVLLTICLLLFPLTALPLDGDQPADQAAERMQAEQHPLFDQKRRCCRFPCPD
T
CRHLCCG (SEQ ID NO:318)

Toxin Sequence:

10 Arg-Cys-Cys-Arg-Phe-Xaa3-Cys-Xaa3-Asp-Thr-Cys-Arg-His-Leu-Cys-Cys-# (SEQ ID
NO:319)

Name: Af3.2

Species: ammiralis

15 **Cloned:** Yes

DNA Sequence:

CAAGAGGGATCGATAGCAGTTCATGATGTTTAAACTGGGAGTCTTGCTGACCATCTG
TCTACTTCTGTTTTCCCTTAATGCTGTTCCGCTGGATGGAGATCAACCTGCAGACCA
20 ACCTGCAGAGCGTCTGCTGGACGACATTCATCTGAAAATAATCCCTTTATGATCC
CGCCAAACGGTGTTCATGACTTGCTTCGGTTGCACACCTTGTTGTGGATGACCAGC
CTCATCAAGTGTCTAACGAATAAGTAAAACGATTGCAGT (SEQ ID NO:320)

Translation:

25 MMFKLGVLLTICLLLFSLNAVPLDGDQPADQPAERLLDDISSENNPFYDPAKRCCMTCF
GCTPCCG (SEQ ID NO:321)

Toxin Sequence:

30 Cys-Cys-Met-Thr-Cys-Phe-Gly-Cys-Thr-Xaa3-Cys-Cys-# (SEQ ID NO:322)

Name: Af3.3

Species: ammiralis

35 **Cloned:** Yes

DNA Sequence:

CAAGAAGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGCCTTGTTGACCATCT
GTCTACTTCTGTTTTCCCTTACTGCTGTTCCGCTGGATGGAGATCAACATGCAGACC
AACCTGCAGAGCGTCTGCAGGACCGCCTTCCAACCTGAAAATCATCCCTTATATGATC
40 CCGTCAAACGGTGTTCGATGATTGCGAATGCGACTATTCTTGCTGGCCTTGCTGTA
TTTTTTCATAACCTTTGTTATCGCGGCCTCATCCTAGTGTCAAATGAATAAGTAAAA
CGATTGCAGT (SEQ ID NO:323)

Translation:

45 MMSKLGALLTICLLLFSLTAVPLDGDQHADQPAERLQDRLPTENHPLYDPVKRCCDDSE
CDYSCWPCCIFS (SEQ ID NO:324)

Toxin Sequence:

Cys-Cys-Asp-Asp-Ser-Xaa1-Cys-Asp-Xaa5-Ser-Cys-Xaa4-Xaa3-Cys-Cys-Ile-Phe-Ser-^ (SEQ ID NO:325)

Name: Af3.4
Species: ammimalis
Cloned: Yes

DNA Sequence:

CAAGAGGGATCGATAGCAGTTCATGATGTTTAAACTCGGAGTCTTGCTGACCATCTG
TCTACTTCTGTTTTCCCTAATtGCTGTTCCGCTGGATGGAGATCAACATGCAGACCAA
CCTGCAGAGCGTCTGCAGGACCGCCTTCCAACCTGAAAATCATCCCTTATATGATCCC
GTCAAACGGTGTGTCAGGTTGTTATGCCTCAGTTGCAACCCTTGTTGTGGATGACCA
GCTTTGTTATCACGGCCTCATCAAGTGTCTAATGAATAAGTAAAACGATTGCAGT
(SEQ ID NO:326)

Translation:

MMFKLGVLLTICLLLFSLIAVPLDGDQHADQPAERLQDRLPTENHPLYDPVKRCCRLLC
LSCNPCCG (SEQ ID NO:327)

Toxin Sequence:

Cys-Cys-Arg-Leu-Leu-Cys-Leu-Ser-Cys-Asn-Xaa3-Cys-Cys-# (SEQ ID NO:328)

Name: Af3.6
Species: ammimalis
Cloned: Yes

DNA Sequence:

CAAGAAGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGCCTTGTTGACCATCT
GTCTACTTCTGTTTTCCCTTACTGCTGTTCCGCTGGATGGAGATCAACATGCAGACC
AACCTGCAGAGCGTCTGCAGGACCGCATTCCAACCTGAAGATCATCCCTTATTTGATC
CCAACAAACGGTGTGTCGATGATTTCGGAATGCGGCTATTCATGCTGGCCTTGCTGTT
ATGGATAAGCTTTGTTATCGCGGCCTCATCCAGTGTCAACGAATAAGTAAAACGATT
GCAGT (SEQ ID NO:329)

Translation:

MMSKLGALLTICLLLFSLTAVPLDGDQHADQPAERLQDRIPTEHDHPLFDPNKRCCDDSE
CGYSCWPCCYG (SEQ ID NO:330)

Toxin Sequence:

Cys-Cys-Asp-Asp-Ser-Xaa1-Cys-Gly-Xaa5-Ser-Cys-Xaa4-Xaa3-Cys-Cys-Xaa5-# (SEQ ID NO:331)

Name: Sf3.1
Species: spurius
Cloned: Yes

5 **DNA Sequence:**

CAAGAAGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGCTGACCATCT
GTCTGCTTCTGTTTCCACGTA CTCTCTTCCGCTGGATGGAGATCAACCTGCAGTCCG
ATCTGCAAAGCGTATGCATTCATCTATACAGCGTCGTTTCTTTGATCCCGTCAAACG
GTGTTGCCCTAGATGCAGCGAGTGCAACCCTTGTTGTGGATGACCAGCTTTGTCATC
10 GCGGCCTCATTAAGTGTCTAATGAATAAGTAAAATGATTGCAGT (SEQ ID NO:332)

Translation:

MMSKLGVLLTICLLLFPR TSLPLDGDQPAVRSAKRMHSSIQRFFDPVKRCCPRCSECNP
15 CCG (SEQ ID NO:333)

Toxin Sequence:

Cys-Cys-Xaa3-Arg-Cys-Ser-Xaa1-Cys-Asn-Xaa3-Cys-Cys-# (SEQ ID NO:334)

20 **Name:** Om3.1
Species: omaria
Cloned: Yes

DNA Sequence:

25 CAAGAGGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTCGTTGACCATCT
GTCTACTTCTATTTTCCCTTACTGCTGTTCCGCTTGATGGAGATCAACATGCAGACCA
ACCTGCAGAGCGTCTGCAGGGCGACATTTTATCTGAAAAGCATCCCTTATTTAATCC
CGTCAAACGGTGTTGCGATGAGGAAGAATGCAGCAGTGCATGCTGGCCTTGTTGTT
GGGGGTGATCAGCTTTGTTATCGCGGCCTCATCAAGTGTCTAATGAATAAGTAAAAT
30 GATTGCAGT (SEQ ID NO:335)

Translation:

MMSKLGVS LTICLLLFSLTAVPLDGDQHADQPAERLQGDILSEKHPLFNPVKRCCDEEE
35 CSSACWPCCWG (SEQ ID NO:336)

Toxin Sequence:

Cys-Cys-Asp-Xaa1-Xaa1-Xaa1-Cys-Ser-Ser-Ala-Cys-Xaa4-Xaa3-Cys-Cys-Xaa4-# (SEQ ID
NO:337)

40 **Name:** Om3.2
Species: omaria
Cloned: Yes

45 **DNA Sequence:**

CAAGAAGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGATCATCTG
TCTACTTCTGTGTCCCTTACTGCTGTTCTGGAGGATGGAGATCAACCTGCAGACCG

ACCTGCAGAGCGTATGCAGGACGACATTTCAACTGAGCATCATCCCTTTTATGATCC
CGTCAAACGGTGTGCAAGTACGGGTGGACATGCTTGCTAGGATGCACTCCTTGTGA
TTGTTGACCAGTTTTGTTATCGCGGCCTCGTCAAGTGTCTAATGAATAAGTAAAACG
ATTGCAGT (SEQ ID NO:338)

5

Translation:

MMSKLGVLLIICLLLCPLTAVLEDGDQPADRPAERMQDDISTEHPFYDPVKRCCKYG
WTCLLGCTPCDC (SEQ ID NO:339)

10 **Toxin Sequence:**

Cys-Cys-Lys-Xaa5-Gly-Xaa4-Thr-Cys-Leu-Leu-Gly-Cys-Thr-Xaa3-Cys-Asp-Cys-[^] (SEQ ID NO:340)

15 **Name:** Om3.3
Species: omaria
Cloned: Yes

DNA Sequence:

20 CAAGAGGGATCGATAGCAGTTCATGATGTCTATACTGGGAGTCTTGTTGATCATCTG
TCTACTTCTGTGTCCCCTTACTGCTGTTCTGGAGGATGGAGATCAACCTGCAGACCG
ACCTGCAGAGCGTATGCAGGACGGCATTTCATCTGAACATCATCCCTTTTTGGATCC
CGTCAAACGGTGTGTCATCTATTGGCATGCCGCTTTGGATGCTCGCCTTGTTGTTG
GTGACCAGCTTTGTTATCGCGGCCTCATCAAGTGTCTAATGAATAAGTAAAACGATT
25 GCAGT (SEQ ID NO:341)

Translation:

MMSILGVLLIICLLLCPLTAVLEDGDQPADRPAERMQDGISSEHHPFLDPVKRCCHLLAC
RFGCSPCCW (SEQ ID NO:342)

30

Toxin Sequence:

Cys-Cys-His-Leu-Leu-Ala-Cys-Arg-Phe-Gly-Cys-Ser-Xaa3-Cys-Cys-Xaa4-[^] (SEQ ID NO:343)

35 **Name:** Om3.4
Species: omaria
Cloned: Yes

DNA Sequence:

40 CAAGAAGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGATCATCTG
TCTACTTCTTTGTCCCCTTACTGCTGTTCCGCAGGATGGAGATCAACCTGCAGACCG
ACCTGCAGAGCGTATGCAGGGCGGCATTTCATCTGAACATCATCCCTTTTTTGGATCC
CGTCAAACGGTGTGTCAGGTACGGGTGGACATGCTGGCTAGGATGCACTCCCTGTG
GTTGTTGACCAGCTTTGTTATCGCGGCCTCATCAAGTGTCTAATGAATAAGTAAAAC
45 GATTGCAGT (SEQ ID NO:344)

Translation:

MMSKLGVLLIICLLLCPLTAVPQDGDQPADRPAERMQGGISSEHHPFFDPVKRCCRYGW
TCWLGCTPCGC (SEQ ID NO:345)

Toxin Sequence:

5 Cys-Cys-Arg-Xaa5-Gly-Xaa4-Thr-Cys-Xaa4-Leu-Gly-Cys-Thr-Xaa3-Cys-Gly-Cys-^ (SEQ ID NO:346)

Name: Ep3.1

10 **Species:** episcopatus

Cloned: Yes

DNA Sequence:

CAAGAAGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTG
15 TCTACTTCTGTTTTCCCTTATTGCTGTTCCGCTTGATGGAGATCAACATGCAGACCAA
CCTGCAGAGCGTCTGCAGGGCGACATTTTATCTGAAAAGCATCCCTTATTTATGCCT
GTCAAACGGTGTGCGATGAGGACGAATGCAACAGTTCATGCTGGCCTTGTTGTTGG
GGGTGATCAGCTTTGTTATCGCGGCCTGATCAAGTGTATAATGAATAAGTAAAACG
ATTGCAGT (SEQ ID NO:347)

20

Translation:

MMSKLGVLLTICLLLFSLIAVPLDGDQHADQPAERLQGDILSEKHPLFMPVKRCCDEDE
CNSSCWPCWG (SEQ ID NO:348)

25 **Toxin Sequence:**

Cys-Cys-Asp-Xaa1-Asp-Xaa1-Cys-Asn-Ser-Ser-Cys-Xaa4-Xaa3-Cys-Cys-Xaa4-# (SEQ ID NO:349)

30 **Name:** Ep3.2

Species: episcopatus

Cloned: Yes

DNA Sequence:

35 CAAGAGGGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTG
TCTACTTCTGTTTTCCCTTATTGCTGTTCCGCTTGATGGAGATCAACATGCAGACCAA
CCTGCAGAGCGTCTGCAGGGCGACATTTTATCTGAAAAGCATCCCTTATTTATGCCT
GTCAAACGGTGTGCGATGAGGACGAATGCAGCAGTTCATGCTGGCCTTGTTGTTGG
GGATGAGCAGCTTTGTTATCGCGGCCTCATCAAGTGTCTAATGAATAAGTAAAACG
40 ATTGCAGT (SEQ ID NO:350)

45 **Translation:**

MMSKLGVLLTICLLLFSLIAVPLDGDQHADQPAERLQGDILSEKHPLFMPVKRCCDEDE
CSSSCWPCCWG (SEQ ID NO:351)

Toxin Sequence:

Cys-Cys-Asp-Xaa1-Asp-Xaa1-Cys-Ser-Ser-Ser-Cys-Xaa4-Xaa3-Cys-Cys-Xaa4-# (SEQ ID NO:352)

5 **Name:** Ep3.3
 Species: episcopatus
 Cloned: Yes

DNA Sequence:

10 CAAGAGGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTG
 TCTACTTCTGTTTTCCCTTACTGCTGTTCCGCTTGATGGAGATCAACATGCAGACCAA
 CCTGCAGAGCGTCTGCAGGGCGACATTTTATCTGAAAAGCATCCCTTATTTAATCCC
 GTCAAACGGTGTGCCCCGGCGGCGGCATGTGCCATGGGATGCAAGCCTTGTTGTGG
 ATGAGCAGCTTTGTTATCGTGGCCTCATCAAGTGTCTAATGAATAAGTAAAACGATT
15 GCAGT (SEQ ID NO:353)

Translation:

MMSKLGVLLTICLLLFSLTAVPLDGDQHADQPAERLQGDILSEKHPLFNPVKRCCPAAA
CAMGCKPCCG (SEQ ID NO:354)

20

Toxin Sequence:

Cys-Cys-Xaa3-Ala-Ala-Ala-Cys-Ala-Met-Gly-Cys-Lys-Xaa3-Cys-Cys-# (SEQ ID NO:355)

25 **Name:** Au3.2
 Species: aulicus
 Cloned: Yes

DNA Sequence:

30 CAAGAGGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTG
 TCTGCTTCTGTTTTCCGTTACTGCTCTTCCGCCGGATGGAGATCAACCTGCAGACCG
 AGCTGCAGAGCGTAGGCAGGTCGAGCAGCATCCCGTGTTTGATCATGAAAGAGGGT
 GTTGCTCGCCACCATGCCACAGTATTTGCGCTGCTTTCTGTTGCGGGTGATGATAAC
 GTGTTGATGACCCACTTTGTCATCACGGCTGCGTCAAGTGTCTAATGAATAAGTAAA
35 ATGATTGCAGT (SEQ ID NO:356)

Translation:

MMSKLGVLLTICLLLF SVTALPPDGDQPADRAAERRQVEQHPVFDHERGCCSPPCHSIC
AAFCCG (SEQ ID NO:357)

40

Toxin Sequence:

Gly-Cys-Cys-Ser-Xaa3-Xaa3-Cys-His-Ser-Ile-Cys-Ala-Ala-Phe-Cys-Cys-# (SEQ ID NO:358)

45 **Name:** Au3.3
 Species: aulicus
 Cloned: Yes

DNA Sequence:

CAAGAGGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTG
TCTACTTCTGTTTTCCCTTACTGCTGTTCCGCTTGATGGAGATCAACATGCAGACCAA
5 CCTGCAGAGCGTCTGCAGGGCGACATTTTATCTGAAAAGCATCCCTTATTTAATCCC
GTCAAACGGTGTGCGGACCGGTGGCATGTGCCATGGGATGCAAGCCTTGTTGTGG
ATGAGCAGCTTTGTTATCGTGGCCTCATCAAGTGTCTAATGAATAAGTAAAATGATT
GCAGT (SEQ ID NO:359)

Translation:

MMSKLGVLLTICLLLFSLTAVPLDGDQHADQPAERLQGDILSEKHPLFNPVKRCCRPVA
CAMGCKPCCG (SEQ ID NO:360)

Toxin Sequence:

15 Cys-Cys-Arg-Xaa3-Val-Ala-Cys-Ala-Met-Gly-Cys-Lys-Xaa3-Cys-Cys-# (SEQ ID NO:361)

Name: Au3.4
Species: aulicus
20 **Cloned:** Yes

DNA Sequence:

CAAGAGGGATCGATAGCAGTTCaTGATGTCTAAACTGGGAGTCTTGTTGATCATCTG
TCTACTTCTGTCTCCCCCTTACTGCTGTTCCGCTGGATGGAGATCAACCTGCAGACCG
25 ACCTGCAGAGCGTATGCAGGACGACATTTTCATCTGAACATCAACCCATGTTTGATGC
CATCAGACAGTGTTGCCCCGGCGGTGGCATGCGCCATGGGATGCGAGCCTTGTTGTG
GATGACCAGCTTTGTTATCGCGGCCTCATCAAGTGTCTAATGAATAAGTAAAATGAT
TGCAGT (SEQ ID NO:362)

Translation:

30 MMSKLGVLLIICLLLSPLTAVPLDGDQPADRP AERMQDDISSEHQPMFDAIRQCCPAVA
CAMGCEPCCG (SEQ ID NO:363)

Toxin Sequence:

35 Xaa2-Cys-Cys-Xaa3-Ala-Val-Ala-Cys-Ala-Met-Gly-Cys-Xaa1-Xaa3-Cys-Cys-# (SEQ ID
NO:364)

Name: Ae3.1
40 **Species:** aureus
Cloned: Yes

DNA Sequence:

45 CAAGAAGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGCCTTGTTGACCATCT
GTCTACTTCTGTTTTCCCTTACTGCTGTTCCGCTGGATGGAGATCAACATGCAGACC
AACATGCAGAGCGTCTGCATGACCGCCTTCCAAGTAAAATCATCCCTTATATGATC
CCGTCAAACGGTGTGCGATGATTGGAATGCGACTATTCTTGCTGGCCTTGCTGTA

TTTTTGGATAACCTTTGTTATCGCGGCCTCATCAAGTGTCAAATGAATAAGTAAAC
GATTGCAGT (SEQ ID NO:365)

Translation:

5 MMSKLGALLTICLLLFSLTAVPLDGDQHADQHAERLHDRLPTENHPLYDPVKRCCDDS
ECDYSCWPCCIFG (SEQ ID NO:366)

Toxin Sequence:

10 Cys-Cys-Asp-Asp-Ser-Xaa1-Cys-Asp-Xaa5-Ser-Cys-Xaa4-Xaa3-Cys-Cys-Ile-Phe-# (SEQ ID
NO:367)

Name: Ae3.2

Species: aureus

15 **Cloned:** Yes

DNA Sequence:

CAAGAGGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGCCTTGTTGACCATCT
GTCTACTTCTGTTTTCCCTAACTGCTGTTCCGCTGGATGGAGATCAACATGCAGACC
20 AACCTGCAGAGCGTCTGCAGGACCGCATTCCAACCTGAAAATCATCCCTTATTTGATC
CGAACAAACGGTGTTGCAATGATTGGAATGCGACGATTCATGCTGGCCTTGCTGTT
ATGGATAACCTTTGTTATCGCGGCCTCATCAAGTGTCAAATGAATAAGTAAAACGAT
TGCAGT (SEQ ID NO:368)

Translation:

25 MMSKLGALLTICLLLFSLTAVPLDGDQHADQPAERLQDRIPTENHPLFDPNKRCCNDWE
CDDSCWPCCYG (SEQ ID NO:369)

Toxin Sequence:

30 Cys-Cys-Asn-Asp-Xaa4-Xaa1-Cys-Asp-Asp-Ser-Cys-Xaa4-Xaa3-Cys-Cys-Xaa5-# (SEQ ID
NO:370)

Name: Cn3.1

35 **Species:** consors

Cloned: Yes

DNA Sequence:

CAAGAGGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTG
40 TTTGCTTCTGTTTCCCCTTACTGCTCTTCCAATGGATGGAGATCAATCTGTAGACCGA
CCTGCAGAGCGTATGCAGGACGACATTTTCATCTGAGCTGCATCCCTTGTTCAATCAG
AAAAGAATGTGTTGCGGCGAAGGTGCGCCATGCCCCAGCTATTTTCAGAAACAGTCA
GATTTGTCATTGTTGTTAAATGACAACGTGTCGATGACCAACTTCGTTATCACGACT
AATGAATAAGTAAAATGATTGCAGT (SEQ ID NO:371)

45

Translation:

MMSKLGVLLTICLLLFPLTALPMDGDQSVDRPAERMQDDISSELHPLFNQKRMCCGEG
APCPSYFRNSQICHCC (SEQ ID NO:372)

Toxin Sequence:

5 Met-Cys-Cys-Gly-Xaa1-Gly-Ala-Xaa3-Cys-Xaa3-Ser-Xaa5-Phe-Arg-Asn-Ser-Gln-Ile-Cys-His-
Cys-Cys-^ (SEQ ID NO:373)

Name: Cn3.3

10 **Species:** consors

Cloned: Yes

DNA Sequence:

TAAGAGGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTG
15 TCTGCTTCTGTTTCCCCTTATTGCTCTTCCAATGGATGGAGATCAACCTGCAGACCGA
CCTGCAGAGCGTATGCAGGACGACATTTTCATCTCAGCAGCATCCCTTGTTTGATAAG
AGAGGCCGCTGTTGCGATGTGCCGAACGCATGCTCCGGCAGATGGTGCAGAGATCA
CGACAATGTTGCGGATGACGATAACGTGTTGATGACCAACTTTGTGATCACGGCTA
CATCAAGTGAATAAGTAAAACGATTGCAGT (SEQ ID NO:374)

Translation:

MMSKLGVLLTICLLLFPLIALPMDGDQPADRPAERMQDDISSQQHPLFDKRGRCCDVPN
ACSGRWCRDHAQCCG (SEQ ID NO:375)

Toxin Sequence:

25 Gly-Arg-Cys-Cys-Asp-Val-Xaa3-Asn-Ala-Cys-Ser-Gly-Arg-Xaa4-Cys-Arg-Asp-His-Ala-Gln-
Cys-Cys-# (SEQ ID NO:376)

30 **Name:** Cn3.4

Species: consors

Cloned: Yes

DNA Sequence:

35 CAAGAGGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGACTGTCTG
TTTGCTTCTGTTTCCCCTTACTGCTCTTCCGATGGATGGAGATCAACCTGCAGACCAA
CCTGCAGAGCGTATGCAGGACGACATTTTCATCTGAGCAGCATCCCTTGTTTGATAAG
AGACAAAGGTGTTGCACTGGGAAGAAGGGGTCATGCTCCGGTAAAGCATGCAAAA
GTCTCAAATGTTGCTCTGGACGATAACGTGTTGATGACCAACTTTGTTATCACGGCT
40 ACGTCAAGTGTCTAGTGAATAAGTAAAACGATTGCAGT (SEQ ID NO:377)

Translation:

MMSKLGVLLTVCLLLFPLTALPMDGDQPADQPAERMQDDISSEQHPLFDKRQRCCTGK
KGSCSGKACKSLKCCSGR (SEQ ID NO:378)

Toxin Sequence:

Xaa2-Arg-Cys-Cys-Thr-Gly-Lys-Lys-Gly-Ser-Cys-Ser-Gly-Lys-Ala-Cys-Lys-Ser-Leu-Lys-Cys-Cys-Ser-# (SEQ ID NO:379)

5 **Name:** Em3.1
Species: emaciatus
Cloned: Yes

DNA Sequence:

10 CAAGAGGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGCTGACCATCTGTCTGCTTCTGTT
 TCCCTTACTGTTCTTCCGATGGATGGAGATCAACCTGCAGACCTACCTGCATTGCGTGCGCAGTTCTT
 TGCACCTGAACATAGTCCCCGGTTTGACCCCGTCAAAACGGTGCTGCTCGCGGGATTGCAGTGTTCAT
 CCCTTGTTGCCCGTATGGATCACCTTGATTATTGCGGCCACGTCAAGTGTCTAATGAATAAGTAAATG
 ATTGCAGT (SEQ ID NO:380)

Translation:

15 MMSKLGVLITICLLFPLTVLPMDGDQPADLPALRAQFFAPEHSPRFPVKRCCSRDCSVCIPCCPYGSP
 (SEQ ID NO:381)

Toxin Sequence:

20 Cys-Cys-Ser-Arg-Asp-Cys-Ser-Val-Cys-Ile-Xaa3-Cys-Cys-Xaa3-Xaa5-Gly-Ser-Xaa3-^ (SEQ
 ID NO:382)

25 -----
 Where:

Xaa1 is Glu or γ -carboxy-Glu

Xaa2 is Gln or pyro-Glu

Xaa3 is Pro or hydroxy-Pro

30 Xaa4 is Trp or bromo-Trp

Xaa5 is Tyr, ¹²⁵I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

^ is free carboxyl or amidated C-terminus, preferably free carboxyl

is free carboxyl or amidated C-terminus, preferably amidated

? = Status of C-term not known.

TABLE2

Alignment of μ -Conopeptides (SEQ ID NO:)

TYPE 1

40	A3.4 (F283)	---CCKVQ-CES--C---TPCC^ (383)
	Ak3.1 (F585)	---CCELP-CGPGFC---VPCC^ (384)
	Ar3.1	---CCERP-CNIG-C---VPCC^ (385)
	Bn3.1 (F586)	---CCNWP-CSMG-C---IPCCYY^ (386)
	Bt3.1	---CCELP-CH-G-C---VPCCWP^ (387)
45	Bt3.2	---CCGLP-CN-G-C---VPCCWPS^ (388)
	Bt3.3	---CCSRN-CAV--C---IPCCPNWPA^ (389)
	bt3a	---CCKQS-CTT--C---MPCCW^ (390)

	bt3b	--ACCXQS-CTT--C---MPCC^ (391)
	bt3c	---CCEQS-CTT--C---MPCCW? (392)
	Ca3.3	R--CCRYP-CPDS-C--HGSCCYK^ (393)
	Ca3.4	---CCPPVACNMG-C---KPCC# (394)
5	Ca3.5	---CCDDSECDYS-C---WPCCMF# (395)
	Ca3.6 (F349)	---CCRR--CYMG-C---IPCCF^ (396)
	Circling	---CCPPVACNMG-C---KPCCG^ (397)
	Comatose/Death	SKQCCHLAACRFG-C---TOCCN^ (398)
	Cp3.1 (F594)	S--CCR--DCGED-C---VGCCR^ (399)
10	Ct3.1 (Z726)	---CCDWP-CIPG-C---TPCCLP^ (400)
	Da3.1	---CCDDSECDYS-C---WPCCILS^ (401)
	Da3.2	Z-QCCPPVACNMG-C---EPCC# (402)
	Da3.3	---CCNAGFCRFG-C---TPCCW^ (403)
	Di3.1	Z--CCVHP-C-P--C---TPCCR^ (404)
15	Fi3.1	---CCPWP-CNIG-C---VPCC^ (405)
	Fi3.2	---CCSKN-CAV--C---IPCCP^ (406)
	Fi3.3	---CCRWP-CP-ARC---GSCCL^ (407)
	Fi3.4	---CCELSRCL-G-C---VPCCTS^ (408)
	Fi3.5	---CCELSKCH-G-C---VPCCIP^ (409)
20	Ge3.1 (F590)	Z--CCTF--CNFG-C---QPCCVP^ (410)
	Ge3.2 (F343/Z734)	Z--CCTF--CNFG-C---QPCCLT^ (411)
	Ge3.3 (F590)	Z--CCTF--CNFG-C---QPCCVP^ (412)
	Gm3.1	---CCDDSECDYS-C---WPCCMF# (413)
	Gm3.2	G--CCHLLACRFG-C---SPCCW^ (414)
25	Gm3.3	---CCSWDVCDHPSC---T-CCG# (415)
	La3.1	---CCDWP-CS-G-C---IPCC^ (416)
	Lp3.1 (F340)	ZINCCPWP-CPST-C--RHQCCH^ (417)
	Lv3.1 (F341)	ZINCCPWP-CPDS-C--HYQCCH^ (418)
	Mr3.2	---CCRLS-CGLG-C---HPCC# (419)
30	Mr3.3	--ECCGSFACRFG-C---VPCCV^ (420)
	Mr3.4	SKQCCHLPAACRFG-C---TPCCW^ (421)
	Mr3.5 (F286)	-MGCCPFP-CKTS-C--TTLCC# (422)
	Ms3.1 (Z738)	--ACCEQS-CTT--C---FPCC^ (423)
	Nb3.1 (F87)	---CCELP-CGPGFC---VPCC^ (424)
35	Pu3.1 (F339)	---CCN-S-CYMG-C---IPCCF^ (425)
	Qc3.1 (F342)	ZR-CCQWP-CPGS-C---RCCRT# (426)
	Qc3.2	ZR-CCRWP-CPGS-C---RCCRYR^ (427)
	Qc3.3	R--CCRYP-CPDS-C--HGSCCYK^ (428)
	QcIIIA	---CCSQD-CLV--C---IOCCPN# (429)
40	QcIIIB	---CCSRH-CWV--C---IOCCPN? (430)
	Ra3.1 (F351)	Z-TCCS-N-CGED-C---DGCCQ^ (431)
	Scratcher I	---CCR-T-C-FG-C---TOCC# (433)
	Ts3.1 (F592)	---CCH-K-CYMG-C---IPCCI^ (434)
	Ts3.2 (F345)	K--CCRPP-CAMS-C-GMARCCY^ (435)
45	Bt3.5 (Z495)	R--CCRWP-CPSI-C-GMARCCFVMITC^ (436)
	Bt3.6 (Z497)	R--CCRWP-CP-SRC-GMARCCFVMITC^ (437)
	Tx3.1	F--CCDSNWCHISDC---ECCY# (438)

	U014	---CCHWNWCDHL-C---SCCGS^ (439)
	U017	--DCCOLPACPGF-C---NOCC# (440)
	U019	---CCAPSACRLG-C---ROCCR^ (441)
	U020	---CCAOSACRLG-C---ROCCR^ (442)
5	U022	---CCAPSACRLG-C---RPCCR^ (443)
	U024	--GCCGSFACRFG-C---VOCCV^ (444)
	U031	---CCSWDVCDHPSC---TCC# (445)
	U032 (F353)	R--CCKFP-CPDS-C--RYLCC# (446)
	Ae3.1	---CCDDSECDYS-C---WPCCIF# (447)
10	Ae3.2	---CCNDWECDDS-C---WPCCY# (448)
	Af3.1	R--CCR-FPCPDT-C---RHLCC# (449)
	Af3.2	---CC--MTC-FG-C---TPCC# (450)
	Af3.3	---CCDDSECDYS-C---WPCCIFS^ (451)
	Af3.4	---CCR-LLC-LS-C---NPCC# (452)
15	Af3.6	---CCDDSECGYS-C---WPCCY# (453)
	Au3.2	G--CCS-PPCHSI-C--AAFCC# (454)
	Au3.3	---CCRPVACAMG-C---KPCC# (455)
	Au3.4	Z--CCPAVACAMG-C---EPCC# (456)
	Em3.1	---CCS-RDC-SV-C---IPCCPYGSP^ (457)
20	Ep3.1	---CCDEDECNSS-C---WPCCW# (458)
	Ep3.2	---CCDEDECSSS-C---WPCCW# (459)
	Ep3.3	---CCPAAACAMG-C---KPCC# (460)
	Om3.1	---CCDEEECSSA-C---WPCCW# (461)
	Om3.3	---CCHLLACRFG-C---SPCCW^ (462)
25	Sf3.1	---CC--PRC-SE-C---NPCC# (463)

TYPE 2

30	Pn3.2 (AA049)	-RCC--KFP-CPDS-C--KYLCC# (464)
	Fd3.2 (Z831)	-RCC--RWP-CPSI-C-GMARCCSS^ (465)
	Pu3.3 (AA405)	--CC--KLL-CYSG-C---TPCCHI^ (466)
	Eb3.1 (Z821)	--CC--EQP-CYMG-C---IPCCF^ (467)
	Eb3.2 (Z822)	--CC--AQP-CYMG-C---IPCCF^ (468)
35	Pu3.2 (AA403)	--CC--V-S-CYMG-C---IPCCF^ (469)
	Mf3.1 (Z882)	--CC--DWP-CSAG-C---YPCCFP^ (470)
	Mf3.2 (Z885)	-GCC--PPM-C-TP-C---FPCCFR^ (471)
	Ra3.2 (AA414)	RGCCAPPRK-CKDRACK-PARCCGP# (472)
	Sm3.3 (AA419)	ZRCCNGRRG-CSSRWCRDHSRCC# (473)
40	Cn3.3	GRCCDVPNA-CSGRWCRDHAQCC# (474)
	Cn3.4	ZRCCTGKKGSCSGKACKSL-KCCS# (475)

TYPE 3

45	A3.1	-MCCGEGRKCPYSYFRNSQICHCC^ (476)
	A3.2 (F84)	--CCR--WPCPRQIDGEY-CGCCCL# (477)
	Bu3.5	-RCCGEGLTCPRYWKNSQICACC^ (478)
	Ca3.1	--CCGPGGSCPVEYFRDNFICGCC^ (479)

	Cr3.1	RKCCGKDGPCPKYFKDNFICGCC^ (480)
	E3.1	--CCS--WPCPRYSNGKLVCFCL# (481)
	M3.2	--CCGPGGSCPVEYFRDNFICGCC^ (482)
	M3.3	-MCCGESAPCPSYFRNSQICHCC^ (483)
5	M3.4	ZKCCGPGGSCPVEYFTDNFICGCC^ (484)
	M3.5	ZKCCGPGGSCPVEYFRDNFICGCC^ (485)
	S3.1	ZKCCGEGSSCPKYFKNNFICGCC^ (486)
	U001	ZKCCS--GGSCPLYFRDRLICPC^ (487)
	U034	ZKCCGPGASCPRYFKDNFICGCC^ (488)
10	Cn3.1	-MCCGEGAPCPSYFRNSQICHCC^ (489)
<u>TYPE 4</u>		
15	A3.3 (F83)	ZK--CCTGK---KGSCSGKACKNL-KCCS# (490)
	A3.5 (Z488)	ZK--CCTGR---KGSCSGKACKNL-KCCS# (491)
	Bu3.1	VTDRCCK----GKREC-GRWCRDHSRCC# (492)
	Bu3.1A	VGDRCCK----GKRGK-GRWCRDHSRCC# (493)
	Bu3.2	VGERCCK---NGKRGK-GRWCRDHSRCC# (494)
20	Bu3.3	IVDRCCN-KGNGKRGK-SRWCRDHSRCC# (495)
	Bu3.4	VGLYCCRPKPNGQMMC-DRWCEKNSRCC# (496)
	Ca3.2	-RD-CCTPP---KK-CKDRQCKPQ-RCCA# (497)
	L3.1	GRD-CCTPP---RK-CKDRACKPQ-RCCG# (498)
	L3.2	ZRL-CCGFP---KS-CRSRQCKPH-RCC# (499)
25	La3.2	-RD-CCTPP---KK-CKDRQCKPA-RCCG# (500)
	La3.3	RPP-CCTYD---GS-CLKESCMRK-ACC# (501)
	La3.3A	RPP-CCTYD---GS-CLKESCKRK-ACC# (502)
	μ -GIIIA	-RD-CCTOO---KK-CKDRQCKOQ-RCCA# (503)
	μ -GIIIB	-RD-CCTOO---RK-CKDRRCKOM-KCCA# (504)
30	μ -GIIIC	-RD-CCTOO---KK-CKDRRCKOL-KCCA# (505)
	μ -PIIIA	ZRL-CCGFO---KS-CRSRQCKOH-RCC# (506)
	M3.1	-RD-CCTPP---KK-CKDRQCKPQ-RCCA# (507)
	Mr3.1	RGG-CCTPP---RK-CKDRACKPA-RCCGP# (508)
	Nb3.2 (F582)	ZK--CCTGK---KGSCSGKACKNL-KCCS# (509)
35	Pr3.1 (Z500)	RGG-CCTPP---KK-CKDRACKPA-RCCGP# (510)
	Pr3.2 (Z501)	-RG-CCTPP---RK-CKDRACKPA-RCCGP# (511)
	R3.1	LOS-CCSLN---LRLCOVOACKRN-OCCT# (512)
	R3.2	ZQR-CCTVK----RICOVOACRSK-OCCKS^ (513)
	R3.3	RGG-CCTPP---RK-CKDRACKPA-RCCGP# (514)
40	Sm3.1	ZK--CCTGK---KGSCSGKACKNL-KCCS# (515)
	T3.1	H-G-CCKGO---EG-CSSRECROQ-HCC# (516)
	T3.2 (Y088)	H-G-CCEGP---KG-CSSRECRPQ-HCC# (517)
	Wi3.1 (M548)	LPS-CCDFE----RLCVVPACIRH-QCCT# (518)

45

Type 5

Om3.2 CCKYGWTCLLGCTPCDC^ (519)

85

Om3 . 4

CCRYGWTICWLGCTPCGC^ (520)

Type 6

5 S3 . 2 (F352)

Z-NCCNGG-CSSKWCRDHARCC# (432)

EXAMPLE 3

Effect of Intrathecal Administration of μ -Conopeptides

10 [0087] Male C57 black mice (20-25g) are obtained from Charles River Laboratories. These mice and the animals are housed in a temperature controlled ($23^{\circ} \pm 3^{\circ} \text{C}$) room with a 12 hour light-dark cycle with free access to food and water. All animals are euthanized in accordance with Public Health Service policies on the humane care of laboratory animals.

15 [0088] Intrathecal (it) drug injections are performed as described (Hylden and Wilcox, 1980). A μ -conopeptide or vehicle is administered in a volume of 5 μl . Duration of hind-limb paralysis is assessed. This experiment reveals that injection of μ -conopeptides into the intrathecal space of C57 black mice produced a paralysis of the animal. The animals in this experiment recovered fully.

20

EXAMPLE 4

Effect of μ -Conopeptides as a Local Anesthetic

25 [0089] Male Hartley guinea pigs (retired breeders) are obtained from Charles River Laboratories. The local anesthetic test is performed essentially as described (Bulbring and Wajda, 1945). On the day prior to test day, a patch on the back of the guinea pig is denuded of hair, first by shaving with electric clippers and subsequently with depilatory cream (Nair®). Depilatory cream is applied for five minutes and removed with a warm washcloth. The guinea pigs are dried and returned to their cages. On the following day, intradermal injections (0.1 ml vols) of lidocaine, bupivacaine, a μ -conopeptide or vehicle (0.5% cyclodextran) are made into the denuded patch. The injection produced a raised wheal on the surface of the skin which is 30 circled with a felt-tipped pen. Typically, four injections are made on the back of each guinea pig. In some cases, guinea pigs are reused following at least one week of recovery and injecting into an unused portion of the skin. The stimulus consists of mild pin pricks (not hard enough to break the skin) with a 26G needle. The response is a localized skin twitch caused by contraction

of cutaneous muscles. A unit test consisted of six uniform pin pricks, 3-5 seconds apart, within the injected area. Unit scores range from 0 (complete anesthesia) to 6 (no anesthesia). For potency experiments, the unit test is repeated at each site at five minute intervals for 30 minutes, and unit test scores summed (with 36 representing no anesthesia to 0 representing complete anesthesia. For duration experiments, unit tests are performed as described over the course of several hours to days.

[0090] μ -Conopeptides of the present invention produce a potent and long lasting local anesthetic effect in the intracutaneous wheal test in the guinea pig. As expected, bupivacaine has a slightly longer duration than lidocaine, consistent with clinical observations.

EXAMPLE 5

Muscle Relaxant Effect of μ -Conopeptides in Anesthetized Monkeys

[0091] μ -Conopeptides are dissolved 0.9 percent saline at a concentration of 2 mg/ml. Rhesus monkeys are anesthetized with halothane, nitrous oxide and oxygen. The maintenance concentration of halothane is 1.0%. Arterial and venous catheters are placed in the femoral vessels for drug administration and recording of the arterial pressure. Controlled ventilation is accomplished via an endotracheal tube. Twitch and tetanic contractions of the tibialis anterior muscle are elicited indirectly via the sciatic nerve. Recordings of arterial pressure, electrocardiogram (lead I), heart rate, and muscle function are made simultaneously. Four to six animals received each listed compound. Four additional animals received succinylcholine chloride or d-tubocurarine chloride as controls. It is seen that the tested μ -conopeptides generally provide similar or better results than those seen for succinylcholine chloride or d-tubocurarine chloride.

EXAMPLE 6

In vivo Activity of μ -Conopeptides in Pain Models

[0092] The anti-pain activity of μ -conopeptides is shown in several animal models. These models include the nerve injury model (Chaplan, et al., 1997), the nociceptive response to s.c. formalin injection in rats (Codene, 1993) and an NMDA-induced persistent pain model (Liu, et al., 1997). In each of these models it is seen that the μ -conopeptides and μ -conopeptides derivatives have analgesic properties.

[0093] More specifically, this study evaluates the effect of intrathecal administration of μ -conopeptides in mice models of nociceptive and neuropathic pain. For nociceptive pain, the effect of the μ -conopeptides is studied in two different tests of inflammatory pain. The first is the formalin test, ideal because it produces a relatively short-lived, but reliable pain behavior that is readily quantified. There are two phases of pain behavior, the second of which is presumed to result largely from formalin-evoked inflammation of the hind paw. A μ -conopeptide is administered 10 minutes prior to injection of formalin. The number of flinches and/or the duration of licking produced by the injection is monitored. Since the first phase is presumed to be due to direct activation of primary afferents, and thus less dependent on long term changes in the spinal cord, μ -conopeptides are presumed to have greatest effect on the magnitude of pain behavior in the second phase.

[0094] The mechanical and thermal thresholds in animals that received an injection of complete Freund's adjuvant into the hind paw are also studied. This produces a localized inflammation including swelling of the hind paw and a profound decrease in mechanical and thermal thresholds, that are detected within 24 hours after injection. The changes in thresholds in rats that receive μ -conopeptides are compared with those of rats that receive vehicle intrathecal injections.

[0095] An important issue is whether the drugs are effective when administered after the pain model has been established, or whether they are effective only if used as a pretreatment. Clearly, the clinical need is for drugs that are effective after the pain has developed. To address this issue, animals are studied in which μ -conopeptides are administered repeatedly, after the inflammation (CFA) or nerve injury has been established. In these experiments, a μ -conopeptide is injected daily by the intrathecal (i.t.) route. The mechanical and thermal thresholds (measured, respectively, with von Frey hairs in freely moving animals and with the Hargreave's test, also in freely moving animals) are repeated for a 2 to 4 week period after the injury is induced and the changes in pain measured monitored over time.

EXAMPLE 7

Effect of μ -Conotoxins in a Pain Model

[0096] Analgesic activity of μ -conotoxins is also tested in pain models as follows.

[0097] Persistent pain (formalin test). Intrathecal (it) drug injections are performed as described by Hylden and Wilcox (1980). An μ -conopeptide or vehicle is administered in a

volume of 5 μ l. Fifteen minutes after the i.t. injection, the right hindpaw is injected with 20 μ l of 5% formalin. Animals are placed in clear plexiglass cylinders backed by mirrors to facilitate observation. Animals are closely observed for 2 minutes per 5 minute period, and the amount of time the animal spent licking the injected paw is recorded in this manner for a total of 45-50 minutes. Results are expressed as licking time in seconds per five minutes. At the end of the experiment, all animals are placed on an accelerating rotorod and the latency to first fall was recorded. μ -Conopeptides are found to be active in this model which is predictive of efficacy for treating neuropathic pain.

[0098] Acute pain (tail-flick). A μ -conopeptide or saline is administered intrathecally (i.t.) according to the method of Hylden and Wilcox (1980) in a constant volume of 5 μ l. Mice are gently wrapped in a towel with the tail exposed. At various time-points following the i.t. injection, the tail is dipped in a water bath maintained at 54° C. and the time to a vigorous tail withdrawal is recorded. If there is no withdrawal by 8 seconds, the tail is removed to avoid tissue damage.

[0099] Neuropathic pain. The partial sciatic nerve ligation model is used to assess the efficacy of μ -conopeptides in neuropathic pain. Nerve injury is produced according to the methods of Malmberg and Basbaum (1998). Animals are anesthetized with a ketamine/xylazine solution, the sciatic nerve is exposed and tightly ligated with 8-0 silk suture around 1/3 to 1/2 of the nerve. In sham-operated mice the nerve is exposed, but not ligated. Animals are allowed to recover for at least 1 week before testing is performed. On the testing day, mice are placed in plexiglass cylinders on a wire mesh frame and allowed to habituate for at least 60 minutes. Mechanical allodynia is assessed with calibrated von Frey filaments using the up-down method as described by Chaplan et al. (1994), and the 50% withdrawal threshold is calculated. Animals that did not respond to any of the filaments in the series are assigned a maximal value of 3.6 grams, which is the filament that typically lifted the hindlimb without bending, and corresponds to approximately 1/10 the animal's body weight.

[0100] The data obtained demonstrate that μ -conopeptides have potent analgesic properties in three commonly used models of pain: acute, persistent/inflammatory and neuropathic pain models.

EXAMPLE 8

Activity of μ -Conopeptide S3.2 on Neuronal Sodium Channels

[0101] μ -Conopeptide S3.2 was tested for activity on sodium channels as follows. S3.2 was administered to mice by intracerebroventricular (ICV) injection. Administration of S3.2 in this manner caused mice to show a spectrum of activity that is characteristic of all sodium channel blockers, including rapid loss of righting reflex, coma-like inactivity and spastic uncontrolled limb movement. Following intrathecal (it) administration to mice, S3.2 causes rapid hindlimb paralysis that spreads to include the entire body over a course of 10-20 minutes followed by death, presumably due to respiratory paralysis. However, unlike classic μ -conopeptides, S3.2 has no significant activity following intravenous administration (iv) to mice. Classic μ -conopeptides, such as GIIIA and PIIIA, cause rapid paralysis and death following iv administration, indicating their activity at skeletal muscle sodium channels. To confirm the selectivity of S3.2, 80 nmol was administered iv to rats. The effect of S3.2 was measured on skeletal muscle contraction, blood pressure and heart rate. S3.2 was found to have no effect on any of these parameters. Controls were performed using classical μ -conopeptides, including Sm3.1, Sm3.3 and Bu3.1 described herein, also administered iv at 80 nmol. These control peptides caused a dramatic decrease in skeletal muscle contractility, as well as a significant drop in systemic blood pressure. Thus, μ -conopeptide S3.2 surprisingly is selective for neuronal sodium channels. The most obvious difference between the S3.2 sequence and the sequences of these other peptides is a shortened first loop (the first loop between cysteine residues) which lacks a charged amino acid.

[0102] It will be appreciated that the methods and compositions of the instant invention can be incorporated in the form of a variety of embodiments, only a few of which are disclosed herein. It will be apparent to the artisan that other embodiments exist and do not depart from the spirit of the invention. Thus, the described embodiments are illustrative and should not be construed as restrictive.

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WHAT IS CLAIMED IS:

1. An isolated peptide selected from the group consisting of:
 - (a) a peptide set forth in Table 1 or Table 2 and
 - (b) a derivative of the peptide in (a).
2. The isolated peptide of claim 1, wherein Xaa₁ is Glu, Xaa₂ is pyro-Glu, Xaa₄ is Trp and Xaa₅ is Tyr.
3. The derivative of the peptide of claim 1, in which the Arg residues may be substituted by Lys, ornithine, homoargine, nor-Lys, N-methyl-Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys or any synthetic basic amino acid; the Lys residues may be substituted by Arg, ornithine, homoargine, nor-Lys, or any synthetic basic amino acid; the Tyr residues may be substituted with meta-Tyr, ortho-Tyr, nor-Tyr, mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr, nitro-Tyr or any synthetic hydroxy containing amino acid; the Ser residues may be substituted with Thr or any synthetic hydroxylated amino acid; the Thr residues may be substituted with Ser or any synthetic hydroxylated amino acid; the Phe residues may be substituted with any synthetic aromatic amino acid; the Trp residues may be substituted with Trp (D), neo-Trp, halo-Trp (D or L) or any aromatic synthetic amino acid; the Asn, Ser, Thr or Hyp residues may be glycosylated; the Tyr residues may also be substituted with the 3-hydroxyl or 2-hydroxyl isomers (meta-Tyr or ortho-Tyr, respectively) and corresponding O-sulpho- and O-phospho-derivatives; the acidic amino acid residues may be substituted with any synthetic acidic amino acid, e.g., tetrazolyl derivatives of Gly and Ala; the aliphatic amino acids may be substituted by synthetic derivatives bearing non-natural aliphatic branched or linear side chains C_nH_{2n+2} up to and including n=8; the Met residues may be substituted by Nle; the Cys residues may be in D or L configuration and may optionally be substituted with homocysteine (D or L); pairs of Cys residues may be replaced pairwise with isoteric lactam or ester-thioether replacements, such as Ser/(Glu or Asp), Lys/(Glu or Asp), Cys/Glu (or Asp) or Cys/Ala combinations; and the peptide may be radioiodinated or radiotriated.

4. A substantially pure μ -conotoxin peptide derivative comprising a permutant of the peptide of claim 1,2 or 3.

5. A substantially pure μ -conotoxin peptide derivative comprising the peptide or peptide derivative of claim 1, 2 or 3 modified to contain an O-glycan, an S-glycan or an N-glycan.

6. A substantially pure μ -conotoxin peptide derivative comprising the peptide derivative of claim 4 modified to contain an O-glycan, an S-glycan or an N-glycan.

7. An isolated nucleic acid encoding a μ -cono peptide propeptide having an amino acid sequence set forth in Table 1.

8. The isolated nucleic acid of claim 7, wherein the nucleic acid comprises a nucleotide sequence set forth in Table 1.

9. An isolated μ -cono peptide propeptide having an amino acid sequence set forth in Table 1.

10. A method for treating or preventing disorders associated with voltage gated ion channel disorders in which comprises administering to a patient in need thereof a therapeutically effective amount of a peptide of claim 1 or a pharmaceutically acceptable salt thereof.

11. The method of claim 10, wherein said disorder is a neurologic disorder.

12. The method of claim 11, wherein said neurologic disorder is Amyotrophic Lateral Sclerosis.

13. The method of claim 11, wherein said neurologic disorder is head trauma.

14. The method of claim 11, wherein said neurologic disorder is epilepsy.

15. The method of claim 11, wherein said neurologic disorder is a neurotoxic injury associated with conditions of hypoxia, anoxia or ischemia.
16. The method of claim 15, wherein said neurotoxic injury is associated with stroke,
5 cerebrovascular accident, brain or spinal cord trauma, myocardial infarct, physical trauma, drownings, suffocation, perinatal asphyxia, or hypoglycemic events.
17. The method of claim 10, wherein said disorder is pain.
- 10 18. The method of claim 17, wherein said pain is migraine, acute pain, persistent pain, chronic pain, neuropathic pain or nociceptive pain.
19. The method of claim 18, wherein the pain is trigeminal neuralgia, diabetic neuropathy, post-herpetic neuralgia, neuroma pain, phantom limb pain.
15
20. The method of claim 17, wherein said pain is burn pain.
21. The method of claim 10, wherein said disorder is a neuromuscular disorder.
- 20 22. The method of claim 21, wherein said neuromuscular disorder is myofacial pain syndrome, chronic muscle spasm, dystonias or spasticity.
23. A method for providing musculoskeletal relaxation in a patient undergoing a surgical procedure requiring anesthesia which comprises administering to a patient in need
25 thereof a therapeutically effective amount of a peptide of claim 1 or a pharmaceutically acceptable salt thereof.
24. A method of alleviating pain which comprises administering to a mammal that is either exhibiting pain or is about to be subjected to a pain-causing event a pain-alleviating
30 amount of a peptide of claim 1 or a pharmaceutically acceptable salt thereof.
25. The method of claim 24, wherein the peptide is administered as a local anesthetic.

26. The method of claim 24, wherein the peptide is administered as an ocular anesthetic.
27. A method for characterizing a pore occlusion site on a sodium channel subtype
5 comprising determining the affinity of said site for a peptide of claim 1.
28. The method of claim 27, wherein said sodium channel subtype is a neuronal sodium
channel subtype and said peptide is μ -conopeptide S3.2 comprising an amino acid
sequence as set forth in SEQ ID NO:211 or SEQ ID NO:432.
- 10 29. A method for screening a small molecule library to identify a small molecule which is a
selective blocking agent of a sodium channel subtype comprising (a) measuring the
blocking activity of a small molecule on said sodium channel subtype, (b) measuring the
blocking activity of a peptide of claim 1 on said sodium channel subtype and (c)
15 comparing the blocking activity of said small molecule with the blocking activity of said
peptide.
30. The method of claim 29, wherein said sodium channel subtype is a neuronal sodium
channel subtype and said peptide is μ -conopeptide S3.2 comprising an amino acid
20 sequence as set forth in SEQ ID NO:211 or SEQ ID NO:432.
31. A method for screening a small molecule library to identify a small molecule which is a
selective blocking agent of a sodium channel subtype comprising (a) measuring the
binding affinity of a small molecule on said sodium channel subtype, (b) measuring the
25 binding affinity of a peptide of claim 1 on said sodium channel subtype and (c)
comparing the binding affinity of said small molecule with the binding affinity of said
peptide.
32. The method of claim 31, wherein said peptide is radiolabeled.

33. The method of claim 31, wherein said sodium channel subtype is a neuronal sodium channel subtype and said peptide is μ -conopeptide S3.2 comprising an amino acid sequence as set forth in SEQ ID NO:211 or SEQ ID NO:432.

5 34. The method of claim 33, wherein said peptide is radiolabeled.

35. A method for screening a small molecule library to identify a small molecule which is a selective blocking agent of a sodium channel subtype comprising (a) allowing a peptide of claim 1 to bind to a sodium channel subtype, (b) adding a small molecule and (c)
10 measuring the amount of displacement of said peptide on said sodium channel subtype by said small molecule.

36. The method of claim 35, wherein said peptide is radiolabeled.

15 37. The method of claim 35, wherein said sodium channel subtype is a neuronal sodium channel subtype and said peptide is μ -conopeptide S3.2 comprising an amino acid sequence as set forth in SEQ ID NO:211 or SEQ ID NO:432.

38. The method of claim 37, wherein said peptide is radiolabeled.

20 39. A method for screening a small molecule library to identify a small molecule which is a selective blocking agent of a sodium channel subtype comprising (a) allowing a small molecule to bind to a sodium channel subtype, (b) adding a peptide of claim 1 and (c) measuring the amount of displacement of said small molecule on said sodium channel
25 subtype by said small peptide.

40. The method of claim 39, wherein said sodium channel subtype is a neuronal sodium channel subtype and said peptide is μ -conopeptide S3.2 comprising an amino acid sequence as set forth in SEQ ID NO:211 or SEQ ID NO:432.

30 41. A method of identifying compounds that mimic the therapeutic activity of a μ -conotoxin, comprising the steps of: (a) conducting a biological assay on a test compound to

determine the therapeutic activity; and (b) comparing the results obtained from the biological assay of the test compound to the results obtained from the biological assay of a μ -conotoxin, wherein said μ -conotoxin is a peptide of claim 1.

- 5 42. The method of claim 41, wherein said μ -conotoxin is S3.2 comprising an amino acid set forth in SEQ ID NO:211 or SEQ IN NO:432.

SEQUENCE LISTING

<110> University of Utah Research Foundation
 Cognetix, Inc.
 Olivera, Baldomero M.
 McIntosh, J. Michael
 Garrett, James E.
 Watkins, Maren
 Cruz, Lourdes J.
 Shon, Ki-Joon
 Jacobsen, Richard
 Jones, Robert M.
 Cartier, G. Edward
 Shen, Greg S.
 Wagstaff, John D.

<120> Mu-Conopeptides

<130> 2314-242

<150> US 60/219,619
 <151> 2000-07-21

<150> US 60/245,157
 <151> 2000-11-03

<150> US 60/264,319
 <151> 2001-01-29

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 20 25 30
 Ala Glu Arg Met Gln Asp Asp Phe Ile Thr Glu His His Pro Leu Phe

35 40 45
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 50 55 60
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 <222> (1)..(14)
 <223> Xaa at residue 3 is Glu or gamma-carboxy Glu; Xaa at residue 5 and 12 is Pro or Hy
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 1 5 10
 <210> 4
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 atttcatctg atcaacatct cttctttgat ctcatcaaac ggtgctgcga gttgccatgc 180
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 <211> 69
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 20 25 30
 Arg Pro Ala Glu Arg Met Gln Asp Ile Ser Ser Asp Gln His Leu Phe
 35 40 45
 Phe Asp Leu Ile Lys Arg Cys Cys Glu Leu Pro Cys Gly Pro Gly Phe
 50 55 60
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 <210> 6
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 <213> Conus atlanticus

3

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 <222> (1)..(15)
 <223> Xaa at residue 3 is Glu or gamma-carboxy Glu; Xaa at residue 5, 8
 and 13 is Pro or Hy

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 1 5 10 15

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 agagcgtatg caggacgaca ttcatctga gcagcatccc ttgtttaatc agaaaagaat 180
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 <213> Conus aurisiacus

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 20 25 30
 Glu Glu Arg Met Gln Asp Asp Ile Ser Ser Glu Gln His Pro Leu Phe
 35 40 45
 Asn Gln Lys Arg Met Cys Cys Gly Glu Gly Arg Lys Cys Pro Ser Tyr
 50 55 60
 Phe Arg Asn Ser Gln Ile Cys His Cys Cys
 65 70

<210> 9
 <211> 22
 <212> PRT
 <213> Conus aurisiacus
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 s Pro or Hyp; Xaa at residue 12 is Tyr, 125I-Tyr, mono-iodo-Tyr,
 di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

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 1 5 10 15

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20

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 <212> DNA
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 gacatttcac ctgagcagca tcgcttgctt aatcagaaaa gaagggtgctg ccggtggcca 180
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 <211> 75
 <212> PRT
 <213> Conus aurisiacus

<400> 11
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 1 5 10 15
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 20 25 30
 Arg Pro Ala Glu Arg Met Gln Asp Asp Ile Ser Ser Glu Gln His Arg
 35 40 45
 Leu Phe Asn Gln Lys Arg Arg Cys Cys Arg Trp Pro Cys Pro Arg Gln
 50 55 60
 Ile Asp Gly Glu Tyr Cys Gly Cys Cys Leu Gly
 65 70 75

<210> 12
 <211> 19
 <212> PRT
 <213> Conus aurisiacus

<220>
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 <223> Xaa at residue 13 is Glu or gamma-carboxy Glu; Xaa at residue 3 and 7 is Pro or Hyp; Xaa at residue 4 is Trp or Bromo Trp; Xaa at residue 14 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

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 1 5 10 15
 Cys Cys Leu

<210> 13
 <211> 262
 <212> DNA
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 gacatttcat ctgagcagta tcccttggtt gataagagac aaaagtgttg cactgggaag 180
 aaggggtcat gctccggcaa agcatgcaaa aatctcaaat gttgctctgg acgataacgt 240
 gttgatgacc aactttctcg ag 262

<210> 14
 <211> 78
 <212> PRT
 <213> Conus aurisiacus

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

<210> 15
 <211> 23
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<220>
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 <222> (1)..(23)
 <223> Xaa at residue 1 is Gln or pyro-Glu

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 1 5 10 15
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<210> 16
 <211> 232
 <212> DNA
 <213> Conus aurisiacus

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 <211> 68
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 <213> Conus aurisiacus

<400> 17

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 20 25 30

Arg His Ala Glu Arg Met His Asp Gly Ile Ser Pro Lys Arg His Pro
 35 40 45

Trp Phe Asp Pro Val Lys Arg Cys Cys Lys Val Gln Cys Glu Ser Cys
 50 55 60

Thr Pro Cys Cys
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<210> 18

<211> 13

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<213> Conus aurisiacus

<220>

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<222> (1)..(13)

<223> Xaa at residue 7 is Glu or gamma-carboxy Glu; Xaa at residue 11 is
 s Pro or Hyp

<400> 18

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<210> 19

<211> 241

<212> DNA

<213> Conus bandus

<400> 19

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<213> Conus bandus

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 20 25 30

Arg Pro Ala Glu Arg Ser Gln Asp Val Ser Ser Glu Gln His Pro Leu
 35 40 45

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<211> 298
<212> DNA
<213> Conus betulinus

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20 25 30

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Cys Trp Pro
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<210> 24
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<212> PRT
<213> Conus betulinus

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1 and 15 is Pro or Hyp; Xaa at residue 14 is Trp or bromo-Trp

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<210> 25

<211> 298

<212> DNA

<213> Conus betulinus

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agagcgtatg caggacattt cacctgaaca gcatccctcg tttgatcccg tcaaacgggtg 180
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<211> 68

<212> PRT

<213> Conus betulinus

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20 25 30
Ala Glu Arg Met Gln Asp Ile Ser Pro Glu Gln His Pro Ser Phe Asp
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50 55 60

Cys Trp Pro Ser
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<210> 27

<211> 16

<212> PRT

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<222> (1)..(16)

<223> Xaa at residue 5, 11 and 15 is Pro or Hyp; Xaa at residue 14 is Trp or bromo-Trp

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1 5 10 15

<210> 28

<211> 282

<212> DNA

<213> Conus betulinus

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 65 70

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 <213> Conus bullatus

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 Ala Glu Arg Met Gln Asp Asp Ile Ser Ser Glu Gln Asn Ser Leu Leu
 35 40 45
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 50 55 60
 Arg Trp Cys Arg Asp His Ser Arg Cys Cys Gly Arg Arg
 65 70 75

<210> 33
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 <222> (1)..(23)
 <223> Xaa at residue 11 is Glu or gamma-carboxy Glu; Xaa at residue 15
 is Trp or bromo-Tr

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 <213> Conus bullatus

<400> 35
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
 1 5 10 15

11

Pro Leu Phe Ala Leu Arg Gln Asp Gly Asp Gln Pro Ala Asp Arg Pro
 20 25 30

Ala Glu Arg Met Gln Asp Asp Ile Ser Ser Glu Gln Asn Pro Leu Leu
 35 40 45

Glu Lys Arg Val Gly Asp Arg Cys Cys Lys Gly Lys Arg Gly Cys Gly
 50 55 60

Arg Trp Cys Arg Asp His Ser Arg Cys Cys Gly Arg Arg
 65 70 75

<210> 36
 <211> 23
 <212> PRT
 <213> Conus bullatus

<220>
 <221> PEPTIDE
 <222> (1)..(23)
 <223> Xaa at residue 15 is Trp or bromo-Trp
 <400> 36

Val Gly Asp Arg Cys Cys Lys Gly Lys Arg Gly Cys Gly Arg Xaa Cys
 1 5 10 15

Arg Asp His Ser Arg Cys Cys
 20

<210> 37
 <211> 331
 <212> DNA
 <213> Conus bullatus

<400> 37
 caagaaggat cgatagcagt tcatgatgtc taaactggga gtcttgttga ccatctgtct 60
 gcttctgttt cccctttttg ctcttcogca ggatggagat caacctgcag accgacctgc 120
 agagcgtatg caggacgaca tttcatctga gcagaatccc ttgcttgaga agagagttgg 180
 tgaaaggtgc tgcaaaaacg ggaagagggg gtgcggcaga tgggtgcagag atcactcacg 240
 ttgttgcggt cgacgataac gtgttgatga ccgaggcttt cgttatcacg gctacatcaa 300
 gtgtctagtg aataagtaaa acgattgcag t 331

<210> 38
 <211> 78
 <212> PRT
 <213> Conus bullatus

<400> 38
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
 1 5 10 15

Pro Leu Phe Ala Leu Pro Gln Asp Gly Asp Gln Pro Ala Asp Arg Pro
 20 25 30

Ala Glu Arg Met Gln Asp Asp Ile Ser Ser Glu Gln Asn Pro Leu Leu
 35 40 45

Glu Lys Arg Val Gly Glu Arg Cys Cys Lys Asn Gly Lys Arg Gly Cys
 50 55 60

Gly Arg Trp Cys Arg Asp His Ser Arg Cys Cys Gly Arg Arg

12

65

70

75

<210> 39
 <211> 24
 <212> PRT
 <213> Conus bullatus

<220>
 <221> PEPTIDE
 <222> (1)..(24)
 <223> Xaa at residue 3 is Glu or gamma-carboxy Glu; Xaa at residue 16 is Trp or bromo-Tr

<400> 39
 Val Gly Xaa Arg Cys Cys Lys Asn Gly Lys Arg Gly Cys Gly Arg Xaa
 1 5 10 15

Cys Arg Asp His Ser Arg Cys Cys
 20

<210> 40
 <211> 337
 <212> DNA
 <213> Conus bullatus

<400> 40
 caagagggat cgatagcagt tcatgatgtc taaactggga gtcttggtga ccattctgtct 60
 gcttctgttt cccctttttg ctcttccgca ggacggagat caacctgcag accgacctgc 120
 agagcgtatg caggacgacc tttcatctga gcagcatccc ttgtttgaga agagaattgt 180
 tgacaggtgc tgcaacaaag ggaacgggaa gagggggtgc agcagatggt gcagagatca 240
 ctacagttgt tgcggtcgac gatgaactgt tgatgaccga ggctttggtt atcacggcta 300
 catcaagtgt ctagtgaata agtaaaacga ttgcagt 337

<210> 41
 <211> 80
 <212> PRT
 <213> Conus bullatus

<400> 41
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
 1 5 10 15

Pro Leu Phe Ala Leu Pro Gln Asp Gly Asp Gln Pro Ala Asp Arg Pro
 20 25 30

Ala Glu Arg Met Gln Asp Asp Leu Ser Ser Glu Gln His Pro Leu Phe
 35 40 45

Glu Lys Arg Ile Val Asp Arg Cys Cys Asn Lys Gly Asn Gly Lys Arg
 50 55 60

Gly Cys Ser Arg Trp Cys Arg Asp His Ser Arg Cys Cys Gly Arg Arg
 65 70 75 80

<210> 42
 <211> 26
 <212> PRT
 <213> Conus bullatus

<220>

13

<221> PEPTIDE

<222> (1)..(26)

<223> Xaa at residue 18 is Trp or bromo-Trp

<400> 42

Ile	Val	Asp	Arg	Cys	Cys	Asn	Lys	Gly	Asn	Gly	Lys	Arg	Gly	Cys	Ser
1				5				10						15	

Arg	Xaa	Cys	Arg	Asp	His	Ser	Arg	Cys	Cys
		20						25	

<210> 43

<211> 337

<212> DNA

<213> Conus bullatus

<400> 43

caagaaggat	cgatagcagt	tcatgatgtc	taaactggga	gtcttgttga	ccatctgtct	60
gcttctgttt	cccccttttg	ctcttccgca	ggatggagat	caacctgcag	accgacctgc	120
tgagcgtatg	caggacgaca	tttcatctga	gcggaatccc	ttgtttgaga	agagcgttgg	180
tttatattgc	tgccgacca	aaccacacgg	gcagatgatg	tgcgacagat	ggtgcgaaaa	240
aaactcacgt	tggtgcggtc	gacgataatg	tgttgatgac	cagctttgtt	atcaaggcta	300
catcaagtat	ctagtgaata	agtaaaacga	ttgcagt			337

<210> 44

<211> 77

<212> PRT

<213> Conus bullatus

<400> 44

Met	Met	Ser	Lys	Leu	Gly	Val	Leu	Leu	Thr	Ile	Cys	Leu	Leu	Leu	Phe
1				5					10					15	

Pro	Leu	Phe	Ala	Leu	Pro	Gln	Asp	Gly	Asp	Gln	Pro	Ala	Asp	Arg	Pro
			20					25					30		

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

Ser	Val	Gly	Cys	Cys	Arg	Pro	Lys	Pro	Asn	Gly	Gln	Met	Met	Cys	Asp
		50				55					60				

Arg	Trp	Cys	Glu	Lys	Asn	Ser	Arg	Cys	Cys	Gly	Arg	Arg
65					70					75		

<210> 45

<211> 27

<212> PRT

<213> Conus bullatus

<220>

<221> PEPTIDE

<222> (1)..(27)

<223> Xaa at residue 21 is Glu or gamma-carboxy Glu; Xaa at residue 8 and 10 is Pro or Hyp; Xaa at residue 19 is Trp or bromo-Trp; Xaa at residue 4 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 45

Val	Gly	Leu	Xaa	Cys	Cys	Arg	Xaa	Lys	Xaa	Asn	Gly	Gln	Met	Met	Cys
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

14

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1           5           10           15
Asp Arg Xaa Cys Xaa Lys Asn Ser Arg Cys Cys
      20           25

<210>  46
<211>  323
<212>  DNA
<213>  Conus bullatus
<400>  46
caagaaggat cgatagcagt tcatgatgtc taaactggga gttttgttga ccatctgtct      60
gtttctgttt ccccttactg ctcttcgat ggatggagat caatctgtag accgacctgc      120
agaacgtatg caggacgacc ttcatctga gcagcatccc ttgtttgttc agaaaagaag      180
gtgttgccgc gaaggcttga catgccccag atattggaaa aacagtcaga tttgtgcttg      240
ttgttaaatag acaacgtgtc gatgaccaac ttcggtatca cgactacgcc aagtgtctaa      300
tgaataagta aaacgattgc agt                                           323

<210>  47
<211>  74
<212>  PRT
<213>  Conus bullatus

<400>  47
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
1           5           10           15
Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Ser Val Asp Arg Pro
      20           25           30
Ala Glu Arg Met Gln Asp Asp Leu Ser Ser Glu Gln His Pro Leu Phe
      35           40           45
Val Gln Lys Arg Arg Cys Cys Gly Glu Gly Leu Thr Cys Pro Arg Tyr
      50           55           60
Trp Lys Asn Ser Gln Ile Cys Ala Cys Cys
65           70

<210>  48
<211>  22
<212>  PRT
<213>  Conus bullatus

<220>
<221>  PEPTIDE
<222>  (1)..(22)
<223>  Xaa at residue 5 is Glu or gamma-carboxy Glu; Xaa at residue 10 is
      Pro or Hyp; Xaa at residue 13 is Trp or bromo-Trp; Xaa at resid
      ue 12 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr
      or O-phospho-Ty

<400>  48
Arg Cys Cys Gly Xaa Gly Leu Thr Cys Xaa Arg Xaa Xaa Lys Asn Ser
1           5           10           15
Gln Ile Cys Ala Cys Cys
      20

<210>  49
<211>  322

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15

<212> DNA

<213> Conus bullatus

<400> 49

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caagagggat cgatagcagt tcatgatgtc taaactggga gtcttggtga ccatctgtct    60
gcttctgttt cccctttttg ctcttccgca ggatggagat caacctgcag accgacctgc    120

tgagcgtatg caggacgaca tttcatctga gcaggatccc ttgtttgttc agaaaagaag    180

gtgttgcggc gaaggcttga catgccccag atattggaaa aacagtcaga tttgtgcttg    240

ttgttaaagt acaacgtgtg atgaccaact tcggtatcac gactacgcca agtgtctaat    300

gaataagtaa aacgattgca gt                                           322

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<210> 50

<211> 74

<212> PRT

<213> Conus bullatus

<400> 50

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Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
1           5           10           15

Pro Leu Phe Ala Leu Pro Gln Asp Gly Asp Gln Pro Ala Asp Arg Pro
          20           25           30

Ala Glu Arg Met Gln Asp Asp Ile Ser Ser Glu Gln Asp Pro Leu Phe
          35           40           45

Val Gln Lys Arg Arg Cys Cys Gly Glu Gly Leu Thr Cys Pro Arg Tyr
          50           55           60

Trp Lys Asn Ser Gln Ile Cys Ala Cys Cys
65           70

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<210> 51

<211> 22

<212> PRT

<213> Conus bullatus

<220>

<221> PEPTIDE

<222> (1)..(22)

<223> Xaa at residue 5 is Glu or gamma-carboxy Glu; Xaa at residue 10 is Pro or Hyp; Xaa at residue 13 is Trp or bromo-Trp; Xaa at residue 12 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 51

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Arg Cys Cys Gly Xaa Gly Leu Thr Cys Xaa Arg Xaa Xaa Lys Asn Ser
1           5           10           15

Gln Ile Cys Ala Cys Cys
          20

```

<210> 52

<211> 238

<212> DNA

<213> Conus capitaneus

<400> 52

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ggatccatga tgtctaaact gggagtcttg gtgaccatct gcttgccttct gtttccctt    60

gctgcttttc cactggatgg aaatcaacct gcagaccacc ctgcaaagcg tacgcaagat    120

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16

gacagttcag ctgccctgat caatacctgg attgatcatt cccattcttg ctgcagggac 180
 tgcggtgaag attgtgttgg ttgttgccgg taacgtgttg atgaccaact ttctcgag 238

<210> 53
 <211> 70
 <212> PRT
 <213> Conus capitaneus.

<400> 53
 Gly Ser Met Met Ser Lys Leu Gly Val Leu Val Thr Ile Cys Leu Leu
 1 5 10 15
 Leu Phe Pro Leu Ala Ala Phe Pro Leu Asp Gly Asn Gln Pro Ala Asp
 20 25 30
 His Pro Ala Lys Arg Thr Gln Asp Asp Ser Ser Ala Ala Leu Ile Asn
 35 40 45
 Thr Trp Ile Asp His Ser His Ser Cys Cys Arg Asp Cys Gly Glu Asp
 50 55 60
 Cys Val Gly Cys Cys Arg
 65 70

<210> 54
 <211> 15
 <212> PRT
 <213> Conus capitaneus

<220>
 <221> PEPTIDE
 <222> (1)..(15)
 <223> Xaa at residue 8 is Glu or gamma-carboxy Glu

<400> 54
 Ser Cys Cys Arg Asp Cys Gly Xaa Asp Cys Val Gly Cys Cys Arg
 1 5 10 15

<210> 55
 <211> 323
 <212> DNA
 <213> Conus characteristicus

<400> 55
 caagagggat c gatagcagt tcatgatgtc taaactggga gtcttgttga ccatctgtct 60
 gcttctgttt ccccttactg ctcttccaat ggatggagat caacctgcag accaacctgc 120
 agatcgtatg caggacgaca tttcatctga gcagtatccc ttgtttgata tgagaaaaag 180
 gtgttgcggc cccggcggtt catgccccgt atatttcaga gacaatttta tttgtggttg 240
 ttgttaaagt acaacgtgtc gatgaccaac ttcattatca cgactacgcc aagtgtctaa 300
 tgaataagta aaatgattgc agt 323

<210> 56
 <211> 74
 <212> PRT
 <213> Conus characteristicus

<400> 56

17

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

<210> 57
 <211> 21
 <212> PRT
 <213> Conus characteristicus
 <220>
 <221> PEPTIDE
 <222> (1)..(21)
 <223> Xaa at residue 4 and 9 is Pro or Hyp; Xaa at residue 11 is Tyr, 1
 25I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 57
 Cys Cys Gly Xaa Gly Gly Ser Cys Xaa Val Xaa Phe Arg Asp Asn Phe
 1 5 10 15
 Ile Cys Gly Cys Cys
 20

<210> 58
 <211> 316
 <212> DNA
 <213> Conus characteristicus

<400> 58
 caagagggat cgatagcagt tcatgatgtc taaactggga gtcttggtga ccatctgtct 60
 gcttctgttt ccccttactg ctcttccgat ggatggagat gaacctgcaa accgacctgt 120
 cgagcgtatg caggacaaca tttcatctga gcagtatccc ttgtttgaga agagacgaga 180
 ttgttgcaact cgcggaaga aatgcaaaga ccgacaatgc aaaccccgaga gatgttgcg 240
 tggacgataa cgtgttgatg accaacttta tcacggctac gtcaagtgtt tagtgaataa 300
 gtaaaatgat tgcagt 316

<210> 59
 <211> 75
 <212> PRT
 <213> Conus characteristicus

<400> 59
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
 1 5 10 15
 Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Glu Pro Ala Asn Arg Pro
 20 25 30
 Val Glu Arg Met Gln Asp Asn Ile Ser Ser Glu Gln Tyr Pro Leu Phe

18

35 40 45
 Glu Lys Arg Arg Asp Cys Cys Thr Pro Pro Lys Lys Cys Lys Asp Arg
 50 55 60

Gln Cys Lys Pro Gln Arg Cys Cys Ala Gly Arg
 65 70 75

<210> 60
 <211> 22
 <212> PRT
 <213> Conus characteristicus

<220>
 <221> PEPTIDE
 <222> (1)..(22)
 <223> Xaa at residue 6, 7 and 17 is Pro or Hyp

<400> 60
 Arg Asp Cys Cys Thr Xaa Xaa Lys Lys Cys Lys Asp Arg Gln Cys Lys
 1 5 10 15

Xaa Gln Arg Cys Cys Ala
 20

<210> 61
 <211> 314
 <212> DNA
 <213> Conus characteristicus

<400> 61
 caagagggat cgatagcagt tcatgatgtc taaactggga gtcttggtga ccatctgtct 60
 gcttctgttt ccccttactg ctcttccact ggatggagat caacctgcag atcaatctgc 120
 agagcgacct gcagagcgta cgcaggacga cattcagcag catccgttat atgatccgaa 180
 aagaaggtgt tgccgttatc catgccccga cagctgccac ggatcttgct gctataagtg 240
 ataacatggt gatggccagc tttgttatca cggccaogtc aagtgtctta atgaataagt 300
 aaaacgattg cagt 314

<210> 62
 <211> 72
 <212> PRT
 <213> Conus characteristicus

<400> 62
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
 1 5 10 15

Pro Leu Thr Ala Leu Pro Leu Asp Gly Asp Gln Pro Ala Asp Gln Ser
 20 25 30
 Ala Glu Arg Pro Ala Glu Arg Thr Gln Asp Asp Ile Gln Gln His Pro
 35 40 45

Leu Tyr Asp Pro Lys Arg Arg Cys Cys Arg Tyr Pro Cys Pro Asp Ser
 50 55 60

Cys His Gly Ser Cys Cys Tyr Lys
 65 70

<210> 63
 <211> 18

<212> PRT
 <213> Conus characteristicus

<220>
 <221> PEPTIDE
 <222> (1)..(18)
 <223> Xaa at residue 6 and 8 is Pro or Hyp; Xaa at residue 5 and 17 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 63
 Arg Cys Cys Arg Xaa Xaa Cys Xaa Asp Ser Cys His Gly Ser Cys Cys
 1 5 10 15

Xaa Lys

<210> 64
 <211> 292
 <212> DNA
 <213> Conus characteristicus

<400> 64
 caagagggat cgatagcagt tcatgatgtc taaactggga gccttggtga ccactgtgtc 60
 acttctgttt tcccttactg ctgttccgct ggatggagat caacatgcag accaacctgc 120
 acagcgtctg caggaccgca ttccaactga agatcatccc ttatttgatc ccaacaaaacg 180
 gtgttgccccg ccggtggcat gcaacatggg atgcaagcct tgttggtggat gaccagcttt 240
 gttatcgcggt tcttcatgaa gtgtcttaat gaataagtaa aatgattgca gt 292

<210> 65
 <211> 69
 <212> PRT
 <213> Conus characteristicus

<400> 65
 Met Met Ser Lys Leu Gly Ala Leu Leu Thr Ile Cys Leu Leu Leu Phe
 1 5 10 15
 Ser Leu Thr Ala Val Pro Leu Asp Gly Asp Gln His Ala Asp Gln Pro
 20 25 30
 Ala Gln Arg Leu Gln Asp Arg Ile Pro Thr Glu Asp His Pro Leu Phe
 35 40 45
 Asp Pro Asn Lys Arg Cys Cys Pro Pro Val Ala Cys Asn Met Gly Cys
 50 55 60

Lys Pro Cys Cys Gly
 65

<210> 66
 <211> 15
 <212> PRT
 <213> Conus characteristicus

<220>
 <221> PEPTIDE
 <222> (1)..(15)
 <223> Xaa at residue 3, 4 and 13 is Pro or Hyp

<400> 66
 Cys Cys Xaa Xaa Val Ala Cys Asn Met Gly Cys Lys Xaa Cys Cys

20

1 5 10 15

<210> 67
 <211> 293
 <212> DNA
 <213> Conus characteristicus

<400> 67
 caagagggat cgatagcagt tcatgatgtc taaactggga gccttggtga ccattctgtct 60
 acttctgttt tccctaactg ctgttccgct ggatggagat caacatgcag accaacctgc 120
 agagcgtctg catgaccgcc ttccaactga aaatcatccc ttatatgata ccgtaaaacg 180
 gtgttgcatg gattcggaat gcgactattc ttgctggcct tgctgtatgt ttggataacc 240
 tttgttatcg cggcctcatc aagtgtctaa tgaataagta aaacgattgc agt 293

<210> 68
 <211> 71
 <212> PRT
 <213> Conus characteristicus

<400> 68
 Met Met Ser Lys Leu Gly Ala Leu Leu Thr Ile Cys Leu Leu Leu Phe
 1 5 10 15
 Ser Leu Thr Ala Val Pro Leu Asp Gly Asp Gln His Ala Asp Gln Pro
 20 25 30
 Ala Glu Arg Leu His Asp Arg Leu Pro Thr Glu Asn His Pro Leu Tyr
 35 40 45
 Asp Pro Val Lys Arg Cys Cys Asp Asp Ser Glu Cys Asp Tyr Ser Cys
 50 55 60
 Trp Pro Cys Cys Met Phe Gly
 65 70

<210> 69
 <211> 17
 <212> PRT
 <213> Conus characteristicus

<220>
 <221> PEPTIDE
 <222> (1)..(17)
 <223> Xaa at residue 6 is Glu or gamma-carboxy Glu; Xaa at residue 13 is
 s Pro or Hyp; Xaa at residue 12 is Trp or bromo-Trp; Xaa at resid
 ue 9 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr o
 r O-phospho-Ty

<400> 69
 Cys Cys Asp Asp Ser Xaa Cys Asp Xaa Ser Cys Xaa Xaa Cys Cys Met
 1 5 10 15
 Phe

<210> 70
 <211> 232
 <212> DNA
 <213> Conus characteristicus

<400> 70
 ggatccatga tgtctaaact gggagtcttg ttgaccatct gtctgcttct gtttcccctt 60

21

actgctgttc cgctggatgg agatcaacct gcagaccgac ctgcagagcg taagcaggac 120
 gtttcatctg aacagcatcc cttctttgat cccgtcaaac ggtggtgccg ccggtgttac 180
 atgggatgca tcccttggtg cttttaacgt gttgatgacc aactttctcg ag 232

<210> 71
 <211> 68
 <212> PRT
 <213> Conus characteristicus

<400> 71
 Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu
 1 5 10 15
 Leu Phe Pro Leu Thr Ala Val Pro Leu Asp Gly Asp Gln Pro Ala Asp
 20 25 30
 Arg Pro Ala Glu Arg Lys Gln Asp Val Ser Ser Glu Gln His Pro Phe
 35 40 45
 Phe Asp Pro Val Lys Arg Cys Cys Arg Arg Cys Tyr Met Gly Cys Ile
 50 55 60
 Pro Cys Cys Phe
 65

<210> 72
 <211> 14
 <212> PRT
 <213> Conus characteristicus

<220>
 <221> PEPTIDE
 <222> (1)..(14)
 <223> Xaa at residue 11 is Pro or Hyp; Xaa at residue 6 is Tyr, 125I-Ty
 r, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 72
 Cys Cys Arg Arg Cys Xaa Met Gly Cys Ile Xaa Cys Cys Phe
 1 5 10
 <210> 73
 <211> 323
 <212> DNA
 <213> Conus circumcisis

<400> 73
 caagaaggat cgatagcagt tcatgatgtc taaactgggg gtattgttga ccatctgtct 60
 gcttctgttt ccccttactg ctcttccaat ggatggagat caacctgcag accaacctgc 120
 agatcgtatg caggacgaca tttcatctga gcagtatccc ttgtttgata agagacgaaa 180
 gtgttgccgc aaagacgggc catgccccaa atatttcaaa gacaatttta tttgtggttg 240
 ttgttaaagt acaacgtgtc gatgaccaac ttcgttatca cgattcgcca agtgtcttaa 300
 tgaataagta aaatgattgc agt 323

<210> 74
 <211> 74
 <212> PRT
 <213> Conus circumcisis

22

<400> 74

Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
 1 5 10 15

Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Pro Ala Asp Gln Pro
 20 25 30

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

Asp Lys Arg Arg Lys Cys Cys Gly Lys Asp Gly Pro Cys Pro Lys Tyr
 50 55 60

Phe Lys Asp Asn Phe Ile Cys Gly Cys Cys
 65 70

<210> 75

<211> 23

<212> PRT

<213> Conus circumciscus

<220>

<221> PEPTIDE

<222> (1)..(23)

<223> Xaa at residue 9 and 11 is Pro or Hyp; Xaa at residue 13 is Tyr,
 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-T
 y

<400> 75

Arg Lys Cys Cys Gly Lys Asp Gly Xaa Cys Xaa Lys Xaa Phe Lys Asp
 1 5 10 15

Asn Phe Ile Cys Gly Cys Cys
 20

<210> 76

<211> 293

<212> DNA

<213> Conus dalli

<400> 76

caagagggat cgatagcagt tcatgatgtc taaactggga gccttgttga ccatctgtct 60

acttctgttt tccctaactg ctgttccgct ggatggagat caacatgcag accaacctgc 120

agagcgtctg caggaccgcc ttccaactga aaatcatccc ttatatgatc ccgtcaaacg 180

gtgttgcatg gattcgggaat gcgactattc ttgctggcct tgctgtattt tatcataacc 240

tttgttatcg cggcctcatc aagtgtcaaa tgaataagta aaatgattgc agt 293

<210> 77

<211> 71

<212> PRT

<213> Conus dalli

<400> 77

Met Met Ser Lys Leu Gly Ala Leu Leu Thr Ile Cys Leu Leu Leu Phe
 1 5 10 15

Ser Leu Thr Ala Val Pro Leu Asp Gly Asp Gln His Ala Asp Gln Pro
 20 25 30

Ala Glu Arg Leu Gln Asp Arg Leu Pro Thr Glu Asn His Pro Leu Tyr
 35 40 45

Asp Pro Val Lys Arg Cys Cys Asp Asp Ser Glu Cys Asp Tyr Ser Cys
 50 55 60

Trp Pro Cys Cys Ile Leu Ser
 65 70

<210> 78
 <211> 18
 <212> PRT
 <213> Conus dalli

<220>
 <221> PEPTIDE
 <222> (1)..(18)
 <223> Xaa at residue 6 is Glu or gamma-carboxy Glu; Xaa at residue 13 is Pro or Hyp; Xaa at residue 12 is Trp or bromo-Trp; Xaa at residue 9 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 78
 Cys Cys Asp Asp Ser Xaa Cys Asp Xaa Ser Cys Xaa Xaa Cys Cys Ile
 1 5 10 15

Leu Ser

<210> 79
 <211> 299
 <212> DNA
 <213> Conus dalli

<400> 79
 caagagggat cgatagcagt tcatgatgtc taaactggga gtcttgttga ccatttgtct 60
 acttctgttt ccccttactg ctgttccact ggatggagat cagcctgcag accgacctgc 120
 agagcgtatg caggacggca tttcatctga acatcatcca ttttttgatt ccgtcaaaaa 180
 gaaacaacag tgttgcccg cgggtggcatg caacatggga tgcgagcctt gttgtggatg 240
 accagctttg ttatcgcggc tcatgaagtg tcctaataaa taagtaaaac gattgcagt 299

<210> 80
 <211> 72
 <212> PRT
 <213> Conus dalli

<400> 80
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
 1 5 10 15

Pro Leu Thr Ala Val Pro Leu Asp Gly Asp Gln Pro Ala Asp Arg Pro
 20 25 30

Ala Glu Arg Met Gln Asp Gly Ile Ser Ser Glu His His Pro Phe Phe
 35 40 45

Asp Ser Val Lys Lys Lys Gln Gln Cys Cys Pro Pro Val Ala Cys Asn
 50 55 60

Met Gly Cys Glu Pro Cys Cys Gly
 65 70

<210> 81
 <211> 17

24

<212> PRT
 <213> Conus dalli

<220>
 <221> PEPTIDE
 <222> (1)..(17)
 <223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 14 is Glu or gamma-carboxy Glu; Xaa at residue 5, 6 and 15 is Pro or Hyp

<400> 81
 Xaa Gln Cys Cys Xaa Xaa Val Ala Cys Asn Met Gly Cys Xaa Xaa Cys
 1 5 10 15

Cys

<210> 82
 <211> 290
 <212> DNA
 <213> Conus dalli

<400> 82
 caagaaggat cgatagcagt tcatgatgtc taaactggga gtcttggtga tcatatgtct 60
 atttctgttt ccccttactg ctgttcagct caatggagat cagcctgcag accaatctgc 120
 agagcgtatg caggacaaaa tttcatotga acatcatccc ttttttgatc ccgtcaaacg 180
 ttgttgcaac gcggggtttt gccgcttcgg atgcacgcct tgttggtggt gaccagcttt 240
 gttatcgcg cctcatcaag tgtctaataa ataagtaaaa tgattgcagt 290

<210> 83
 <211> 69
 <212> PRT
 <213> Conus dalli

<400> 83
 Met Met Ser Lys Leu Gly Val Leu Leu Ile Ile Cys Leu Phe Leu Phe
 1 5 10 15
 Pro Leu Thr Ala Val Gln Leu Asn Gly Asp Gln Pro Ala Asp Gln Ser
 20 25 30
 Ala Glu Arg Met Gln Asp Lys Ile Ser Ser Glu His His Pro Phe Phe
 35 40 45
 Asp Pro Val Lys Arg Cys Cys Asn Ala Gly Phe Cys Arg Phe Gly Cys
 50 55 60
 Thr Pro Cys Cys Trp
 65

<210> 84
 <211> 16
 <212> PRT
 <213> Conus dalli

<220>
 <221> PEPTIDE
 <222> (1)..(16)
 <223> Xaa at residue 13 is Pro or Hyp; Xaa at residue 16 is Trp or brom o-Tr

<400> 84
 Cys Cys Asn Ala Gly Phe Cys Arg Phe Gly Cys Thr Xaa Cys Cys Xaa
 1 5 10 15

25

<210> 85
 <211> 288
 <212> DNA
 <213> Conus distans

<400> 85
 caagagggat cgatagcagt tcatgatgtc taaactggga gtcttgctga ccatctttct 60
 gcttctgttt ccccttactg ctgttccgct ggatggagat caaccgcag acggacttgc 120
 agagcgcag caggacgaca gttcagctgc actgattaga gactggcttc ttcaaaccgc 180
 acagtgttgt gtgcatccat gcccatgcac gccttgctgt agatgaccag ctttgtcatc 240
 gcggctacgt caagtatcta atgaataagt aagtaaacg attgcagt 288

<210> 86
 <211> 67
 <212> PRT
 <213> Conus distans

<400> 86
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Phe Leu Leu Phe
 1 5 10 15
 Pro Leu Thr Ala Val Pro Leu Asp Gly Asp Gln Pro Ala Asp Gly Leu
 20 25 30
 Ala Glu Arg Met Gln Asp Asp Ser Ser Ala Ala Leu Ile Arg Asp Trp
 35 40 45
 Leu Leu Gln Thr Arg Gln Cys Cys Val His Pro Cys Pro Cys Thr Pro
 50 55 60
 Cys Cys Arg
 65

<210> 87
 <211> 14
 <212> PRT
 <213> Conus distans

<220>
 <221> PEPTIDE
 <222> (1)..(14)
 <223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 6, 8 and 11 is Pro or Hy

<400> 87
 Xaa Cys Cys Val His Xaa Cys Xaa Cys Thr Xaa Cys Cys Arg
 1 5 10

<210> 88
 <211> 303
 <212> DNA
 <213> Conus ermineus

<400> 88
 acctcaagag ggatcgatcg cagttcatga tgtctaaact gggagccttg ttgaccatct 60
 gtctgcttct gtttccatt actgctcttc tgatggatgg agatcagcct gcagaccgac 120
 ctgcagagcg tacggaggat gacatttcat ctgactacat tccctgttgc agttggccat 180

26

gcccccgata ctccaacggt aaacttggtt gtttttggtg ccttggtatga taatgtgttg 240
 atgaccaact ttgttatcac ggctacgtca agtgtctact gaataagtaa aatgattgca 300
 gta 303

<210> 89
 <211> 67
 <212> PRT
 <213> Conus ermineus

<400> 89
 Met Met Ser Lys Leu Gly Ala Leu Leu Thr Ile Cys Leu Leu Leu Phe
 1 5 10 15
 Pro Ile Thr Ala Leu Leu Met Asp Gly Asp Gln Pro Ala Asp Arg Pro
 20 25 30
 Ala Glu Arg Thr Glu Asp Asp Ile Ser Ser Asp Tyr Ile Pro Cys Cys
 35 40 45
 Ser Trp Pro Cys Pro Arg Tyr Ser Asn Gly Lys Leu Val Cys Phe Cys
 50 55 60
 Cys Leu Gly
 65

<210> 90
 <211> 20
 <212> PRT
 <213> Conus ermineus

<220>
 <221> PEPTIDE
 <222> (1)..(20)
 <223> Xaa at residue 5 and 7 is Pro or Hyp; Xaa at residue4 is Trp or
 bromo-Trp; Xaa at residue 9 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-i
 odo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 90
 Cys Cys Ser Xaa Xaa Cys Xaa Arg Xaa Ser Asn Gly Lys Leu Val Cys
 1 5 10 15
 Phe Cys Cys Leu
 20

<210> 91
 <211> 241
 <212> DNA
 <213> Conus generalis

<400> 91
 ggatccatga tgtctaaact gggagtcttg ttgaccatct gtctggttct gtttcccctt 60
 actgctcttc cactggatgg agaacaacct gtagaccgac atgccgagca tatgcaggat 120
 gacaattcag ctgcacagaa cccctggggtt attgccatca gacagtgttg cacgttctgc 180
 aactttggat gccaaccttg ttgcctcacc tgataacgtg ttgatgacca acttttctcga 240
 g 241

<210> 92
 <211> 70
 <212> PRT

<213> Conus generalis

<400> 92

Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Val
1 5 10 15

Leu Phe Pro Leu Thr Ala Leu Pro Leu Asp Gly Glu Gln Pro Val Asp
20 25 30

Arg His Ala Glu His Met Gln Asp Asp Asn Ser Ala Ala Gln Asn Pro
35 40 45

Trp Val Ile Ala Ile Arg Gln Cys Cys Thr Phe Cys Asn Phe Gly Cys
50 55 60

Gln Pro Cys Cys Leu Thr
65 70

<210> 93

<211> 16

<212> PRT

<213> Conus generalis

<220>

<221> PEPTIDE

<222> (1)..(16)

<223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 12 is Pro or
Hy

<400> 93

Xaa Cys Cys Thr Phe Cys Asn Phe Gly Cys Gln Xaa Cys Cys Leu Thr
1 5 10 15

<210> 94

<211> 241

<212> DNA

<213> Conus generalis

<400> 94

ggatccatga tgtctaaact gggagtcttg ttgaccatct gtctggttct gtttcccctt 60

actgctcttc cactggatgg agaacaacct gtagaccgac atgccgagca tatgcaggat 120

gacaattcag ctgcacagaa cccctgggtt attgccatca gacagtgttg cacgttctgc 180

aactttggat gccagccttg ttgcgtcccc tgataacgtg ttgatgacca actttctcga 240

g 241

<210> 95

<211> 70

<212> PRT

<213> Conus generalis

<400> 95

Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Val
1 5 10 15

Leu Phe Pro Leu Thr Ala Leu Pro Leu Asp Gly Glu Gln Pro Val Asp
20 25 30

Arg His Ala Glu His Met Gln Asp Asp Asn Ser Ala Ala Gln Asn Pro
35 40 45

Trp Val Ile Ala Ile Arg Gln Cys Cys Thr Phe Cys Asn Phe Gly Cys

28

50 55 60

Gln Pro Cys Cys Val Pro
65 70

<210> 96
<211> 16
<212> PRT
<213> *Conus generalis*

<220>
<221> PEPTIDE
<222> (1)..(16)
<223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 12 and 16 is Pro or Hy

<400> 96
Xaa Cys Cys Thr Phe Cys Asn Phe Gly Cys Gln Xaa Cys Cys Val Xaa
1 5 10 15

<210> 97
<211> 862
<212> DNA
<213> *Conus geographus*

<400> 97
gtcgactcta gaggatccga caacaaagag tcaacccac tgccacgtca agagcgaagc 60
gccacagcta agacaagagg gatcgatagc agttcatgat gtctaaactg ggagtcttgt 120
tgaccatctg tctgcttctg tttcccctta ctgctcttcc gatggatgga gatgaacctg 180
caaaccgacc tgtcgagcgt atgcaggaca acatttcattc tgagcagtat cccttggttg 240
agaagagacg agattgttgc actccgccga agaaatgcaa agaccgacaa tgcaaacccc 300
agagatgttg cgctggacga taacgtgttg atgaccaact ttatcacggc tacgtcaagt 360
gtttagttaa taagtaaaat gattgcagtc ttgctcagat ttgcttttgt gttttggtct 420
aaagatcaat gaccaaaccg ttgttttgat gcggtattgtc atatatttct cgattccaat 480
ccaacactag atgatttaat cacgatagat taattttcta tcaatgcctt gatttttctgt 540
ctgtcatatc agttttgttt atatttatatt tttcgtcact gtctacacaa acgcatgcat 600
gcacgcatgc acgcacacac gcacgcacgc tcgcacaaac atgcgcgcgc acgcacacac 660
acacacacac acacaaacac acacacaagc aatcacacaa ttattgacat tatttattta 720
ttcattgatg tatttggtat tcgtttgctt gtttttagaa tagtttgagg ccgtcttttt 780
ggatttatatt gaactgcttt attgtatacg agtacttcgt gctttgaaac actgctgaaa 840
ataaaaacaaa cactgacgta gc 862

<210> 98
<211> 75
<212> PRT
<213> *Conus geographus*

<400> 98
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
1 5 10 15

29

Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Glu Pro Ala Asn Arg Pro
 20 25 30

Val Glu Arg Met Gln Asp Asn Ile Ser Ser Glu Gln Tyr Pro Leu Phe
 35 40 45

Glu Lys Arg Arg Asp Cys Cys Thr Pro Pro Lys Lys Cys Lys Asp Arg
 50 55 60

Gln Cys Lys Pro Gln Arg Cys Cys Ala Gly Arg
 65 70 75

<210> 99
 <211> 22
 <212> PRT
 <213> Conus geographus

<220>
 <221> PEPTIDE
 <222> (1)..(22)
 <223> Xaa at residue 6, 7 and 17 is Pro or Hyp

<400> 99
 Arg Asp Cys Cys Thr Xaa Xaa Lys Lys Cys Lys Asp Arg Gln Cys Lys
 1 5 10 15

Xaa Gln Arg Cys Cys Ala
 20

<210> 100
 <211> 860
 <212> DNA
 <213> Conus geographus

<400> 100
 ggccagacga caacaaagag tcaacccac tgccacgtca agagcgaagc gccacagcta 60
 agacaagagg gatcgatagc agttcatgat gtctaaactg ggagtcttgt tgaccatctg 120
 tctgcttctg tttccctta ctgctcttcc gatggatgga gatgaacctg caaaccgacc 180
 tgtcgagcgt atgcaggaca acatttcatac tgagcagtat cccttgtttg agaagagacg 240
 agattgtttgc actccgccga ggaaatgcaa agaccgacga tgcaaaccga tgaaatgttg 300
 cgctggacga taacgtgttg atgaccaact ttatcacggc tagctcagtg tttagtgaat 360
 aagtaaaatg attgcagtct tgctcagatt gcttttgtgt tttggtctaa gatcaatgac 420
 caaacgcttg ttttgatgcg gattgtcata tatttctoga ttccaatcca aactagatg 480
 atttaatcac gatagattaa ttttctatca atgccttgat ttttcgtctg tcatatcagt 540
 tttgtttata tttatTTTTT cgtcaactgtc tacacaaacg catgcatgca cgcattgcacg 600
 cacacacgca cgcacgctcg cacaaacatg cgcgcgcacg cacacacaca cacacacaca 660
 aacacacaca cgaagcaatc acacaattag ttgacattat ttattttattc attgatgtat 720
 ttgttattcg tttgcttggt tttagaatag tttgaggccg tcttttttga tttatttgaa 780
 ctgctttatt gtatacgagt acttcgtgct ttgaaacact gctgaaaata aaacaaacac 840
 tgacgtagca aaaaaaaaaa 860

30

<210> 101
 <211> 75
 <212> PRT
 <213> Conus geographus

<400> 101
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
 1 5 10 15
 Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Glu Pro Ala Asn Arg Pro
 20 25 30
 Val Glu Arg Met Gln Asp Asn Ile Ser Ser Glu Gln Tyr Pro Leu Phe
 35 40 45
 Glu Lys Arg Arg Asp Cys Cys Thr Pro Pro Arg Lys Cys Lys Asp Arg
 50 55 60
 Arg Cys Lys Pro Met Lys Cys Cys Ala Gly Arg
 65 70 75

<210> 102
 <211> 22
 <212> PRT
 <213> Conus geographus

<220>
 <221> PEPTIDE
 <222> (1)..(22)
 <223> Xaa at residue 6, 7 and 17 is Pro or Hyp

<400> 102
 Arg Asp Cys Cys Thr Xaa Xaa Arg Lys Cys Lys Asp Arg Arg Cys Lys
 1 5 10 15
 Xaa Met Lys Cys Cys Ala
 20

<210> 103
 <211> 22
 <212> PRT
 <213> Conus geographus

<220>
 <221> PEPTIDE
 <222> (1)..(22)
 <223> Xaa at residue 6, 7 and 17 is Pro or Hyp

<400> 103
 Arg Asp Cys Cys Thr Xaa Xaa Lys Lys Cys Lys Asp Arg Arg Cys Lys
 1 5 10 15
 Xaa Leu Lys Cys Cys Ala
 20

<210> 104
 <211> 321
 <212> DNA
 <213> Conus gloriamaris

<400> 104
 ctcactatag gaattcgagc tcggtacacg ggatcgatag cagttcatga tgtctaaact 60
 gggagccttg ttgaccatct gtctacttct gttttcccta actgctgttc cgctggatgg 120

31

agatcaacat gcagaccaac ctgcagagcg tctgcatgac cgccttccaa ctgaaaatca 180
 tcccttatat gatcccgta aacgggtgttg cgatgattcg gaatgcgact attcttgctg 240
 gccttgctgt atgtttggat aacctttggt atcgcggcct cgataagtgt ctaatgaata 300
 agtaaaacga ttgcagtagg c 321

<210> 105
 <211> 71
 <212> PRT
 <213> Conus gloriamaris

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

<210> 106
 <211> 17
 <212> PRT
 <213> Conus gloriamaris

<220>
 <221> PEPTIDE
 <222> (1)..(17)
 <223> Xaa at residue is 6 Glu or gamma-carboxy Glu; Xaa at residue 13 is
 s Pro or Hyp; Xaa at residue 12 is Trp or bromo-Trp; Xaa at resid
 ue 9 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr o
 r O-phospho-Ty

<400> 106
 Cys Cys Asp Asp Ser Xaa Cys Asp Xaa Ser Cys Xaa Xaa Cys Cys Met
 1 5 10 15

Phe

<210> 107
 <211> 257
 <212> DNA
 <213> Conus gloriamaris

<400> 107
 gttcatgatg tctaaactgg gagtcttggt gatcatctgt ctacttctgt ttccccttac 60
 tgctgttccg ctggatggag atcaacctgc agaccgatat gcagagcgta tgcaggacga 120
 catttcatct gaacatcatc ccatgtttga tgccgtcaga ggggtgttgcc atctgttggc 180
 atgccgcttc ggatgctcgc cttgttggtg gtgatcagct ttgttatcgc ggcctcatca 240
 agtgactcta atgcaaa 257
 <210> 108
 <211> 69

32

<212> PRT

<213> Conus gloriamaris

<400> 108

Met Met Ser Lys Leu Gly Val Leu Leu Ile Ile Cys Leu Leu Leu Phe
 1 5 10 15

Pro Leu Thr Ala Val Pro Leu Asp Gly Asp Gln Pro Ala Asp Arg Tyr
 20 25 30

Ala Glu Arg Met Gln Asp Asp Ile Ser Ser Glu His His Pro Met Phe
 35 40 45

Asp Ala Val Arg Gly Cys Cys His Leu Leu Ala Cys Arg Phe Gly Cys
 50 55 60

Ser Pro Cys Cys Trp
 65

<210> 109

<211> 17

<212> PRT

<213> Conus gloriamaris

<220>

<221> PEPTIDE

<222> (1)..(17)

<223> Xaa at residue 14 is Pro or Hyp; Xaa at residue 17 is Trp or bromo-Trp

<400> 109

Gly Cys Cys His Leu Leu Ala Cys Arg Phe Gly Cys Ser Xaa Cys Cys
 1 5 10 15

Xaa

<210> 110

<211> 471

<212> DNA

<213> Conus gloriamaris

<400> 110

gagacgacaa ggaacagtca accccacagc cacgccaaga gcagacagcc acagctacgt 60

gaagaagggg ggagagaggt tcgtgatggt gaaaatggga gtgggtgctat tcattcttctt 120

gggtactgttt cccctggcaa cgctccagct ggatgcagat caacctgtag aacgatatgc 180

ggagaacaaa cagctcctca acccagatga aaggaggggaa atcatattgc atgctctggg 240

gacgcgatgc tgttcttggg atgtgtgcga ccaccogagt tgtacttgct gcggcgggta 300

gcgccgaaca tccatggcgc tgtgctgggc gggttttatcc aacaacgaca gcgtttgttg 360

atttcatgta tcattgcgcc cagctctctt gtctaagaat gacgaacatg attgcactct 420

ggttcagatt tcgtgttctt ttctgacaat aaatgacaaa actccaaaaa a 471

<210> 111

<211> 71

<212> PRT

<213> Conus gloriamaris

<400> 111

Met Leu Lys Met Gly Val Val Leu Phe Ile Phe Leu Val Leu Phe Pro

33

1 5 10 15
 Leu Ala Thr Leu Gln Leu Asp Ala Asp Gln Pro Val Glu Arg Tyr Ala
 20 25 30
 Glu Asn Lys Gln Leu Leu Asn Pro Asp Glu Arg Arg Glu Ile Ile Leu
 35 40 45
 His Ala Leu Gly Thr Arg Cys Cys Ser Trp Asp Val Cys Asp His Pro
 50 55 60
 Ser Cys Thr Cys Cys Gly Gly
 65 70
 <210> 112
 <211> 16
 <212> PRT
 <213> *Conus gloriamaris*
 <220>
 <221> PEPTIDE
 <222> (1)..(16)
 <223> Xaa at residue 10 is Pro or Hyp; Xaa at residue 4 is Trp or bromo
 -Tr
 <400> 112
 Cys Cys Ser Xaa Asp Val Cys Asp His Xaa Ser Cys Thr Cys Cys Gly
 1 5 10 15
 <210> 113
 <211> 304
 <212> DNA
 <213> *Conus laterculatus*
 <400> 113
 cgacctcaag aaggatcgat agcagttcat gatgtctaaa ctgggagtct tgttgaccat 60
 ctgtctgctt ctgtttcccc ttactgctct tccgatggat ggagatcaac ctgcagaccg 120
 acctgcagag cgtatgcagg acgtttcatc tgaacagcat cccttgatg atcccgtaa 180
 acggtgttgc gactggccat gcagcggatg catcccttgt tgctaatagt aacaacgtgt 240
 tgataaccaa ctttcttacc acgactacgt caagtgtcta atgaataagt aaaatgattg 300
 cagt 304
 <210> 114
 <211> 65
 <212> PRT
 <213> *Conus laterculatus*
 <400> 114
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
 1 5 10 15
 Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Pro Ala Asp Arg Pro
 20 25 30
 Ala Glu Arg Met Gln Asp Val Ser Ser Glu Gln His Pro Leu Tyr Asp
 35 40 45
 Pro Val Lys Arg Cys Cys Asp Trp Pro Cys Ser Gly Cys Ile Pro Cys
 50 55 60
 Cys

65

<210> 115
 <211> 13
 <212> PRT
 <213> Conus laterculatus

<220>
 <221> PEPTIDE
 <222> (1)..(13)
 <223> Xaa at residue 5 and 11 is Pro or Hyp; Xaa at residue 4 is Trp or bromo-Trp

<400> 115
 Cys Cys Asp Xaa Xaa Cys Ser Gly Cys Ile Xaa Cys Cys
 1 5 10

<210> 116
 <211> 313
 <212> DNA
 <213> Conus laterculatus

<400> 116
 cgacctcaag aaggatcgat agcagttcat gatgtctaaa ctgggagtct tgttgaccat 60
 ctgtctgctt ctgtttcccc ttactgctct ggatggagat caacctgcag accgacttgc 120
 agagcgtatg caggacgaca tttcatctga gcagcatccc ttgaaaaga gacgagactg 180
 ttgcacacct ccgaagaaat gcagagaccg acaatgcaaa cctgcacgtt gttgcggagg 240
 ataacgtggt gatgaccaac ttgttatca cggctacgtc aagtgtctag tgaataagta 300
 aaacgattgc agt 313

<210> 117
 <211> 71
 <212> PRT
 <213> Conus laterculatus

<400> 117
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
 1 5 10 15
 Pro Leu Thr Ala Leu Asp Gly Asp Gln Pro Ala Asp Arg Leu Ala Glu
 20 25 30
 Arg Met Gln Asp Asp Ile Ser Ser Glu Gln His Pro Phe Glu Lys Arg
 35 40 45
 Arg Asp Cys Cys Thr Pro Pro Lys Lys Cys Arg Asp Arg Gln Cys Lys
 50 55 60
 Pro Ala Arg Cys Cys Gly Gly
 65 70

<210> 118
 <211> 22
 <212> PRT
 <213> Conus laterculatus

<220>
 <221> PEPTIDE
 <222> (1)..(22)
 <223> Xaa at residue 6, 17 and 17 is Pro or Hyp

35

<400> 118

Arg Asp Cys Cys Thr Xaa Xaa Lys Lys Cys Arg Asp Arg Gln Cys Lys
 1 5 10 15

Xaa Ala Arg Cys Cys Gly
 20

<210> 119

<211> 314

<212> DNA

<213> Conus laterculatus

<400> 119

gggatcgata gcagttcatg atgtctaaac tgggagtctt gttgaccatc tgtctgcttc 60
 tgtttccct tactgctctt ccgatggatg gagatcaact tgcacgccga tctgcagagc 120
 gtatgcagga caacatttca tctgagcagc atcacctctt tgaaaagaga cgaccacat 180
 gttgcaccta tgacgggagt tgcctaaaag aatcatgcat gcgtaaagct tgttgccgat 240
 gataacgtgt tgatgaccaa ctttgttatc acggtactc aagtgtctaa tgaataagta 300
 aaatgattgc agta 314

<210> 120

<211> 74

<212> PRT

<213> Conus laterculatus

<400> 120

Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
 1 5 10 15

Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Leu Ala Arg Arg Ser
 20 25 30

Ala Glu Arg Met Gln Asp Asn Ile Ser Ser Glu Gln His His Leu Phe
 35 40 45

Glu Lys Arg Arg Pro Pro Cys Cys Thr Tyr Asp Gly Ser Cys Leu Lys
 50 55 60

Glu Ser Cys Met Arg Lys Ala Cys Cys Gly
 65 70

<210> 121

<211> 22

<212> PRT

<213> Conus laterculatus

<220>

<221> PEPTIDE

<222> (1)..(22)

<223> Xaa at residue 14 is Glu or gamma-carboxy Glu; Xaa at residue 2 and 3 is Pro or Hyp; Xaa at residue 7 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 121

Arg Xaa Xaa Cys Cys Thr Xaa Asp Gly Ser Cys Leu Lys Xaa Ser Cys
 1 5 10 15

Met Arg Lys Ala Cys Cys
 20

<210> 122
 <211> 314
 <212> DNA
 <213> Conus laterculatus

<400> 122
 gggatcgata gcagttcatg atgtctaaac tgggagtctt gttgaccacc tgtctgcttc 60
 tgtttccctt tactgctctt ccgatggatg gagatcaact tgcacgccga cctgcagagc 120
 gtatgcagga caacatttca totgagcagc atcccttctt tgaaaggaga cgaccacccat 180
 gttgcaccta tgacgggagt tgcctaaaag aatcatgcaa gcgtaaagct tgttgcggtat 240
 aataacgtgt tgatgaccaa ctttggtatc acggctactc aagtgtctaa tgaataagta 300
 aaatgattgc agta 314

<210> 123
 <211> 74
 <212> PRT
 <213> Conus laterculatus

<400> 123
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Thr Cys Leu Leu Leu Phe
 1 5 10 15
 Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Leu Ala Arg Arg Pro
 20 25 30
 Ala Glu Arg Met Gln Asp Asn Ile Ser Ser Glu Gln His Pro Phe Phe
 35 40 45
 Glu Arg Arg Arg Pro Pro Cys Cys Thr Tyr Asp Gly Ser Cys Leu Lys
 50 55 60
 Glu Ser Cys Lys Arg Lys Ala Cys Cys Gly
 65 70

<210> 124
 <211> 22
 <212> PRT
 <213> Conus laterculatus

<220>
 <221> PEPTIDE
 <222> (1)..(22)
 <223> Xaa at residue 14 is Glu or gamma-carboxy Glu; Xaa at residue 2 and 3 is Pro or Hyp; Xaa at residue 7 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 124
 Arg Xaa Xaa Cys Cys Thr Xaa Asp Gly Ser Cys Leu Lys Xaa Ser Cys
 1 5 10 15
 Lys Arg Lys Ala Cys Cys
 20

<210> 125
 <211> 247
 <212> DNA
 <213> Conus leopardus

<400> 125

37

ggatccatga tgtctaaact gggagtcttg ttgaccgtct gtctgcttct gtttcccctt 60
 actgctcttc ggctggttgg agatcaacct gcagagcgac ctgcaaagcg tacgcaggac 120
 gacattccag atggacagca tccgttaaata gataggcaga taaactgttg cccgtggcca 180
 tgccctagta catgccgcca tcaatgctgc cattaatgat aacgtgttga tgaccaactt 240
 tctcgag 247

<210> 126
 <211> 71
 <212> PRT
 <213> Conus leopardus

<400> 126
 Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Val Cys Leu Leu
 1 5 10 15
 Leu Phe Pro Leu Thr Ala Leu Arg Leu Val Gly Asp Gln Pro Ala Glu
 20 25 30
 Arg Pro Ala Lys Arg Thr Gln Asp Asp Ile Pro Asp Gly Gln His Pro
 35 40 45
 Leu Asn Asp Arg Gln Ile Asn Cys Cys Pro Trp Pro Cys Pro Ser Thr
 50 55 60
 Cys Arg His Gln Cys Cys His
 65 70

<210> 127
 <211> 19
 <212> PRT
 <213> Conus leopardus
 <220>
 <221> PEPTIDE
 <222> (1)..(19)
 <223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 6, 8 and 10 is Pro or Hyp; Xaa at residue 7 is Trp or bromo-Trp

<400> 127
 Xaa Ile Asn Cys Cys Xaa Xaa Xaa Cys Xaa Ser Thr Cys Arg His Gln
 1 5 10 15
 Cys Cys His

<210> 128
 <211> 244
 <212> DNA
 <213> Conus lividus

<400> 128
 ggatccatga tgtctaaact gggagtcttg ttgaccgtct gtctgcttct gtttcccctt 60
 actgctcttc ggctggtttag agatcaacct gcagagcgac ctgcaaagcg tacgcaggac 120
 gacattccaa atggacagga tccgttaatt gataggcaga taaattgttg cccttggcca 180
 tgccctgatt catgccacta tcaatgctgc cactgataac gtgttgatga ccaactttct 240
 cgag 244

<210> 129

38

<211> 71
 <212> PRT
 <213> Conus lividus

<400> 129
 Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Val Cys Leu Leu
 1 5 10 15
 Leu Phe Pro Leu Thr Ala Leu Arg Leu Val Arg Asp Gln Pro Ala Glu
 20 25 30
 Arg Pro Ala Lys Arg Thr Gln Asp Asp Ile Pro Asn Gly Gln Asp Pro
 35 40 45
 Leu Ile Asp Arg Gln Ile Asn Cys Cys Pro Trp Pro Cys Pro Asp Ser
 50 55 60
 Cys His Tyr Gln Cys Cys His
 65 70

<210> 130
 <211> 19
 <212> PRT
 <213> Conus lividus

<220>
 <221> PEPTIDE
 <222> (1)..(19)
 <223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 6, 8 and 10 is Pro or Hyp; Xaa at residue 7 is Trp or bromo-Trp; Xaa at residue 15 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 130
 Xaa Ile Asn Cys Cys Xaa Xaa Xaa Cys Xaa Asp Ser Cys His Xaa Gln
 1 5 10 15

Cys Cys His

<210> 131
 <211> 275
 <212> DNA
 <213> Conus lynceus

<400> 131
 aaggatcgat agcagttcat gatgtctaaa ctgggagtct tgttgaccat ctgtctgctt 60
 ctgtttcccc ttactgtctt tccgatggat ggagatcaat ctgcagaccg acttgacagag 120
 cgtatgcagg acaacatttc atctgagcag catcccttct ttgaaaagag aggacgagac 180
 tgttgcacac ctccgaggaa atgcagagac cgagcctgca aacctcaacg ttgttgcgga 240
 ggataagctg ttgatgacca actttgttat acggc 275

<210> 132
 <211> 75
 <212> PRT
 <213> Conus lynceus

<400> 132
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
 1 5 10 15
 Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Ser Ala Asp Arg Leu

39

20 25 30

Ala Glu Arg Met Gln Asp Asn Ile Ser Ser Glu Gln His Pro Phe Phe
35 40 45

Glu Lys Arg Gly Arg Asp Cys Cys Thr Pro Pro Arg Lys Cys Arg Asp
50 55 60

Arg Ala Cys Lys Pro Gln Arg Cys Cys Gly Gly
65 70 75

<210> 133
<211> 23
<212> PRT
<213> Conus lynceus

<220>
<221> PEPTIDE
<222> (1)..(23)
<223> Xaa at residue 7, 8 and 18 is Pro or Hyp

<400> 133
Gly Arg Asp Cys Cys Thr Xaa Xaa Arg Lys Cys Arg Asp Arg Ala Cys
1 5 10 15

Lys Xaa Gln Arg Cys Cys Gly
20

<210> 134
<211> 803
<212> DNA
<213> Conus magus

<400> 134
caagagggat cgatagcagt tcatgatgtc taaactggga gtcttggtga ccatctgtct 60
gcttctgttt ccccttactg ctcttccgat ggatggagat gaacctgcaa accgacctgt 120
cgagcgtatg caggacaaca tttcatctga gcagtatccc ttgtttgaga agagacgaga 180
ttgttgact cgcgcaaga aatgcaaaga ccgacaatgc aaacccaga gatgttgccg 240
tggacgataa cgtgttgatg accaacttta tcacggctac gtcaagtgtt tagtgaataa 300
gtaaaatgat tgcagtcttg ctcagatttg cttttgtgtt ttggtctaaa gatcaatgac 360
caaaccgttg ttttgatgcg gattgtcata tatttctoga ttccaatcca acactagatg 420
atttaatcac gatagattaa ttttctatca atgccttgat ttttcgtctg tcatatcagt 480
tttgtttata tttatTTTTT cgtcactgtc tacacaaaacg catgcatgca cgcattgcacg 540
cacacacgca cgcacgctcg cacaacatg cgcgcgcacg cacacacaca cacacacaca 600
caaacacaca cacgaagcaa tcacacaatt agttgacatt atttatttat tcattgatgt 660
atgtgttatt cgtttgcttg tttttagaat agtttgaggc cgtctttttg gatttatttg 720
aactgcttta ttgtatacga gtacttcgtg cggggaaaca ctgctgaaaa taaaacaaac 780
actgacgtag caaaaaaaaaaaa aaa 803

<210> 135
<211> 75
<212> PRT

40

<213> Conus magus

<400> 135

Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
 1 5 10 15

Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Glu Pro Ala Asn Arg Pro
 20 25 30

Val Glu Arg Met Gln Asp Asn Ile Ser Ser Glu Gln Tyr Pro Leu Phe
 35 40 45

Glu Lys Arg Arg Asp Cys Cys Thr Pro Pro Lys Lys Cys Lys Asp Arg
 50 55 60

Gln Cys Lys Pro Gln Arg Cys Cys Ala Gly Arg
 65 70 75

<210> 136

<211> 22

<212> PRT

<213> Conus magus

<220>

<221> PEPTIDE

<222> (1)..(22)

<223> Xaa at residue 6 and 7 is Pro or Hyp

<400> 136

Arg Asp Cys Cys Thr Xaa Xaa Lys Lys Cys Lys Asp Arg Gln Cys Lys
 1 5 10 15

Xaa Gln Arg Cys Cys Ala
 20

<210> 137

<211> 656

<212> DNA

<213> Conus magus

<400> 137

caagagggat cgatagcagt tcatgatgtc taaactggga gtcttggtga ccatctgtct 60
 gcttctgttt ccccttactg ctcttccaat ggatggagat caacctgcag accaacctgc 120
 agatcgtatg caggacgaca tttcatctga gcagtatccc ttgtttgata tgagaaaaag 180
 gtgttgcggc cccggcggtt catgccccgt atatttcaga gacaatttta tttgtggttg 240
 ttgttaaagt acaacgtgtc gatgaccaac ttcatatca cgactacgcc aagtgtctaa 300
 tgaataaata aaatgattgc agtctcgtc agatttgctt ttgtattttg gtctaaagat 360
 caatgaccaa accgttggtt tgggtgtgat tttcatatat ttctcgagtc ctatccaaca 420
 ctagatgatt taatcacgat agatctgatt tttttatcaa aggcttggtt tttcgtctgt 480
 cacatcagtt ttgtttatat ttaatttttc gtcactgatt acacacacgc atgaacgcac 540
 agagtactaa cacatacaca cacacacaca cacacacaca cacacacaca cacacacaca 600
 cacacacaca cagcgcgcg cgcgcgcca tctagtagcg ccgcgacgac acacac 656

<210> 138

<211> 74

<212> PRT

41

<213> Conus magus

<400> 138

Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
 1 5 10 15

Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Pro Ala Asp Gln Pro
 20 25 30

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

Asp Met Arg Lys Arg Cys Cys Gly Pro Gly Gly Ser Cys Pro Val Tyr
 50 55 60

Phe Arg Asp Asn Phe Ile Cys Gly Cys Cys
 65 70

<210> 139

<211> 21

<212> PRT

<213> Conus magus

<220>

<221> PEPTIDE

<222> (1)..(21)

<223> Xaa at residue 4 and 9 is Pro or Hyp; Xaa at residue is 11 Tyr, 1
 25I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 139

Cys Cys Gly Xaa Gly Gly Ser Cys Xaa Val Xaa Phe Arg Asp Asn Phe
 1 5 10 15

Ile Cys Gly Cys Cys
 20

<210> 140

<211> 594

<212> DNA

<213> Conus magus

<400> 140

caagagggat cgatagcagt tcatgatgtc taaactggga gtcttggtga ccatctgttt 60

gcttctgttt ccccttactg ctcttccgag ggatggagat caatctgtag accgacctgc 120

agagcgtatg caggacgaca tttcatctga gctgcatccc ttgtcaatca gaaaaagaat 180

gtgttgccggc gagagtgcgc catgccccag ctatttcaga aacagtcaga tttgtcattg 240

ttgttaaagt acaacgtgtc gatgaccacc ttcgttatca cgactaatga taagtaaaat 300

gattgcagtc tcgctcagat ttgcttttgt attttgggtc aaagatcaat gaccaaaccg 360

ttgttttgat gtggattttc atatatttct cgagtcctat ccaacactag atgatttaat 420

cacgatagat ctgatttttt tatcaaagcc ttgggttttc gtctgtcaca tcagttttgt 480

ttatatattaa tttttcgtca ctgattacac acacgcatga acgcacagac gtactaacac 540

atacacacac acacacacac acacacacac acacacacac acacacacac acac 594

<210> 141

<211> 74

42

<212> PRT

<213> Conus magus

<400> 141

Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
 1 5 10 15

Pro Leu Thr Ala Leu Pro Arg Asp Gly Asp Gln Ser Val Asp Arg Pro
 20 25 30

Ala Glu Arg Met Gln Asp Asp Ile Ser Ser Glu Leu His Pro Leu Ser
 35 40 45

Ile Arg Lys Arg Met Cys Cys Gly Glu Ser Ala Pro Cys Pro Ser Tyr
 50 55 60

Phe Arg Asn Ser Gln Ile Cys His Cys Cys
 65 70

<210> 142

<211> 22

<212> PRT

<213> Conus magus

<220>

<221> PEPTIDE

<222> (1)..(22)

<223> Xaa at residue 5 is Glu or gamma-carboxy Glu; Xaa at residue 8 and
 10 is Pro or Hyp; Xaa at residue 12 is Tyr, 125I-Tyr, mono-iodo-
 -Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 142

Met Cys Cys Gly Xaa Ser Ala Xaa Cys Xaa Ser Xaa Phe Arg Asn Ser
 1 5 10 15

Gln Ile Cys His Cys Cys
 20

<210> 143

<211> 501

<212> DNA

<213> Conus magus

<400> 143

caagagggat c gatagcagt tcatgatgtc taaactggga gtcttggtga ccatctgtct 60

gcttctgttt ccccttactg ctcttccaat ggatggagat caacctgcag accaacctgc 120

agatcgtatg caggacgaca tttcatctga gcagtatccc ttgtttgata agagacaaaa 180

gtgttgcggc cccggcggtt catgccccgt atatttcaca gacaatttta tttgtggttg 240

ttgttaaagt acaacgtgtc gatgaccaac ttcattatca cgactacgcc aagtgtctaa 300

tgaataaata aaatgattgc agtctcgctc agatttgctt ttgtatttgg tctaaagatc 360

aatgacaaa ccgttggttt ggtgctggat tttcatatat ttctcgattc ctatccaaca 420

ctagatgatt taatcacgat agatctgatt ttttatcaa tgccttaatt ttttgctctg 480

tcatatcagt tttgtttata t 501

<210> 144

<211> 74

<212> PRT

43

<213> Conus magus

<400> 144

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Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
1          5          10          15

Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Pro Ala Asp Gln Pro
          20          25          30

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

Asp Lys Arg Gln Lys Cys Cys Gly Pro Gly Gly Ser Cys Pro Val Tyr
          50          55          60

Phe Thr Asp Asn Phe Ile Cys Gly Cys Cys
65          70
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<210> 145

<211> 23

<212> PRT

<213> Conus magus

<220>

<221> PEPTIDE

<222> (1)..(23)

<223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 6 and 11 is P
ro or Hyp; Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-
iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 145

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Xaa Lys Cys Cys Gly Xaa Gly Gly Ser Cys Xaa Val Xaa Phe Thr Asp
1          5          10          15

Asn Phe Ile Cys Gly Cys Cys
          20
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<210> 146

<211> 454

<212> DNA

<213> Conus magus

<400> 146

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caagagggat cgatagcagt tcatgatgtc taaactggga gtcttggtga ccatctgtct      60
gcttctgttt ccccttactg ctcttccaat ggatggagat caacctgcag accaacctgc      120
agatcgtatg caggacgaca tttcatctga gcagtatccc ttgtttgata agagacaaaa      180
gtgttgcggc cccggcggtt catgccccgt atatttcaga gacaatttta tttgtggttg      240
ttgttaaagt acaacgtgtc gatgaccatc ttcattatca cgactacgcc aagtgtctaa      300
tgaataaata aaatgattgc agtctcgtc agatttgctt ttgtattttg gtctaaagat      360
caatgaccaa accgttggtt tgggtgtggat tttcatatat ttctcgattc ctatccaaca      420
ctagatgatt taatcacgat agatctgatt tttt                                454
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<210> 147

<211> 74

<212> PRT

<213> Conus magus

<400> 147

44

Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
 1 5 10 15

Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Pro Ala Asp Gln Pro
 20 25 30

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

Asp Lys Arg Gln Lys Cys Cys Gly Pro Gly Gly Ser Cys Pro Val Tyr
 50 55 60

Phe Arg Asp Asn Phe Ile Cys Gly Cys Cys
 65 70

<210> 148

<211> 23

<212> PRT

<213> Conus magus

<220>

<221> PEPTIDE

<222> (1)..(23)

<223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 6 and 11 is P
 ro or Hyp; Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-
 iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 148

Xaa Lys Cys Cys Gly Xaa Gly Gly Ser Cys Xaa Val Xaa Phe Arg Asp
 1 5 10 15

Asn Phe Ile Cys Gly Cys Cys
 20

<210> 149

<211> 22

<212> PRT

<213> Conus magus

<220>

<221> PEPTIDE

<222> (1)..(22)

<223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 10 and 20 is
 Pro or Hyp; Xaa at residue 12 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-
 iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 149

Xaa Lys Cys Cys Ser Gly Gly Ser Cys Xaa Leu Xaa Phe Arg Asp Arg
 1 5 10 15

Leu Ile Cys Xaa Cys Cys
 20

<210> 150

<211> 19

<212> PRT

<213> Conus marmoreus

<220>

<221> PEPTIDE

<222> (1)..(19)

<223> Xaa at residue 16 is Pro or Hyp

<400> 150

Ser Lys Gln Cys Cys His Leu Ala Ala Cys Arg Phe Gly Cys Thr Xaa
 1 5 10 15

Cys Cys Asn

<210> 151
 <211> 321
 <212> DNA
 <213> Conus marmoreus
 <400> 151
 caagaaggat cgatagcagt tcatgatgtc taaactggga gtcttgttga ccatctgtct 60
 gcttctgttt cccgttactg ctcttccgat ggatggatgat caacctgcag accgacttgt 120
 agagcgtatg caggacaaca tttcatctga gcagcatccc ttctttgaaa agagaagagg 180
 aggctgttgc acacctccga ggaaatgcaa agaccgagcc tgcaaacctg cacgttgctg 240
 cggcccagga taacgtgttg atgaccaact ttgttatcac ggctacgtca agtgtctagt 300
 gaataagtaa aacgattgca g 321

<210> 152
 <211> 76
 <212> PRT
 <213> Conus marmoreus
 <400> 152
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
 1 5 10 15
 Pro Val Thr Ala Leu Pro Met Asp Gly Asp Gln Pro Ala Asp Arg Leu
 20 25 30
 Val Glu Arg Met Gln Asp Asn Ile Ser Ser Glu Gln His Pro Phe Phe
 35 40 45
 Glu Lys Arg Arg Gly Gly Cys Cys Thr Pro Pro Arg Lys Cys Lys Asp
 50 55 60
 Arg Ala Cys Lys Pro Ala Arg Cys Cys Gly Pro Gly
 65 70 75

<210> 153
 <211> 24
 <212> PRT
 <213> Conus marmoreus
 <220>
 <221> PEPTIDE
 <222> (1)..(24)
 <223> Xaa at residue 3, 8, 18 and 24 is Pro or Hyp

<400> 153
 Arg Gly Gly Cys Cys Thr Xaa Xaa Arg Lys Cys Lys Asp Arg Ala Cys
 1 5 10 15
 Lys Xaa Ala Arg Cys Cys Gly Xaa
 20

<210> 154
 <211> 296
 <212> DNA
 <213> Conus marmoreus
 <400> 154
 gagctcggta ccccgacctc aagagggatc gatagcagtt catgatgtct aaactgggaa 60

46

tcttgttgac catctgtcta cttctatttc cccttactgc tgttccgctg gatggagatc 120
 aacctgcaga ccgacctgca gagcgtatgc aggaacgacat ttcacatgaa catcatccct 180
 tttttgatcc cgtcaaacgg tgttgcaggt tatcatgcgg cctgggatgc cacccttggt 240
 gtggatgacc agctttgtta tcgcggcctc atcaagtgtc taatgaataa gtaaaa 296

<210> 155
 <211> 68
 <212> PRT
 <213> Conus marmoreus

<400> 155
 Met Met Ser Lys Leu Gly Ile Leu Leu Thr Ile Cys Leu Leu Leu Phe
 1 5 10 15
 Pro Leu Thr Ala Val Pro Leu Asp Gly Asp Gln Pro Ala Asp Arg Pro
 20 25 30
 Ala Glu Arg Met Gln Asp Asp Ile Ser Ser Glu His His Pro Phe Phe
 35 40 45
 Asp Pro Val Lys Arg Cys Cys Arg Leu Ser Cys Gly Leu Gly Cys His
 50 55 60

Pro Cys Cys Gly
 65

<210> 156
 <211> 14
 <212> PRT
 <213> Conus marmoreus

<220>
 <221> PEPTIDE
 <222> (1)..(14)
 <223> Xaa at residue 12 is Pro or Hyp

<400> 156
 Cys Cys Arg Leu Ser Cys Gly Leu Gly Cys His Xaa Cys Cys
 1 5 10

<210> 157
 <211> 355
 <212> DNA
 <213> Conus marmoreus

<400> 157
 ggcctacacc aagcttgcat gcctgcaggt cgactctaga ggatccccga tcgatagcag 60
 ttcacatgatg ctagactggg agtcttggtg accatctgtc tacttctgtt tccccttact 120
 gctgttccgc tggatggaga tcaacctgcg gaccgacctg cagagcgcct gcaggacgac 180
 atttcatctg aacatcatcc ccattttgat tccggcagag agtggtgcgg ttcggttcgca 240
 tgccgctttg gatgcgtgcc ttgttggtga tgaccagctt tgttatcacg gcctcatcga 300
 gtgtctaata aataagtaaa acgattgcag taggggggta ccgagctcga attcc 355

<210> 158
 <211> 69
 <212> PRT

47

<213> Conus marmoreus

<400> 158

Met Met Ser Arg Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
 1 5 10 15

Pro Leu Thr Ala Val Pro Leu Asp Gly Asp Gln Pro Ala Asp Arg Pro
 20 25 30

Ala Glu Arg Leu Gln Asp Asp Ile Ser Ser Glu His His Pro His Phe
 35 40 45

Asp Ser Gly Arg Glu Cys Cys Gly Ser Phe Ala Cys Arg Phe Gly Cys
 50 55 60

Val Pro Cys Cys Val
 65

<210> 159

<211> 17

<212> PRT

<213> Conus marmoreus

<220>

<221> PEPTIDE

<222> (1)..(17)

<223> Xaa at residue 1 is Glu or gamma-carboxy Glu; Xaa at residue 14 is Pro or Hy

<400> 159

Xaa Cys Cys Gly Ser Phe Ala Cys Arg Phe Gly Cys Val Xaa Cys Cys
 1 5 10 15

Val

<210> 160

<211> 295

<212> DNA

<213> Conus marmoreus

<400> 160

cgacctcaag agggatcgat agcagttcat gatgtctaaa ctgggagtct tgttgaccat 60

ctgtctactt ctatttcccc ttactgctgt tccgctggat ggagaccaac ctgcagaccg 120

acctgcagag cgtatgcagg acgacatttc atctgaacgt catccttttt ttgatcgag 180

caaacagtgt tgccatctgc cggcatgccg cttcggatgt acgccttggt gttggtgatc 240

agctttgtta tcgcgtcctc atcaagtgtc taatgaataa gtaaaatgat tgcag 295

<210> 161

<211> 67

<212> PRT

<213> Conus marmoreus

<400> 161

Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
 1 5 10 15

Pro Leu Thr Ala Val Pro Leu Asp Gly Asp Gln Pro Ala Asp Arg Pro
 20 25 30

Ala Glu Arg Met Gln Asp Asp Ile Ser Ser His Pro Phe Phe Asp Arg
 35 40 45

Ser Lys Gln Cys Cys His Leu Pro Ala Cys Arg Phe Gly Cys Thr Pro
 50 55 60

Cys Cys Trp
 65

<210> 162

<211> 19

<212> PRT

<213> Conus marmoreus

<220>

<221> PEPTIDE

<222> (1)..(19)

<223> Xaa at residue 8 and 16 is Pro or Hyp; Xaa at residue 19 is Trp o
 r bromo-Tr

<400> 162

Ser Lys Gln Cys Cys His Leu Xaa Ala Cys Arg Phe Gly Cys Thr Xaa
 1 5 10 15

Cys Cys Xaa

<210> 163

<211> 235

<212> DNA

<213> Conus marmoreus

<400> 163

ggatccatga tgtctaaact gggagtcttg ttgaccatct gtctgcttct gtttcccctt 60

actgctcttc cgctggatgg agatcaacct gcagaccaac gtgcagagcg tacgcaggcc 120

gagaagcatt ccttgctga tccgagaatg ggctgttgcc cgtttccatg caaaaccagt 180

tgcactactt tgtgttgcg gtgatgataa cgtgttgatg accaactttc tcgag 235

<210> 164

<211> 67

<212> PRT

<213> Conus marmoreus

<400> 164

Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu
 1 5 10 15

Leu Phe Pro Leu Thr Ala Leu Pro Leu Asp Gly Asp Gln Pro Ala Asp
 20 25 30

Gln Arg Ala Glu Arg Thr Gln Ala Glu Lys His Ser Leu Pro Asp Pro
 35 40 45

Arg Met Gly Cys Cys Pro Phe Pro Cys Lys Thr Ser Cys Thr Thr Leu
 50 55 60

Cys Cys Gly
 65

<210> 165

<211> 17

<212> PRT

<213> Conus marmoreus

<220>

<221> PEPTIDE

<222> (1)..(17)

<223> Xaa at residue 5 and 7 is Pro or Hyp

<400> 165

Met Gly Cys Cys Xaa Phe Xaa Cys Lys Thr Ser Cys Thr Thr Leu Cys
1 5 10 15

Cys

<210> 166

<211> 16

<212> PRT

<213> Conus marmoreus

<220>

<221> PEPTIDE

<222> (1)..(16)

<223> Xaa at residue 4 and 6 is Trp or bromo-Trp

<400> 166

Cys Cys His Xaa Asn Xaa Cys Asp His Leu Cys Ser Cys Cys Gly Ser
1 5 10 15

<210> 167

<211> 357

<212> DNA

<213> Conus marmoreus

<400> 167

gccaaagcttg catgcctgca ggatgactct agaggatccc cacctcaaga gggatcgata 60
gcagttcatg atgtctaaac tgggagtctt gttgaccatc tgtctacttc tgtttgcct 120
tactgctggt cgcgtggatg gagatcaacc tgcagaccga cctgcagaac gtatgcagga 180
cgacatttca tctgaacgtc atcccatggt tgatgcogtc agagattggt gcccgttgcc 240
ggcatgcccc tttggatgca acccttgttg tggatgacca gctttgttat cgggacctca 300
tcaagtgtct aatgaataag taaaaaacga ttcgagtggg taccgagctc gaattcc 357

<210> 168

<211> 67

<212> PRT

<213> Conus marmoreus

<400> 168

Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
1 5 10 15

Ala Leu Thr Ala Val Pro Leu Asp Gly Asp Gln Pro Ala Asp Arg Pro
20 25 30

Ala Glu Arg Met Gln Asp Asp Ile Ser Ser His Pro Met Phe Asp Ala
35 40 45

Val Arg Asp Cys Cys Pro Leu Pro Ala Cys Pro Phe Gly Cys Asn Pro
50 55 60

Cys Cys Gly
65

<210> 169

<211> 16

50

<212> PRT
<213> Conus marmoreus

<220>
<221> PEPTIDE
<222> (1)..(16)
<223> Xaa at residue 4, 6, 9 and 14 is Pro or Hyp

<400> 169
Asp Cys Cys Xaa Leu Xaa Ala Cys Xaa Phe Gly Cys Asn Xaa Cys Cys
1 5 10 15

<210> 170
<211> 16
<212> PRT
<213> Conus marmoreus

<220>
<221> PEPTIDE
<222> (1)..(16)
<223> Xaa at residue 4 and 13 is Pro or Hyp

<400> 170
Cys Cys Ala Xaa Ser Ala Cys Arg Leu Gly Cys Arg Xaa Cys Cys Arg
1 5 10 15

<210> 171
<211> 16
<212> PRT
<213> Conus marmoreus

<220>
<221> PEPTIDE
<222> (1)..(16)
<223> Xaa at residue 4 and 13 is Pro or Hyp

<400> 171
Cys Cys Ala Xaa Ser Ala Cys Arg Leu Gly Cys Arg Xaa Cys Cys Arg
1 5 10 15

<210> 172
<211> 16
<212> PRT
<213> Conus marmoreus

<220>
<221> PEPTIDE
<222> (1)..(16)
<223> Xaa at residue 4 and 13 is Pro or Hyp

<400> 172
Cys Cys Ala Xaa Ser Ala Cys Arg Leu Gly Cys Arg Xaa Cys Cys Arg
1 5 10 15

<210> 173
<211> 17
<212> PRT
<213> Conus marmoreus

<220>
<221> PEPTIDE
<222> (1)..(17)
<223> Xaa at residue 14 is Pro or Hyp

<400> 173

51

Gly Cys Cys Gly Ser Phe Ala Cys Arg Phe Gly Cys Val Xaa Cys Cys
 1 5 10 15

Val

<210> 174
 <211> 244
 <212> DNA
 <213> Conus nobilis

<400> 174
 ggatccatga tgtctaaact gggagtcttg ttgaccatct gtctacttct gtttcccctt 60
 actgctcttc cgctggatga agatcaaccg gtacaccgac ctgcagagcg tatgcaggac 120
 atttcacttg atcaacatct cttctttgat ctcatcaaac ggtgctgcga gttgccatgc 180
 gggccaggct tttgcgtccc ttgttgctga catcaataac gtgttgatga ccaactttct 240
 cgag 244

<210> 175
 <211> 69
 <212> PRT
 <213> Conus nobilis

<400> 175
 Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu
 1 5 10 15
 Leu Phe Pro Leu Thr Ala Leu Pro Leu Asp Glu Asp Gln Pro Val His
 20 25 30
 Arg Pro Ala Glu Arg Met Gln Asp Ile Ser Ser Asp Gln His Leu Phe
 35 40 45
 Phe Asp Leu Ile Lys Arg Cys Cys Glu Leu Pro Cys Gly Pro Gly Phe
 50 55 60
 Cys Val Pro Cys Cys
 65

<210> 176
 <211> 15
 <212> PRT
 <213> Conus nobilis

<220>
 <221> PEPTIDE
 <222> (1)..(15)
 <223> Xaa at residue 3 is Glu or gamma-carboxy Glu; Xaa at residue 5, 8
 adn 13 is Pro or Hy

<400> 176
 Cys Cys Xaa Leu Xaa Cys Gly Xaa Gly Phe Cys Val Xaa Cys Cys
 1 5 10 15

<210> 177
 <211> 262
 <212> DNA
 <213> Conus nobilis

<400> 177
 ggatccatga tgtctaaact gggagtcttg ttgaccatct gtctacttct gtttcccctt 60

52

actgcttttc cgatggatgg agatcaacct gcagaccaac ctgcagatcg tatgcaggac 120
 gacatttcat ctgagcagta tcccttggtt gataagagac aaaagtgttg cactgggaag 180
 aaggggtcat gctccggcaa agcatgcaaa aatctcaaat gttgctctgg acgataacgt 240
 gttgatgacc aactttctcg ag 262

<210> 178
 <211> 78
 <212> PRT
 <213> Conus nobilis

<400> 178
 Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu
 1 5 10 15
 Leu Phe Pro Leu Thr Ala Phe Pro Met Asp Gly Asp Gln Pro Ala Asp
 20 25 30
 Gln Pro Ala Asp Arg Met Gln Asp Asp Ile Ser Ser Glu Gln Tyr Pro
 35 40 45
 Leu Phe Asp Lys Arg Gln Lys Cys Cys Thr Gly Lys Lys Gly Ser Cys
 50 55 60
 Ser Gly Lys Ala Cys Lys Asn Leu Lys Cys Cys Ser Gly Arg
 65 70 75

<210> 179
 <211> 23
 <212> PRT
 <213> Conus nobilis

<220>
 <221> PEPTIDE
 <222> (1)..(23)
 <223> Xaa at residue 1 is Gln or pyro-Glu

<400> 179
 Xaa Lys Cys Cys Thr Gly Lys Lys Gly Ser Cys Ser Gly Lys Ala Cys
 1 5 10 15
 Lys Asn Leu Lys Cys Cys Ser
 20

<210> 180
 <211> 238
 <212> DNA
 <213> Conus pulicarius

<400> 180
 ggatccatga tgtctaaact gggagttttg ttgaccatct gtctgcttct gtttcccctt 60
 actgctgttc cgctggatgg agatcaacct gcagaccgac ctgcagagcg tatgcaggac 120
 attgcaactg aacagcatcc cttctttgat cccgtcaaac ggtgttgcaa cagctgttac 180
 atgggatgca tcccttggtg cttctagtaa taacgtgttg atgaccaact ttctcgag 238

<210> 181
 <211> 68
 <212> PRT
 <213> Conus pulicarius

53

<400> 181

Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu
 1 5 10 15

Leu Phe Pro Leu Thr Ala Val Pro Leu Asp Gly Asp Gln Pro Ala Asp
 20 25 30

Arg Pro Ala Glu Arg Met Gln Asp Ile Ala Thr Glu Gln His Pro Phe
 35 40 45

Phe Asp Pro Val Lys Arg Cys Cys Asn Ser Cys Tyr Met Gly Cys Ile
 50 55 60

Pro Cys Cys Phe
 65

<210> 182

<211> 14

<212> PRT

<213> Conus pulicarius

<220>

<221> PEPTIDE

<222> (1)..(14)

<223> Xaa at residue 11 is Pro or Hyp; Xaa at residue 5 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 182

Cys Cys Asn Ser Cys Xaa Met Gly Cys Ile Xaa Cys Cys Phe
 1 5 10

<210> 183

<211> 238

<212> DNA

<213> Conus quercinus

<400> 183

ggatccatga tgtctaaact gggagtcttg ttgaccatct gtctgcttct gtttcccott 60

acagctcttc agctggatgg agatcaacct gcagaccgac ctgcagagcg tacgcaggac 120

attgcatctg aacagtatcg aaagtttgat cagagacaga ggtgttgcca gtggccatgc 180

cccggtagtt gcagatgctg ccgtactggt taacgtgttg atgaccaact ttctcgag 238

<210> 184

<211> 70

<212> PRT

<213> Conus quercinus

<400> 184

Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu
 1 5 10 15

Leu Phe Pro Leu Thr Ala Leu Gln Leu Asp Gly Asp Gln Pro Ala Asp
 20 25 30

Arg Pro Ala Glu Arg Thr Gln Asp Ile Ala Ser Glu Gln Tyr Arg Lys
 35 40 45

Phe Asp Gln Arg Gln Arg Cys Cys Gln Trp Pro Cys Pro Gly Ser Cys
 50 55 60

Arg Cys Cys Arg Thr Gly
 65 70

<210> 185
 <211> 17
 <212> PRT
 <213> Conus quercinus

<220>
 <221> PEPTIDE
 <222> (1)..(17)
 <223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 7 and 9 is Pr
 o or Hyp; Xaa at residue 6 is Trp or bromo-Tr

<400> 185
 Xaa Arg Cys Cys Gln Xaa Xaa Cys Xaa Gly Ser Cys Arg Cys Cys Arg
 1 5 10 15

Thr

<210> 186
 <211> 15
 <212> PRT
 <213> Conus quercinus

<220>
 <221> PEPTIDE
 <222> (1)..(15)
 <223> Xaa at residue 11 and 14 is Pro or Hyp

<400> 186
 Cys Cys Ser Gln Asp Cys Leu Val Cys Ile Xaa Cys Cys Xaa Asn
 1 5 10 15

<210> 187
 <211> 15
 <212> PRT
 <213> Conus quercinus

<220>
 <221> PEPTIDE
 <222> (1)..(15)
 <223> Xaa at residue 11 14 is Pro or Hyp; Xaa at residue 7 is Trp or br
 omo-Tr

<400> 187
 Cys Cys Ser Arg His Cys Xaa Val Cys Ile Xaa Cys Cys Xaa Asn
 1 5 10 15

<210> 188
 <211> 323
 <212> DNA
 <213> Conus radiatus

<400> 188
 tcaagaagga tcgatagcag ttcgatgatgt ctaaactggg agtcttggtg accatctgtc 60
 tgctttctggt tccccttact gctcttccga tggatggaga tcaacctgta gaccgacttg 120
 cagagcgtat gcaggacaac atttcatctg agcagcatac cttctttgaa aagagactac 180
 catcgtggtg ctcccttaac ttgcggcttt gccagtagc agcatgcaaa cgtaaccctt 240
 gttgcacagg ataacgtggt gatgaccaac tttgttatca cggctacgtc aagtgtctag 300
 tgaataagta aaacgattgc agt 323

55

<210> 189
 <211> 76
 <212> PRT
 <213> Conus radiatus

<400> 189
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
 1 5 10 15
 Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Pro Val Asp Arg Leu
 20 25 30
 Ala Glu Arg Met Gln Asp Asn Ile Ser Ser Glu Gln His Thr Phe Phe
 35 40 45
 Glu Lys Arg Leu Pro Ser Cys Cys Ser Leu Asn Leu Arg Leu Cys Pro
 50 55 60
 Val Pro Ala Cys Lys Arg Asn Pro Cys Cys Thr Gly
 65 70 75

<210> 190
 <211> 24
 <212> PRT
 <213> Conus radiatus

<220>
 <221> PEPTIDE
 <222> (1)..(24)
 <223> Xaa at residue 2, 13, 15 and 21 is Pro or Hyp

<400> 190
 Leu Xaa Ser Cys Cys Ser Leu Asn Leu Arg Leu Cys Xaa Val Xaa Ala
 1 5 10 15
 Cys Lys Arg Asn Xaa Cys Cys Thr
 20

<210> 191
 <211> 336
 <212> DNA
 <213> Conus radiatus

<400> 191
 aggtcgactc tagaggatcc ccaaggatcg atagcagttc atgatgtcta aactgggagt 60
 cttgttgacc atctgtctgc ttctgtttcc ccttactgct cttccgatgg atggagatca 120
 acctgcagac cgacttgacg agcgtatgca ggacgacatt tcatctgagc agcatccctt 180
 ctttaaaaag agacaacaaa gatgttgacg cgtaaagagg atttgtccag taccagcatg 240
 cagaagtaaa ccttgttgca aatcataacg tattgatgac caactttgtt atcacggcta 300
 cgtcaagtgt ctagtgaata agtaaaatga ttgcag 336

<210> 192
 <211> 75
 <212> PRT
 <213> Conus radiatus

<400> 192
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
 1 5 10 15

56

Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Pro Ala Asp Arg Leu
20 25 30

Ala Glu Arg Met Gln Asp Asp Ile Ser Ser Glu Gln His Pro Phe Phe
35 40 45

Lys Lys Arg Gln Gln Arg Cys Cys Thr Val Lys Arg Ile Cys Pro Val
50 55 60

Pro Ala Cys Arg Ser Lys Pro Cys Cys Lys Ser
65 70 75

<210> 193

<211> 24

<212> PRT

<213> Conus radiatus

<220>

<221> PEPTIDE

<222> (1)..(24)

<223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 12, 14 and 20
is Pro or Hy

<400> 193

Xaa Gln Arg Cys Cys Thr Val Lys Arg Ile Cys Xaa Val Xaa Ala Cys
1 5 10 15

Arg Ser Lys Xaa Cys Cys Lys Ser
20

<210> 194

<211> 326

<212> DNA

<213> Conus radiatus

<400> 194

acctcaagaa ggatcgatag cagttcatga tgtctaaact gggagtcttg ttgaccatct 60

gtctgcttct gtttcccggt actgctcttc cgatggatgg tgatcaacct gcagaccgac 120

ttgtagagcg tatgcaggac aacatttcat ctgagcagca tcccttcttt gaaaagagaa 180

gaggaggctg ttgcacacct ccgaggaaat gcaaagaccg agcctgcaaa cctgcacgtt 240

gctgcgggccc aggataacgt gttgatgacc aactttgtta tcacggctac gtcaagtgtc 300

tagtgaataa gtaaaacgat tgcagt 326

<210> 195

<211> 76

<212> PRT

<213> Conus radiatus

<400> 195

Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
1 5 10 15

Pro Val Thr Ala Leu Pro Met Asp Gly Asp Gln Pro Ala Asp Arg Leu
20 25 30

Val Glu Arg Met Gln Asp Asn Ile Ser Ser Glu Gln His Pro Phe Phe
35 40 45

Glu Lys Arg Arg Gly Gly Cys Cys Thr Pro Pro Arg Lys Cys Lys Asp
50 55 60

57

Arg Ala Cys Lys Pro Ala Arg Cys Cys Gly Pro Gly
65 70 75

<210> 196
<211> 24
<212> PRT
<213> Conus radiatus

<220>
<221> PEPTIDE
<222> (1)..(24)
<223> Xaa at residue 7, 8, 18 and 24 is Pro or Hyp

<400> 196
Arg Gly Gly Cys Cys Thr Xaa Xaa Arg Lys Cys Lys Asp Arg Ala Cys
1 5 10 15

Lys Xaa Ala Arg Cys Cys Gly Xaa
20

<210> 197
<211> 238
<212> DNA
<213> Conus rattus

<400> 197
ggatccatga tgtctaaact gggagtcttg gtgaccatct gcttgcttct gttccctctt 60
gctgcttttc cactggatgg agatcaacct gcagaccacc ctgcaaagcg tacgcaagat 120
gacagttcag ctgcctgat caatgcctgg cttgatgaat cccagacttg ctgcagtaac 180
tgcggtgaag attgtgatgg ttgttgccag taacgtgttg atgaccaact ttctcgag 238

<210> 198
<211> 70
<212> PRT
<213> Conus rattus

<400> 198
Gly Ser Met Met Ser Lys Leu Gly Val Leu Val Thr Ile Cys Leu Leu
1 5 10 15

Leu Phe Pro Leu Ala Ala Phe Pro Leu Asp Gly Asp Gln Pro Ala Asp
20 25 30

His Pro Ala Lys Arg Thr Gln Asp Asp Ser Ser Ala Ala Leu Ile Asn
35 40 45

Ala Trp Leu Asp Glu Ser Gln Thr Cys Cys Ser Asn Cys Gly Glu Asp
50 55 60

Cys Asp Gly Cys Cys Gln
65 70

<210> 199
<211> 16
<212> PRT
<213> Conus rattus

<220>
<221> PEPTIDE
<222> (1)..(16)
<223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 9 is Glu or gamma-carboxy Gl

<400> 199

Xaa Thr Cys Cys Ser Asn Cys Gly Xaa Asp Cys Asp Gly Cys Cys Gln
 1 5 10 15

<210> 200

<211> 327

<212> DNA

<213> *Conus stercusmuscarum*

<400> 200

gacctcaaga gggatcgata gcagttcgtg atgtctaaac tgggagtctt gttgaccatc 60
 tgtctgcttc tgtttcctct tactgctctt ccgatggatg gagatcaacc tgcagaccaa 120
 cctgcagatc gtatgcagga cgacatttca tctgagcagt atcccttggt tgataagaga 180
 caaaagtgtt gcactgggaa gaaggggtca tgctccggca aagcatgcaa aaatctcaaa 240
 tgttgctctg gacgataacg tgttgatgac caactttggt atcacggcta cgtcaagtgt 300
 ctaatgaata agtaaaacga ttgcagt 327

<210> 201

<211> 75

<212> PRT

<213> *Conus stercusmuscarum*

<400> 201

Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe Pro
 1 5 10 15

Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Pro Ala Asp Gln Pro Ala
 20 25 30

Asp Arg Met Gln Asp Asp Ile Ser Ser Glu Gln Tyr Pro Leu Phe Asp
 35 40 45

Lys Arg Gln Lys Cys Cys Thr Gly Lys Lys Gly Ser Cys Ser Gly Lys
 50 55 60

Ala Cys Lys Asn Leu Lys Cys Cys Ser Gly Arg
 65 70 75

<210> 202

<211> 23

<212> PRT

<213> *Conus stercusmuscarum*

<220>

<221> PEPTIDE

<222> (1)..(23)

<223> Xaa at residue 1 is Gln or pyro-Glu

<400> 202

Xaa Lys Cys Cys Thr Gly Lys Lys Gly Ser Cys Ser Gly Lys Ala Cys
 1 5 10 15

Lys Asn Leu Lys Cys Cys Ser
 20

<210> 203

<211> 316

<212> DNA

<213> *Conus stercusmuscarum*

59

<400> 203
 gatcgatagc agttcgtgat gtctaaactg ggagtccttgt tgaccatctg tctgcttctg 60
 tttcccctta ctgctcttcc gatggatgga gatcaacctg cagaccaacc tgcagatcgt 120
 atgcagaacg acatttcatac tgagcagtat cccttgtttg ataagagaca aaagtgttgc 180
 ggccccggcg cgtcatgccc cagatatattc aaagacaatt ttatttgtgg ttgttggttaa 240
 atgacaacgt gtcgatgacc aacttcgtta tcacgacttc gccaaagtgc taatgaataa 300
 gtaaaaacgat tgcagt 316

<210> 204
 <211> 73
 <212> PRT
 <213> Conus stercusmuscarum

<400> 204
 Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe Pro
 1 5 10 15
 Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Pro Ala Asp Gln Pro Ala
 20 25 30
 Asp Arg Met Gln Asn Asp Ile Ser Ser Glu Gln Tyr Pro Leu Phe Asp
 35 40 45
 Lys Arg Gln Lys Cys Cys Gly Pro Gly Ala Ser Cys Pro Arg Tyr Phe
 50 55 60
 Lys Asp Asn Phe Ile Cys Gly Cys Cys
 65 70

<210> 205
 <211> 23
 <212> PRT
 <213> Conus stercusmuscarum

<220>
 <221> PEPTIDE
 <222> (1)..(23)
 <223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 6 and 11 is P
 ro or Hyp; Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-
 iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 205
 Xaa Lys Cys Cys Gly Xaa Gly Ala Ser Cys Xaa Arg Xaa Phe Lys Asp
 1 5 10 15
 Asn Phe Ile Cys Gly Cys Cys
 20

<210> 206
 <211> 331
 <212> DNA
 <213> Conus striatus

<400> 206
 cgacctttca agagggatcg atagcagttc gcgatgtcta aactgggggt attgttgacc 60
 atctgtctgc ttctgtttcc cttactgct cttccgatgg atgaagatca acctgcagac 120
 caacttgaag atcgtatgca ggacgacatt tcatctgagc agtatccctc gtttgtagg 180
 agacaaaagt gttgcggcga aggtcgtca tgccccaaat atttcaaaaa caattttatt 240

60

tgtggttggtt gttaaataac aacgtgtcga tgaccaactt cgttatcacg actacgccaa 300

gtgtcttgctc taatgataat aaaatgattc c 331

<210> 207

<211> 73

<212> PRT

<213> Conus striatus

<400> 207

Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe Pro
1 5 10 15

Leu Thr Ala Leu Pro Met Asp Glu Asp Gln Pro Ala Asp Gln Leu Glu
20 25 30

Asp Arg Met Gln Asp Asp Ile Ser Ser Glu Gln Tyr Pro Ser Phe Val
35 40 45

Arg Arg Gln Lys Cys Cys Gly Glu Gly Ser Ser Cys Pro Lys Tyr Phe
50 55 60

Lys Asn Asn Phe Ile Cys Gly Cys Cys
65 70

<210> 208

<211> 23

<212> PRT

<213> Conus striatus

<220>

<221> PEPTIDE

<222> (1)..(23)

<223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 6 is Glu or gamma-carboxy Glu; Xaa at residue 11 is Pro or Hyp; Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 208

Xaa Lys Cys Cys Gly Xaa Gly Ser Ser Cys Xaa Lys Xaa Phe Lys Asn
1 5 10 15

Asn Phe Ile Cys Gly Cys Cys
20

<210> 209

<211> 256

<212> DNA

<213> Conus striatus

<400> 209

ggatccatga tgtctaaact gggagtcttg ttgaccgtct gtctgcttct gtttcccctt 60

actgctcttc cgctggatgg agatcaacct gcagaccgac ctgcagagcg tatgcaggac 120

gacatttcac ctgacgagca tcccttggtt gataagagac aaaactgttg caatggggga 180

tgctccagca aatggtgcag agatcacgca cgttgttgcg gtcgatgata acgtgttgat 240

gaccaacttt ctcgag 256

<210> 210

<211> 75

<212> PRT

<213> *Conus striatus*

<400> 210

Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Val Cys Leu Leu
1 5 10 15

Leu Phe Pro Leu Thr Ala Leu Pro Leu Asp Gly Asp Gln Pro Ala Asp
20 25 30

Arg Pro Ala Glu Arg Met Gln Asp Asp Ile Ser Ser Asp Glu His Pro
35 40 45

Leu Phe Asp Lys Arg Gln Asn Cys Cys Asn Gly Gly Cys Ser Ser Lys
50 55 60

Trp Cys Arg Asp His Ala Arg Cys Cys Gly Arg
65 70 75

<210> 211

<211> 20

<212> PRT

<213> *Conus striatus*

<220>

<221> PEPTIDE

<222> (1)..(20)

<223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 12 is Trp or
bromo-Tr

<400> 211

Xaa Asn Cys Cys Asn Gly Gly Cys Ser Ser Lys Xaa Cys Arg Asp His
1 5 10 15

Ala Arg Cys Cys
20

<210> 212

<211> 235

<212> DNA

<213> *Conus tessulatus*

<400> 212

ggatccatga tgtctaaact gggagtcttg ttgaccatgt gtctgcttct gtttcccctt 60

actgctgttc cgctggatgg agatcaacct gcagaccgac ctgcagagcg taggcaggac 120

attgcaactg acgatcatcc tttgtttgat ccggtcaaac ggtgctgcc aaatgctat 180

atgggatgca tcccttggtg catttagtaa cgtgttgatg accaactttc tcgag 235

<210> 213

<211> 68

<212> PRT

<213> *Conus tessulatus*

<400> 213

Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Met Cys Leu Leu
1 5 10 15

Leu Phe Pro Leu Thr Ala Val Pro Leu Asp Gly Asp Gln Pro Ala Asp
20 25 30

Arg Pro Ala Glu Arg Arg Gln Asp Ile Ala Thr Asp Asp His Pro Leu
35 40 45

62

Phe Asp Pro Val Lys Arg Cys Cys His Lys Cys Tyr Met Gly Cys Ile
 50 55 60

Pro Cys Cys Ile
 65

<210> 214
 <211> 14
 <212> PRT
 <213> Conus tessulatus

<220>
 <221> PEPTIDE
 <222> (1)..(14)
 <223> Xaa at residue 11 is Pro or Hyp; Xaa at residue 6 is Tyr, 125I-Ty
 r, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 214
 Cys Cys His Lys Cys Xaa Met Gly Cys Ile Xaa Cys Cys Ile
 1 5 10

<210> 215
 <211> 238
 <212> DNA
 <213> Conus tessulatus

<400> 215
 ggatccatga tgtctaaact gggagtcttg ttgaccatct gtgtgcttct gtttcccctt 60
 actgctgttc cgctggatgg agatcaacct gcagaccaac ctgcagagcg tacgcagaac 120
 gagcagcatc ccttgtatga tcagaaaaga aagtgttgcc ggccgccatg cgccatgagc 180
 tgcggcatgg ctaggtgttg ctattaatga taacgtgttg atgaccaact ttctcgag 238

<210> 216
 <211> 68
 <212> PRT
 <213> Conus tessulatus

<400> 216
 Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Val Leu
 1 5 10 15

Leu Phe Pro Leu Thr Ala Val Pro Leu Asp Gly Asp Gln Pro Ala Asp
 20 25 30

Gln Pro Ala Glu Arg Thr Gln Asn Glu Gln His Pro Leu Tyr Asp Gln
 35 40 45

Lys Arg Lys Cys Cys Arg Pro Pro Cys Ala Met Ser Cys Gly Met Ala
 50 55 60

Arg Cys Cys Tyr
 65

<210> 217
 <211> 18
 <212> PRT
 <213> Conus tessulatus

<220>
 <221> PEPTIDE
 <222> (1)..(18)
 <223> Xaa at residue 5 and 6 is Pro or Hyp; Xaa at residue 18 is Tyr, 1

63

25I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 217

Lys	Cys	Cys	Arg	Xaa	Xaa	Cys	Ala	Met	Ser	Cys	Gly	Met	Ala	Arg	Cys
1				5					10					15	

Cys Xaa

<210> 218

<211> 564

<212> DNA

<213> Conus textile

<400> 218

gagtc	aaccc	actgt	cacgc	caagag	cggga	cgccac	agct	aaggca	agaa	ggatc	gatag	60
cagtt	catga	tgtct	aaact	gggag	ccttg	ttgacc	atct	gtctac	ttct	gttttc	ccctt	120
actgc	tgttc	cgctg	gatgg	agatca	aacat	gcagac	caaac	ctgcac	agcg	tctgc	caggac	180
cgcatt	ccaa	ctgaag	atca	tccctt	atatt	gatccca	aaca	aacggt	gttg	cccgcc	gggtg	240
gcatg	caaca	tgggat	gcaa	gccttg	tttgt	ggatga	caccag	ctttgt	tatc	gcggtc	tcat	300
gaagt	gtcta	atgaata	agt	aaaac	gattg	cagttt	cggt	cagattt	tgct	gttgtat	ttt	360
ggtcta	aaaga	ttaatg	acca	aactgt	ttctt	ttgatc	cgga	ttttcac	gta	tttctc	gatt	420
cctatt	caac	actaga	taag	ttaatc	acga	cagatc	tgat	tttccat	caa	tgcttg	ctt	480
tttgg	tctgt	catata	aatc	ttgttt	tatat	ttaattt	tctc	gtcactt	tca	acacgc	acac	540
acacac	acac	acgcgc	gcgc									564

<210> 219

<211> 69

<212> PRT

<213> Conus textile

<400> 219

Met	Met	Ser	Lys	Leu	Gly	Ala	Leu	Leu	Thr	Ile	Cys	Leu	Leu	Leu	Phe
1				5					10					15	

Ser	Leu	Thr	Ala	Val	Pro	Leu	Asp	Gly	Asp	Gln	His	Ala	Asp	Gln	Pro
			20					25					30		

Ala	Gln	Arg	Leu	Gln	Asp	Arg	Ile	Pro	Thr	Glu	Asp	His	Pro	Leu	Phe
		35					40					45			

Asp	Pro	Asn	Lys	Arg	Cys	Cys	Pro	Pro	Val	Ala	Cys	Asn	Met	Gly	Cys
	50					55					60				

Lys	Pro	Cys	Cys	Gly
65				

<210> 220

<211> 16

<212> PRT

<213> Conus textile

<220>

<221> PEPTIDE

<222> (1)..(16)

<223> Xaa at residue 3, 4 and 13 is Pro or Hyp

<400> 220

Cys Cys Xaa Xaa Val Ala Cys Asn Met Gly Cys Lys Xaa Cys Cys Gly
 1 5 10 15

<210> 221

<211> 780

<212> DNA

<213> Conus textile

<400> 221

ggatccagac gacaaagaag agtcaaccca ctgccacgtc aagagcagag cccacagcta 60
 agacaagaag gatcgatagc agttcatgat gtttaaactg ggagtcttgt tgaccatctg 120
 tctccttctg ttttccctta atgctgttcc gttggatgga gatcaacctg cagaccaacc 180
 tgcagagcgt ctgctggacg acatttcatt tgaaaataat cccttttatg atcccgccaa 240
 acggtgttgc aggacttgct tcggttgac accttgttgt ggatgaccag cctcatcaag 300
 tgtctaacga ataagtaaag cgattgcagt ctogttcaga ttacttttg tattctggtc 360
 taaagattaa tgaccaaact cttcttttga tcgggatgta catatatattc tcgattccta 420
 tccaacgcta gataagctaa tcacgacaga tctgatatttc tgtcaatgcc ttgctttttg 480
 gtctctcata tcactcttgt ttatatttaa tttctogtca ctatatatat atatacacac 540
 acacacacac ggaattccga ttgtccagta ccgttcttgg gatcgaggta ttgctgcat 600
 ggcttattct gtactctttt cttctgcgct tgatagtgat gtcttctact cccatctgtg 660
 ctacccttg cttgatcttt gataggcgtg tgcccttcac tggttataaa cccctctgat 720
 cctactctct ggacgcctcg ggggcccaac ctccaaataa agcgacatcc aatgaaaaaa 780

<210> 222

<211> 66

<212> PRT

<213> Conus textile

<400> 222

Met Met Phe Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
 1 5 10 15

Ser Leu Asn Ala Val Pro Leu Asp Gly Asp Gln Pro Ala Asp Gln Pro
 20 25 30

Ala Glu Arg Leu Leu Asp Asp Ile Ser Phe Glu Asn Asn Pro Phe Tyr
 35 40 45

Asp Pro Ala Lys Arg Cys Cys Arg Thr Cys Phe Gly Cys Thr Pro Cys
 50 55 60

Cys Gly
 65

<210> 223

<211> 12

<212> PRT

<213> Conus textile

<220>

<221> PEPTIDE

65

<222> (1)..(12)

<223> Xaa at residue 10 is Pro or Hyp

<400> 223

Cys	Cys	Arg	Thr	Cys	Phe	Gly	Cys	Thr	Xaa	Cys	Cys
1				5					10		

<210> 224

<211> 456

<212> DNA

<213> Conus textile

<400> 224

ggaacagtca	acccacagc	cacgccaaga	gcagacagcc	acagctacgt	gaagaagggt	60
ggagagaggt	tcatgatgtt	gaaaatggga	gtggtgctat	tcatctttct	ggtactgttt	120
cccctggcaa	cgctccagct	ggatgcagat	caacctgtag	aacgatatgc	ggagaacaaa	180
cagctcctca	accagatga	aaggagggaa	atcctattgc	ctgctctgag	gaagttctgc	240
tgtgattcga	attggtgcc	catttcggat	tgtgagtgt	gctacgggta	gcgccgaaca	300
tccatggcac	tgtgctgggc	ggtttcatcc	caacaacgac	agcgtttgtt	gatttcatgt	360
atcattgcgc	ccacgtctct	tgtctaagaa	tgacgaacat	gattgcactc	tggttcagat	420
ttcgtgttct	tttctgacaa	taaatgacaa	acctcc			456

<210> 225

<211> 70

<212> PRT

<213> Conus textile

<400> 225

Met	Met	Leu	Lys	Met	Gly	Val	Val	Leu	Phe	Ile	Phe	Leu	Val	Leu	Phe
1				5					10					15	

Pro	Leu	Ala	Thr	Leu	Gln	Leu	Asp	Ala	Asp	Gln	Pro	Val	Glu	Arg	Tyr
			20					25					30		

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

Leu	Pro	Ala	Leu	Arg	Lys	Phe	Cys	Cys	Asp	Ser	Asn	Trp	Cys	His	Asp
	50					55					60				

Cys	Glu	Cys	Cys	Tyr	Gly
65					70

<210> 226

<211> 17

<212> PRT

<213> Conus textile

<220>

<221> PEPTIDE

<222> (1)..(17)

<223> Xaa at residue 14 is Glu or gamma-carboxy Glu; Xaa at residue 7 is Trp or bromo-Trp; Xaa at residue 17 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 226

Phe	Cys	Cys	Asp	Ser	Asn	Xaa	Cys	His	Ile	Ser	Asp	Cys	Xaa	Cys	Cys
1				5					10					15	

66

Xaa

<210> 227
 <211> 456
 <212> DNA
 <213> Conus textile

<220>
 <221> misc_feature
 <222> (1)..(456)
 <223> n may be any nucleotide

<400> 227
 caaggaacag tcaaccccac agccacgccca agagcagaca gccacagcta cgtgaagaag 60
 ggtggagaga ggttcgtgat gttgaaaatg ggagtgggtgc tattcatctt cctggtactg 120
 tttcccctgg caacgctcca gctggatgca gatcaacctg tagaacgata tgcggagaac 180
 aaacagctcc tcagcccaga tgaaaggagg gaaatcatat tgcattgctct ggggacgcga 240
 tgctgttctt gggatgtgtg cgaccacccg agttgtactt gctgcggtta gcgccgaaca 300
 tccatggcgc tgtgctgggc ggttttatcc caacaacgac agcgtttgtt gatttcatgt 360
 atcattgcgc ccacgtctct tgtctaagaa tgacgaacat gattgcactc tggttcagat 420
 ttcgtgttct tttctgacaa taaatgacaa aacncc 456

<210> 228
 <211> 70
 <212> PRT
 <213> Conus textile

<400> 228
 Met Leu Lys Met Gly Val Val Leu Phe Ile Phe Leu Val Leu Phe Pro
 1 5 10 15
 Leu Ala Thr Leu Gln Leu Asp Ala Asp Gln Pro Val Glu Arg Tyr Ala
 20 25 30
 Glu Asn Lys Gln Leu Leu Ser Pro Asp Glu Arg Arg Glu Ile Ile Leu
 35 40 45
 His Ala Leu Gly Thr Arg Cys Cys Ser Trp Asp Val Cys Asp His Pro
 50 55 60
 Ser Cys Thr Cys Cys Gly
 65 70

<210> 229
 <211> 15
 <212> PRT
 <213> Conus textile

<220>
 <221> PEPTIDE
 <222> (1)..(15)
 <223> Xaa at residue 10 is Pro or Hyp; Xaa at residue 4 is Trp or bromo
 -Tr

<400> 229
 Cys Cys Ser Xaa Asp Val Cys Asp His Xaa Ser Cys Thr Cys Cys
 1 5 10 15

67

<210> 230
 <211> 235
 <212> DNA
 <213> Conus textile

<400> 230
 ggatccatga tgtctaaact gggagtcttg ttgaccatct gtctgcttct gtttcccctt 60
 actgctcttc cgctggatgg agatcaaccc gcagaccaag ctgcagagcg tatgcaggcc 120
 gagcagcatc ccttgtttga tcagaaaaga cggtgctgca agtttccatg ccccgatagt 180
 tgcagatatt tgtgttgcggt gtgatgataa cgtgttgatg accaactttc tcgag 235

<210> 231
 <211> 67
 <212> PRT
 <213> Conus textile

<400> 231
 Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu
 1 5 10 15
 Leu Phe Pro Leu Thr Ala Leu Pro Leu Asp Gly Asp Gln Pro Ala Asp
 20 25 30
 Gln Ala Ala Glu Arg Met Gln Ala Glu Gln His Pro Leu Phe Asp Gln
 35 40 45
 Lys Arg Arg Cys Cys Lys Phe Pro Cys Pro Asp Ser Cys Arg Tyr Leu
 50 55 60
 Cys Cys Gly
 65

<210> 232
 <211> 16
 <212> PRT
 <213> Conus textile

<220>
 <221> PEPTIDE
 <222> (1)..(16)
 <223> Xaa at residue 3 and 8 is Pro or Hyp; Xaa at residue 13 is Tyr, 1
 25I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 232
 Arg Cys Cys Lys Phe Xaa Cys Xaa Asp Ser Cys Arg Xaa Leu Cys Cys
 1 5 10 15

<210> 233
 <211> 321
 <212> DNA
 <213> Conus tulipa

<400> 233
 cgacctcaag agggatcgat agcagttcat gtctaaactg ggagtcttgt tgacaatctg 60
 tctgcttctg tttcccctta ctgctctgcc gatggatgga gatgaacctg cagaccgacc 120
 tgcagagcgt atgcaggaca acatttcacg tgagcagcat cccttggttg aggagagaca 180
 cggatgttgc aaggggcccg aaggatgctc ctccagagaa tgcagacccc aacattgttg 240

68

cggtcgacga taacgtgttg agggccaact ttgttatcac ggctacgtca agtgtttagt 300
gaataagtaa aatgattgca g 321

<210> 234
<211> 74
<212> PRT
<213> Conus tulipa

<400> 234
Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe Pro
1 5 10 15
Leu Thr Ala Leu Pro Met Asp Gly Asp Glu Pro Ala Asp Arg Pro Ala
20 25 30
Glu Arg Met Gln Asp Asn Ile Ser Ser Glu Gln His Pro Leu Phe Glu
35 40 45
Glu Arg His Gly Cys Cys Lys Gly Pro Glu Gly Cys Ser Ser Arg Glu
50 55 60
Cys Arg Pro Gln His Cys Cys Gly Arg Arg
65 70

<210> 235
<211> 21
<212> PRT
<213> Conus tulipa

<220>
<221> PEPTIDE
<222> (1)..(21)
<223> Xaa at residue 8 and 14 is Glu or gamma-carboxy Glu; Xaa at residue 7 and 17 is Pro or Hy

<400> 235
His Gly Cys Cys Lys Gly Xaa Xaa Gly Cys Ser Ser Arg Xaa Cys Arg
1 5 10 15
Xaa Gln His Cys Cys
20

<210> 236
<211> 287
<212> DNA
<213> Conus figulinus

<400> 236
caagaaggat cgaatagcagt tcatgatgtc taaactggga gtcttgctga ccatctgtct 60
gcttctgatt ccccttactg ctctttcgct ggatggagat caacctgcag accgacctgc 120
agagcgtatg caggatggaa tttcatctga acagcatccc atgtttgatc ccgtcagacg 180
gtgttgccccg tggccatgca acataggatg cgtaccttgt tggtgatgac cagttttgtt 240
atcgcggcct catcaaagt ctaatgaata agtaaaacga ttgcagt 287

<210> 237
<211> 67
<212> PRT
<213> Conus figulinus

<400> 237

69

Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Ile
1 5 10 15

Pro Leu Thr Ala Leu Ser Leu Asp Gly Asp Gln Pro Ala Asp Arg Pro
20 25 30

Ala Glu Arg Met Gln Asp Gly Ile Ser Ser Glu Gln His Pro Met Phe
35 40 45

Asp Pro Val Arg Arg Cys Cys Pro Trp Pro Cys Asn Ile Gly Cys Val
50 55 60

Pro Cys Cys
65

<210> 238

<211> 14

<212> PRT

<213> Conus figulinus

<220>

<221> PEPTIDE

<222> (1)..(14)

<223> Xaa at residue 3, 5 and 12 is Pro or Hyp; Xaa at residue 4 is Trp
or bromo-Tr

<400> 238

Cys Cys Xaa Xaa Xaa Cys Asn Ile Gly Cys Val Xaa Cys Cys
1 5 10

<210> 239

<211> 283

<212> DNA

<213> Conus figulinus

<400> 239

caagagggat cgatagcagt tcatgatgtt taaactggga gtctgttga ccatctgtat 60

gcttctgttt ccctttactg ctcttccgct ggatggagag caacctgcag accaacctgc 120

agagcgcgatg cagtatgaca tgttacgtgc aatgaatccc tggtttgatc ccgtaaaaag 180

gtgctgctcg aagaactgcg cagtatgcat cccttggtgc ccgtaactga ccagcttgat 240

tatcgcggcc aaggctctaa tgaataagta aaacgattgc agt 283

<210> 240

<211> 67

<212> PRT

<213> Conus figulinus

<400> 240

Met Met Phe Lys Leu Gly Val Leu Leu Thr Ile Cys Met Leu Leu Phe
1 5 10 15

Pro Phe Thr Ala Leu Pro Leu Asp Gly Glu Gln Pro Ala Asp Gln Pro
20 25 30

Ala Glu Arg Met Gln Tyr Asp Met Leu Arg Ala Met Asn Pro Trp Phe
35 40 45

Asp Pro Val Lys Arg Cys Cys Ser Lys Asn Cys Ala Val Cys Ile Pro
50 55 60

Cys Cys Pro

70

65

<210> 241
 <211> 14
 <212> PRT
 <213> Conus figulinus

<220>
 <221> PEPTIDE
 <222> (1)..(14)
 <223> Xaa at residue 11 and 14 is Pro or Hyp

<400> 241
 Cys Cys Ser Lys Asn Cys Ala Val Cys Ile Xaa Cys Cys Xaa
 1 5 10

<210> 242
 <211> 286
 <212> DNA
 <213> Conus figulinus

<400> 242
 caagagggat cgatagcagt tcatgatgtc taaactgaga gtcttgttga ccttatgtct 60
 gcttctgttt ccccttactg ctcttccgct gaatgaagat caacctgcag agcgtatgca 120
 ggacgacaat tcatctgagc agcaccctt gtatgaccac aaacgaaagt gttgccggtg 180
 gccatgcccc gcaagatgcg gctcttgttg cctgtaataa cgtgttggcc aactttgtta 240
 tcacggccac gtcaaatgtt taatgaataa gtaaaacgat tgcagt 286

<210> 243
 <211> 64
 <212> PRT
 <213> Conus figulinus

<400> 243
 Met Met Ser Lys Leu Arg Val Leu Leu Thr Leu Cys Leu Leu Leu Phe
 1 5 10 15

Pro Leu Thr Ala Leu Pro Leu Asn Glu Asp Gln Pro Ala Glu Arg Met
 20 25 30

Gln Asp Asp Asn Ser Ser Glu Gln His Pro Leu Tyr Asp His Lys Arg
 35 40 45

Lys Cys Cys Arg Trp Pro Cys Pro Ala Arg Cys Gly Ser Cys Cys Leu
 50 55 60

<210> 244
 <211> 15
 <212> PRT
 <213> Conus figulinus

<220>
 <221> PEPTIDE
 <222> (1)..(15)
 <223> Xaa at residue 5 and 7 is Pro or Hyp; Xaa at residue 4 is Trp or bromo-Tr

<400> 244
 Cys Cys Arg Xaa Xaa Cys Xaa Ala Arg Cys Gly Ser Cys Cys Leu
 1 5 10 15

<210> 245

71

<211> 301
 <212> DNA
 <213> Conus figulinus

<400> 245
 caagagggat cgatagcagt tcatgatgtc taaactggga gtcttggtga ccttatgtct 60
 gcttctgttt cccctgactg ctcttccgct ggatgaagat caagctgcag accgacctgc 120
 agagcgtatg cagggcatgt catctgaaca gcatcccttc tttgatcccg tcaaacgggtg 180
 ttgcgagttg tcacgctgcc ttggatgcgt cccttggttg acatcttaat aacgtgtgga 240
 tgaccaactg tgttatcacg gccacgtcaa gtgtctaata aataagtaaa atgattgcag 300
 t 301

<210> 246
 <211> 68
 <212> PRT
 <213> Conus figulinus

<400> 246
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Leu Cys Leu Leu Leu Phe
 1 5 10 15
 Pro Leu Thr Ala Leu Pro Leu Asp Glu Asp Gln Ala Ala Asp Arg Pro
 20 25 30
 Ala Glu Arg Met Gln Gly Met Ser Ser Glu Gln His Pro Phe Phe Asp
 35 40 45
 Pro Val Lys Arg Cys Cys Glu Leu Ser Arg Cys Leu Gly Cys Val Pro
 50 55 60
 Cys Cys Thr Ser
 65

<210> 247
 <211> 16
 <212> PRT
 <213> Conus figulinus

<220>
 <221> PEPTIDE
 <222> (1)..(16)
 <223> Xaa at residue 3 and 12 is Pro or Hyp

<400> 247
 Cys Cys Xaa Leu Ser Arg Cys Leu Gly Cys Val Xaa Cys Cys Thr Ser
 1 5 10 15

<210> 248
 <211> 301
 <212> DNA
 <213> Conus figulinus

<400> 248
 caagagggat cgatagcagt tcatgatgtc taaactggga gtcttggtga ccttatgtct 60
 gcttctgttt cccctgactg ctcttccgct ggatgaagat caacctgcag accgacctgc 120
 agagcgtatg cagggcatgt catctgaaca gcatcccttc tttgatcccg tcaaacgggtg 180
 ttgcgagttg tcaaaatgcc atggatgcgt cccttggttg ataccttaat aacgtgcgga 240

72

tgaccaactg tgttatcacg gccacgtcaa gtgtctaataa aataagtaaa atgattgcag 300
t 301

<210> 249
<211> 68
<212> PRT
<213> Conus figulinus

<400> 249
Met Met Ser Lys Leu Gly Val Leu Leu Thr Leu Cys Leu Leu Leu Phe
1 5 10 15
Pro Leu Thr Ala Leu Pro Leu Asp Glu Asp Gln Pro Ala Asp Arg Pro
20 25 30
Ala Glu Arg Met Gln Gly Met Ser Ser Glu Gln His Pro Phe Phe Asp
35 40 45
Pro Val Lys Arg Cys Cys Glu Leu Ser Lys Cys His Gly Cys Val Pro
50 55 60
Cys Cys Ile Pro
65

<210> 250
<211> 16
<212> PRT
<213> Conus figulinus

<220>
<221> PEPTIDE
<222> (1)..(16)
<223> Xaa at residue 3 is Glu or gamma-carboxy Glu; Xaa at residue 12 and 16 is Pro or Hy

<400> 250
Cys Cys Xaa Leu Ser Lys Cys His Gly Cys Val Xaa Cys Cys Ile Xaa
1 5 10 15

<210> 251
<211> 298
<212> DNA
<213> Conus quercinus

<400> 251
caagagggat c gatagcagt tcatgatgtc taaactcgga gtcttgttga ccatctgtct 60
ggttctgttt ccccttacag ctcttcagct ggatggagat caacctgcag accgacctgc 120
agagcgtacg caggacattt catctgaaca gtatcgaaag tttgatcaga gacagaggtg 180
ttgccggtgg ccatgccccg gtagttgcag atgctgccgt tatcggttaac gtgttgggtga 240
ccagctttgt tatcacgacc acgccaagtg tctaacgaat aagtaaaatg attgcagt 298

<210> 252
<211> 68
<212> PRT
<213> Conus quercinus

<400> 252
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Val Leu Phe
1 5 10 15
Pro Leu Thr Ala Leu Gln Leu Asp Gly Asp Gln Pro Ala Asp Arg Pro

73

20 25 30

Ala Glu Arg Thr Gln Asp Ile Ser Ser Glu Gln Tyr Arg Lys Phe Asp
35 40 45

Gln Arg Gln Arg Cys Cys Arg Trp Pro Cys Pro Gly Ser Cys Arg Cys
50 55 60

Cys Arg Tyr Arg
65

<210> 253
<211> 18
<212> PRT
<213> Conus quercinus

<220>
<221> PEPTIDE
<222> (1)..(18)
<223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 7 and 9 is Pr
o or Hyp; Xaa at residue 6 is Trp or bromo-Trp; Xaa at residue 17
is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-
phospho-Ty

<400> 253
Xaa Arg Cys Cys Arg Xaa Xaa Cys Xaa Gly Ser Cys Arg Cys Cys Arg
1 5 10 15

Xaa Arg

<210> 254
<211> 313
<212> DNA
<213> Conus quercinus

<400> 254
caagagggat cgatagcagt tcatgatgtc taaactggga gtcttggtga ccattctgtct 60
gcttctgttt ccccttactg ctcttccact ggatggagat caacctgcag atcaatctgc 120
agagcgacct gcagagcgta cgcaggacga cattcagcag catccgttat atgatccgaa 180
aagaaggtgt tgccgttatc catgccccga cagctgccac ggatcttgct gctataagtg 240
ataacatggt gatggccagc tttgttatca cggccacgtc aagtgtctaa tgaataagta 300
aaacgattgc agt 313

<210> 255
<211> 72
<212> PRT
<213> Conus quercinus

<400> 255
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
1 5 10 15

Pro Leu Thr Ala Leu Pro Leu Asp Gly Asp Gln Pro Ala Asp Gln Ser
20 25 30

Ala Glu Arg Pro Ala Glu Arg Thr Gln Asp Asp Ile Gln Gln His Pro
35 40 45

Leu Tyr Asp Pro Lys Arg Arg Cys Cys Arg Tyr Pro Cys Pro Asp Ser
50 55 60

Cys His Gly Ser Cys Cys Tyr Lys
65 70

<210> 256
<211> 18
<212> PRT
<213> Conus quercinus

<220>
<221> PEPTIDE
<222> (1)..(18)
<223> Xaa at residue 6 and 8 is Pro or Hyp; Xaa at residue 5 and 17 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 256
Arg Cys Cys Arg Xaa Xaa Cys Xaa Asp Ser Cys His Gly Ser Cys Cys
1 5 10 15

Xaa Lys

<210> 257
<211> 256
<212> DNA
<213> Conus wittigi

<400> 257
ggatccatga tgtctaaact gggagtcttg ttgaccatct gtctgcttct gtttcccatt 60
actgctcttc cgggtgggtgg agatcagcct gcagaccgac ttgcagagcg tatgcaggac 120
gacacttcat ctgagcagca tccctttgaa aagagactac catcatgttg cgactttgag 180
aggctttgcg tagtaccagc atgcatacgt catcagtgtt gcacaggata acgtgttgat 240
gaccaacttt ctcgag 256

<210> 258
<211> 74
<212> PRT
<213> Conus wittigi

<400> 258
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
1 5 10 15

Pro Ile Thr Ala Leu Pro Val Gly Gly Asp Gln Pro Ala Asp Arg Leu
20 25 30

Ala Glu Arg Met Gln Asp Asp Thr Ser Ser Glu Gln His Pro Phe Glu
35 40 45

Lys Arg Leu Pro Ser Cys Cys Asp Phe Glu Arg Leu Cys Val Val Pro
50 55 60

Ala Cys Ile Arg His Gln Cys Cys Thr Gly
65 70

<210> 259
<211> 23
<212> PRT
<213> Conus wittigi

<220>

75

<221> PEPTIDE
 <222> (1)..(23)
 <223> Xaa at residue 8 is Glu or gamma-carboxy Glu; Xaa at residue 2 and 14 is Pro or Hy

<400> 259
 Leu Xaa Ser Cys Cys Asp Phe Xaa Arg Leu Cys Val Val Xaa Ala Cys
 1 5 10 15

Ile Arg His Gln Cys Cys Thr
 20

<210> 260
 <211> 14
 <212> PRT
 <213> Conus betulinus

<220>
 <221> PEPTIDE
 <222> (1)..(14)
 <223> Xaa at residue 11 is Pro or Hyp; Xaa at residue 14 is Trp or bromo-Tr

<400> 260
 Cys Cys Lys Gln Ser Cys Thr Thr Cys Met Xaa Cys Cys Xaa
 1 5 10

<210> 261
 <211> 259
 <212> DNA
 <213> Conus tulipa

<220>
 <221> misc_feature
 <222> (1)..(259)
 <223> n may be any nucleotide

<400> 261
 ggatccatga tgtctaaact gggagtcttg ttgacaatct gtctgcttct gtttcccctt 60
 actgctctgc cgatggatgg agatgaacct gcagaccgac ctgcagagcg tatgcaggac 120
 aacatttcat ctgagcagca tcccttggtt gaggagagac acggatgttg cgaggggccg 180
 aagggatgct cctccagaga atgcagaccc caacattggt gcggtcgacg ataacgtgtt 240
 gatgaccaac tntctcgag 259

<210> 262
 <211> 75
 <212> PRT
 <213> Conus tulipa

<400> 262
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
 1 5 10 15

Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Glu Pro Ala Asp Arg Pro
 20 25 30

Ala Glu Arg Met Gln Asp Asn Ile Ser Ser Glu Gln His Pro Leu Phe
 35 40 45

Glu Glu Arg His Gly Cys Cys Glu Gly Pro Lys Gly Cys Ser Ser Arg
 50 55 60

76

Glu Cys Arg Pro Gln His Cys Cys Gly Arg Arg
65 70 75

<210> 263
<211> 21
<212> PRT
<213> Conus tulipa

<220>
<221> PEPTIDE
<222> (1)..(21)
<223> Xaa at residue 5 and 14 is Glu or gamma-carboxy Glu; Xaa at residue 7 and 17 is Pro or Hy

<400> 263
His Gly Cys Cys Xaa Gly Xaa Lys Gly Cys Ser Ser Arg Xaa Cys Arg
1 5 10 15

Xaa Gln His Cys Cys
20

<210> 264
<211> 262
<212> DNA
<213> Conus aurisiacus

<220>
<221> misc_feature
<222> (1)..(262)
<223> n may be any nucleotide

<400> 264
ggatccatga tgtctaaact gggagtccttg ttgaccatct gtctacttct gtttcccctt 60
actgcttttc cgatggatgg agatcaacct gcagaccaac ctgcagatcg tatgcaggac 120
gacatttcac ctgagcagta tcccttggtt gataagagac aaaagtgttg cactgggagg 180
aaggggtcat gctccggcaa agcatgcaaa aatctcaaat gttgctctgg acgataacgt 240
gttgatgacc aactttctcg an 262

<210> 265
<211> 76
<212> PRT
<213> Conus aurisiacus

<400> 265
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
1 5 10 15

Pro Leu Thr Ala Phe Pro Met Asp Gly Asp Gln Pro Ala Asp Gln Pro
20 25 30

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

Asp Lys Arg Gln Lys Cys Cys Thr Gly Arg Lys Gly Ser Cys Ser Gly
50 55 60

Lys Ala Cys Lys Asn Leu Lys Cys Cys Ser Gly Arg
65 70 75

<210> 266

77

<211> 23
 <212> PRT
 <213> Conus aurisiacus

<220>
 <221> PEPTIDE
 <222> (1)..(23)
 <223> Xaa at residue 1 is Gln or pyro-Glu

<400> 266
 Xaa Lys Cys Cys Thr Gly Arg Lys Gly Ser Cys Ser Gly Lys Ala Cys
 1 5 10 15
 Lys Asn Leu Lys Cys Cys Ser
 20

<210> 267
 <211> 239
 <212> DNA
 <213> Conus betulinus

<400> 267
 ggatccatga tgtctaaact gggagtcttg ttgaccatct gtctgcttct gtttcccctt 60
 actgctgttc cgttggatgg agatcaacct gcagaccaac ctgcagagcg tatgcagaac 120
 gagcagcatc cctcgtttga tcagaaaaga aggtgctgcc ggtggccatg cccaggtata 180
 tgcggcatgg ctagggtgtg ctctgctcatg ataacgtgtt gatgaccaac tttctcgag 239

<210> 268
 <211> 71
 <212> PRT
 <213> Conus betulinus

<400> 268
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
 1 5 10 15
 Pro Leu Thr Ala Val Pro Leu Asp Gly Asp Gln Pro Ala Asp Gln Pro
 20 25 30
 Ala Glu Arg Met Gln Asn Glu Gln His Pro Ser Phe Asp Gln Lys Arg
 35 40 45
 Arg Cys Cys Arg Trp Pro Cys Pro Ser Ile Cys Gly Met Ala Arg Cys
 50 55 60
 Cys Phe Val Met Ile Thr Cys
 65 70

<210> 269
 <211> 23
 <212> PRT
 <213> Conus betulinus

<220>
 <221> PEPTIDE
 <222> (1)..(23)
 <223> Xaa at residue 6 and 8 is Pro or Hyp; Xaa at residue 5 is Trp or
 bromo-Tr

<400> 269
 Arg Cys Cys Arg Xaa Xaa Cys Xaa Ser Ile Cys Gly Met Ala Arg Cys
 1 5 10 15

Cys Phe Val Met Ile Thr Cys
20

<210> 270
<211> 226
<212> DNA
<213> Conus betulinus

<220>
<221> misc_feature
<222> (1)..(226)
<223> n may be any nucleotide

<400> 270
ggatccatga tgtctaaact gggagtcttg ttgatcatct gtctgcttct gtttcccctt 60
actgctgttc cgctggatgg agatcagcct gcagagcgta cgcagatcga gcagcatccc 120
ttgtttgacc agaaaagaag gtgttgccgg tggccatgcc ccagtagatg cggcatggct 180
aggtgttgct tcgtcatgat aacgtgttga tganccacct ctcnag 226

<210> 271
<211> 67
<212> PRT
<213> Conus betulinus

<400> 271
Met Met Ser Lys Leu Gly Val Leu Leu Ile Ile Cys Leu Leu Leu Phe
1 5 10 15
Pro Leu Thr Ala Val Pro Leu Asp Gly Asp Gln Pro Ala Glu Arg Thr
20 25 30
Gln Ile Glu Gln His Pro Leu Phe Asp Gln Lys Arg Arg Cys Cys Arg
35 40 45
Trp Pro Cys Pro Ser Arg Cys Gly Met Ala Arg Cys Cys Phe Val Met
50 55 60

Ile Thr Cys
65

<210> 272
<211> 23
<212> PRT
<213> Conus betulinus

<220>
<221> PEPTIDE
<222> (1)..(23)
<223> Xaa at residue 6 and 8 is Pro or Hyp; Xaa at residue 5 is Trp or
bromo-Trp

<400> 272
Arg Cys Cys Arg Xaa Xaa Cys Xaa Ser Arg Cys Gly Met Ala Arg Cys
1 5 10 15
Cys Phe Val Met Ile Thr Cys
20

<210> 273
<211> 262
<212> DNA
<213> Conus parius

79

<400> 273
 ggatccatga tgtctaaact gggagtcttg ttgaccatct gtctgcttct gtttcccctt 60
 actgctcttc cgatggatgg tgatcaacct gcagaccgac ttgtagagcg tatgcaggac 120
 aacatttcac ctgagcagca tcccttcttt gaaaagagaa gaggaggctg ttgcacacct 180
 ccgaagaaat gcaaagaccg agcctgcaaa cctgcacgtt gctgcggccc aggataacgt 240
 gttgatgacc aactttctcg cc 262

<210> 274
 <211> 76
 <212> PRT
 <213> Conus parius

<400> 274
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
 1 5 10 15
 Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Pro Ala Asp Arg Leu
 20 25 30
 Val Glu Arg Met Gln Asp Asn Ile Ser Ser Glu Gln His Pro Phe Phe
 35 40 45
 Glu Lys Arg Arg Gly Gly Cys Cys Thr Pro Pro Lys Lys Cys Lys Asp
 50 55 60
 Arg Ala Cys Lys Pro Ala Arg Cys Cys Gly Pro Gly
 65 70 75

<210> 275
 <211> 24
 <212> PRT
 <213> Conus parius

<220>
 <221> PEPTIDE
 <222> (1)..(24)
 <223> Xaa at residue 7, 8, 18 and 24 is Pro or Hyp

<400> 275
 Arg Gly Gly Cys Cys Thr Xaa Xaa Lys Lys Cys Lys Asp Arg Ala Cys
 1 5 10 15
 Lys Xaa Ala Arg Cys Cys Gly Xaa
 20

<210> 276
 <211> 259
 <212> DNA
 <213> Conus parius
 <400> 276
 ggatccatga tgtctaaact gggagtcttg ttgaccatct gtctgcttct gtttcccctt 60
 actgctcttc cgatggatgg tgatcaacct gcagaccgac ttgtagagcg tatgcaggac 120
 aacatttcac ctgagcagca tcccttcttt gaaaagagaa gaggctgttg cacacctccg 180
 aggaaatgca aagaccgagc ctgcaaacct gcacgttggtt ggggccaggg ataacgtgtt 240
 gatgaccaac tttctcgag 259

80

<210> 277
 <211> 75
 <212> PRT
 <213> Conus parius

<400> 277
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
 1 5 10 15
 Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Pro Ala Asp Arg Leu
 20 25 30
 Val Glu Arg Met Gln Asp Asn Ile Ser Ser Glu Gln His Pro Phe Phe
 35 40 45
 Glu Lys Arg Arg Gly Cys Cys Thr Pro Pro Arg Lys Cys Lys Asp Arg
 50 55 60
 Ala Cys Lys Pro Ala Arg Cys Cys Gly Pro Gly
 65 70 75

<210> 278
 <211> 23
 <212> PRT
 <213> Conus parius

<220>
 <221> PEPTIDE
 <222> (1)..(23)
 <223> Xaa at residue 6, 7, 17 and 23 is Pro or Hyp

<400> 278
 Arg Gly Cys Cys Thr Xaa Xaa Arg Lys Cys Lys Asp Arg Ala Cys Lys
 1 5 10 15
 Xaa Ala Arg Cys Cys Gly Xaa
 20

<210> 279
 <211> 241
 <212> DNA
 <213> Conus coronatus

<400> 279
 ggatccatga tgtctaaact gggagtcttg ttgaccatct gtctgcttct gtttccaatt 60
 actgcccttc cgctggatga agatcaacct gcagaccgac ctgcagagcg tatgcaggac 120
 attgcaactg aacagcatcc cttgtttgat cccgtcaaac ggtgctgcga ttggccatgc 180
 atcccaggat gcaccccttg ttgcttgccct tgataacgtg ttgatgacca actttctcga 240
 g 241

<210> 280
 <211> 68
 <212> PRT
 <213> Conus coronatus

<400> 280
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
 1 5 10 15
 Pro Ile Thr Ala Leu Pro Leu Asp Glu Asp Gln Pro Ala Asp Arg Pro
 20 25 30

<210>	284
<211>	14
<212>	PRT

<213> Conus musicus

<220>

<221> PEPTIDE

<222> (1)..(14)

<223> Xaa at residue4 is Glu or gamma-carboxy Glu; Xaa at residue 12 is Pro or Hy

<400> 284

Ala Cys Cys Xaa Gln Ser Cys Thr Thr Cys Phe Xaa Cys Cys
1 5 10

<210> 285

<211> 14

<212> PRT

<213> Conus betulinus

<220>

<221> PEPTIDE

<222> (1)..(14)

<223> Xaa at residue 4 is Glu or gamma-carboxy Glu; Xaa at residue 12 is Pro or Hy

<400> 285

Ala Cys Cys Xaa Gln Ser Cys Thr Thr Cys Met Xaa Cys Cys
1 5 10

<210> 286

<211> 14

<212> PRT

<213> Conus betulinus

<220>

<221> PEPTIDE

<222> (1)..(14)

<223> Xaa at residue 3 is Glu or gamma-carboxy Glu; Xaa at residue 11 is Pro or Hyp; Xaa at residue 14 is Trp or bromo-Tr

<400> 286

Cys Cys Xaa Gln Ser Cys Thr Thr Cys Met Xaa Cys Cys Xaa
1 5 10

<210> 287

<211> 235

<212> DNA

<213> Conus pennaceus

<400> 287

ggatccatga tgtctaaact gggagtcttg ttgaccatct gtctgcttct gtttcccctt 60

actgctcttc cgctggatgg agatcaacct gcataccaag ctgcagagcg tatgcaggcc 120

gagcatcatc ccttgtttga tcagaaaaga cggtgctgca agtttccatg ccccgatagt 180

tgcaaattatt tgtgttgcgg gtgatgataa catgttgatg accaactttc ttgag 235

<210> 288

<211> 65

<212> PRT

<213> Conus pennaceus

<400> 288

Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
1 5 10 15

83

Pro Leu Thr Ala Leu Pro Leu Asp Gly Asp Gln Pro Ala Tyr Gln Ala
20 25 30

Ala Glu Arg Met Gln Ala Glu His His Pro Leu Phe Asp Gln Lys Arg
35 40 45

Arg Cys Cys Lys Phe Pro Cys Pro Asp Ser Cys Lys Tyr Leu Cys Cys
50 55 60

Gly
65

<210> 289

<211> 16

<212> PRT

<213> Conus pennaceus

<220>

<221> PEPTIDE

<222> (1)..(16)

<223> Xaa at residue 6 and 8 is Pro or Hyp; Xaa at residue 13 is Tyr, 1
25I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 289

Arg Cys Cys Lys Phe Xaa Cys Xaa Asp Ser Cys Lys Xaa Leu Cys Cys
1 5 10 15

<210> 290

<211> 241

<212> DNA

<213> Conus pulicarius

<400> 290

ggatccatga tgtctaaact gggagtcttg ttgaccatct gtctgcttct gtttcccctt 60

actgctcttc cgatggatgg tgatcaactt gcagaccgac ttgtagagcg tatgcaggac 120

aacatttcat ctgagcagca tcccttcttt gatcccgta aacggtgttg cgtcagctgt 180

tacatgggat gcatcccttg ttgcttctag taataacgtg ttgatgacca actttctcga 240

g 241

<210> 291

<211> 67

<212> PRT

<213> Conus pulicarius

<400> 291

Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
1 5 10 15

Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Leu Ala Asp Arg Leu
20 25 30

Val Glu Arg Met Gln Asp Asn Ile Ser Ser Glu Gln His Pro Phe Phe
35 40 45

Asp Pro Val Lys Arg Cys Cys Val Ser Cys Tyr Met Gly Cys Ile Pro
50 55 60

Cys Cys Phe
65

84

<210> 292
 <211> 14
 <212> PRT
 <213> Conus pulicarius

 <220>
 <221> PEPTIDE
 <222> (1)..(14)
 <223> Xaa at residue 11 is Pro or Hyp; Xaa at residue 6 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

 <400> 292
 Cys Cys Val Ser Cys Xaa Met Gly Cys Ile Xaa Cys Cys Phe
 1 5 10

 <210> 293
 <211> 244
 <212> DNA
 <213> Conus pulicarius

 <400> 293
 ggatccatga tgtctaaact gggagtottg ttgaccgtct gtctgcttct gtgtccctt 60
 actgctcttc cactggatga agatcaactt gcagaccgac ctgcagagcg tatgcaggat 120
 gacacttcag ctgcacagat tttcgggttt gatcccgatca aacggtgctg caaattgcta 180
 tgctactcgg gatgcactcc ttgttgccat atttgataac gtgttgatga ccaactttct 240
 cgag 244

 <210> 294
 <211> 67
 <212> PRT
 <213> Conus pulicarius

 <400> 294
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Val Cys Leu Leu Leu Cys
 1 5 10 15
 Pro Leu Thr Ala Leu Pro Leu Asp Glu Asp Gln Leu Ala Asp Arg Pro
 20 25 30
 Ala Glu Arg Met Gln Asp Asp Thr Ser Ala Ala Gln Ile Phe Gly Phe
 35 40 45
 Asp Pro Val Lys Arg Cys Cys Lys Leu Leu Cys Gly Cys Thr Pro Cys
 50 55 60
 Cys His Ile
 65

 <210> 295
 <211> 16
 <212> PRT
 <213> Conus pulicarius

 <220>
 <221> PEPTIDE
 <222> (1)..(16)
 <223> Xaa at residue 12 is Pro or Hyp; Xaa at residue 7 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

 <400> 295
 Cys Cys Lys Leu Leu Cys Xaa Ser Gly Cys Thr Xaa Cys Cys His Ile

85

1 5 10 15

<210> 296
 <211> 259
 <212> DNA
 <213> Conus rattus

<400> 296
 ggatccatga tgtctaaact gggagtcttg ttgaccatct gtctgcttgt gtttccgctt 60
 actgctcttc cgatggatgg tgatcaacct gcagaccgac ttgtagagcg tatacaggac 120
 aacatttcat ctgagcagca tcccttcttt gaaaagagaa gaggctgttg cgcacctccg 180
 aggaaatgca aagaccgagc ctgcaaacct gcacgttgct ggggccagg ataacgtgtt 240
 gatgaccaac tttctcgag 259

<210> 297
 <211> 75
 <212> PRT
 <213> Conus rattus

<400> 297
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Val Phe
 1 5 10 15
 Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Pro Ala Asp Arg Leu
 20 25 30
 Val Glu Arg Ile Gln Asp Asn Ile Ser Ser Glu Gln His Pro Phe Phe
 35 40 45
 Glu Lys Arg Arg Gly Cys Cys Ala Pro Pro Arg Lys Cys Lys Asp Arg
 50 55 60
 Ala Cys Lys Pro Ala Arg Cys Cys Gly Pro Gly
 65 70 75

<210> 298
 <211> 23
 <212> PRT
 <213> Conus rattus

<220>
 <221> PEPTIDE
 <222> (1)..(23)
 <223> Xaa at residue 6, 7, 17 and 23 is Pro or Hyp

<400> 298
 Arg Gly Cys Cys Ala Xaa Xaa Arg Lys Cys Lys Asp Arg Ala Cys Lys
 1 5 10 15
 Xaa Ala Arg Cys Cys Gly Xaa
 20

<210> 299
 <211> 262
 <212> DNA
 <213> Conus stercusmuscarum

<400> 299
 ggatccatga tgtctaaact gggagtcttg ttgacaatct gtctgcttct gtttcccctt 60
 attgctcttc cgctggatgg agatcaacct gcagaccgac ctgcagagcg tatgcaggac 120

86

gacatttcat ctgagaagca tcccttggtt gataagagac aacggtgttg caatgggcgg 180
 aggggatgct ccagcagatg gtgcagagat cactcacgtt gttgcggtcg acgataacgt 240
 gttgatgacc aactttctcg ag 262

<210> 300
 <211> 76
 <212> PRT
 <213> Conus stercusmuscarum

<400> 300
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
 1 5 10 15
 Pro Leu Ile Ala Leu Pro Leu Asp Gly Asp Gln Pro Ala Asp Arg Pro
 20 25 30
 Ala Glu Arg Met Gln Asp Asp Ile Ser Ser Glu Lys His Pro Leu Phe
 35 40 45
 Asp Lys Arg Gln Arg Cys Cys Asn Gly Arg Arg Gly Cys Ser Ser Arg
 50 55 60
 Trp Cys Arg Asp His Ser Arg Cys Cys Gly Arg Arg
 65 70 75

<210> 301
 <211> 22
 <212> PRT
 <213> Conus stercusmuscarum

<220>
 <221> PEPTIDE
 <222> (1)..(22)
 <223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 14 is Trp or
 bromo-Tr

<400> 301
 Xaa Arg Cys Cys Asn Gly Arg Arg Gly Cys Ser Ser Arg Xaa Cys Arg
 1 5 10 15
 Asp His Ser Arg Cys Cys
 20

<210> 302
 <211> 241
 <212> DNA
 <213> Conus ebraceus

<400> 302
 ggatccatga tgtctaaact gggagtcttg ttgaccatct gtctgcttct gtttcccctt 60
 actgctcttc cactggatga aggtcaacct gcagacctac ctgcagagcg tatgcaggac 120
 attgcaactg aacagcatcc cttgtttgat cctgtcaaac ggtgttgcca gcagccatgc 180
 tacatgggat gcatcccttg ttgcttctaa taataacgtg ttgatgacca acttttctcg 240
 g 241

<210> 303
 <211> 67
 <212> PRT

<213> Conus ebraceus

<400> 303

Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
1 5 10 15

Pro Leu Thr Ala Leu Pro Leu Asp Glu Gly Gln Pro Ala Asp Leu Pro
20 25 30

Ala Glu Arg Met Gln Asp Ile Ala Thr Glu Gln His Pro Leu Phe Asp
35 40 45

Pro Val Lys Arg Cys Cys Glu Gln Pro Cys Tyr Met Gly Cys Ile Pro
50 55 60

Cys Cys Phe
65

<210> 304

<211> 15

<212> PRT

<213> Conus ebraceus

<220>

<221> PEPTIDE

<222> (1)..(15)

<223> Xaa at residue 3 is Glu or gamma-carboxy Glu; Xaa at residue 5 and 12 is Pro or Hyp; Xaa at residue 7 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 304

Cys Cys Xaa Gln Xaa Cys Xaa Met Gly Cys Ile Xaa Cys Cys Phe
1 5 10 15

<210> 305

<211> 241

<212> DNA

<213> Conus ebraceus

<400> 305

ggatccatga tgtctaaact gggagtcttg ttgacccatct gtctgcttct gtttcccctt 60

actgctcttc cactggatga agatcaacct gcagacctac ctgcagagcg tatgcaggac 120

attgcaactg aacagcatcc cttgtttgat cctgtcaaac ggtgctgcgc gcagccatgc 180

tacatgggat gcatcccttg ttgcttctaa taataacgtg ttgatgacca actttctcga 240

g 241

<210> 306

<211> 67

<212> PRT

<213> Conus ebraceus

<400> 306

Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
1 5 10 15

Pro Leu Thr Ala Leu Pro Leu Asp Glu Asp Gln Pro Ala Asp Leu Pro
20 25 30

Ala Glu Arg Met Gln Asp Ile Ala Thr Glu Gln His Pro Leu Phe Asp
35 40 45

Pro Val Lys Arg Cys Cys Ala Gln Pro Cys Tyr Met Gly Cys Ile Pro

88

50 55 60

Cys Cys Phe
65

<210> 307
<211> 15
<212> PRT
<213> Conus ebraceus

<220>
<221> PEPTIDE
<222> (1)..(15)
<223> Xaa at residue 5 and 12 is Pro or Hyp; Xaa at residue 7 is Tyr, 1
25I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 307
Cys Cys Ala Gln Xaa Cys Xaa Met Gly Cys Ile Xaa Cys Cys Phe
1 5 10 15

<210> 308
<211> 238
<212> DNA
<213> Conus flavidus

<400> 308
ggatccatga tgtctaaact gggagtcttg ttgaccatct gtctgcttct gtttcccctt 60
actgctgttc cggtggatgg agatcaacct gcagaccagc ctgcagagcg tatgcagaac 120
gagcagcatc ccttgtttga tcagaaaaga aggtgctgcc ggtggccatg cccagtata 180
tgcggcacatg ctaggtgttg ctcgtcatga taacgtgttg atgaccaact ttctcgag 238

<210> 309
<211> 67
<212> PRT
<213> Conus flavidus

<400> 309
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
1 5 10 15
Pro Leu Thr Ala Val Pro Leu Asp Gly Asp Gln Pro Ala Asp Gln Pro
20 25 30
Ala Glu Arg Met Gln Asn Glu Gln His Pro Leu Phe Asp Gln Lys Arg
35 40 45
Arg Cys Cys Arg Trp Pro Cys Pro Ser Ile Cys Gly Met Ala Arg Cys
50 55 60

Cys Ser Ser
65

<210> 310
<211> 19
<212> PRT
<213> Conus flavidus

<220>
<221> PEPTIDE
<222> (1)..(19)
<223> Xaa at residue 6 and 8 is Pro or Hyp; Xaa at residue 5 is Trp or

bromo-Tr

<400> 310
 Arg Cys Cys Arg Xaa Xaa Cys Xaa Ser Ile Cys Gly Met Ala Arg Cys
 1 5 10 15

Cys Ser Ser

<210> 311
 <211> 245
 <212> DNA
 <213> Conus miliaris

<220>
 <221> misc_feature
 <222> (1)..(245)
 <223> n may be any nucleotide

<400> 311
 ggatccatga tgtctaaact gggagtcttg ttgaccatct gtctgcttct gtttccaatt 60
 actgcccttc cactggatga agatcaacct gcagaccgac ctgcagagcg tatgcaggac 120
 attgcaactg aacagcatcc cttgtttgat cccgtcaaac ggtgttgcca ttggccatgc 180
 agcgcaggat gctacccttg ttgcttcctt taataacgtg ttgatgacca actnangnaa 240
 aaaaaa 245

<210> 312
 <211> 68
 <212> PRT
 <213> Conus miliaris

<400> 312
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
 1 5 10 15
 Pro Ile Thr Ala Leu Pro Leu Asp Glu Asp Gln Pro Ala Asp Arg Pro
 20 25 30
 Ala Glu Arg Met Gln Asp Ile Ala Thr Glu Gln His Pro Leu Phe Asp
 35 40 45
 Pro Val Lys Arg Cys Cys Asp Trp Pro Cys Ser Ala Gly Cys Tyr Pro
 50 55 60

Cys Cys Phe Pro
 65

<210> 313
 <211> 16
 <212> PRT
 <213> Conus miliaris

<220>
 <221> PEPTIDE
 <222> (1)..(16)
 <223> Xaa at residue 5, 12 and 16 is Pro or Hyp; Xaa at residue 4 is Trp or bromo-Trp; Xaa at residue 11 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 313
 Cys Cys Asp Xaa Xaa Cys Ser Ala Gly Cys Xaa Xaa Cys Cys Phe Xaa
 1 5 10 15

90

<210> 314
 <211> 230
 <212> DNA
 <213> *Conus miliaris*

<220>
 <221> misc_feature
 <222> (1)..(230)
 <223> n may be any nucleotide
 <400> 314
 ggatccatga tgtctaaact gggagtgggtg ccattcgtct ttctggtcct gtttcccctg 60
 gcaacactcc aactggatgc agatcaacct gcagaccgac ctgcgcgtaa aaagggcatt 120
 gcaactaaac ggcatccctt gtctgatact gtcagagggt gttgccctcc aatgtgcaca 180
 ccatgcttcc cttgctgttt tcgttaataa cgtgttgatg natgatgna 230

<210> 315
 <211> 66
 <212> PRT
 <213> *Conus miliaris*

<400> 315
 Met Met Ser Lys Leu Gly Val Val Pro Phe Val Phe Leu Val Leu Phe
 1 5 10 15
 Pro Leu Ala Thr Leu Gln Leu Asp Ala Asp Gln Pro Ala Asp Arg Pro
 20 25 30
 Ala Arg Lys Lys Gly Ile Ala Thr Lys Arg His Pro Leu Ser Asp Pro
 35 40 45
 Val Arg Gly Cys Cys Pro Pro Met Cys Thr Pro Cys Phe Pro Cys Cys
 50 55 60
 Phe Arg
 65

<210> 316
 <211> 16
 <212> PRT
 <213> *Conus miliaris*

<220>
 <221> PEPTIDE
 <222> (1)..(16)
 <223> Xaa at residue 4, 9 and 12 is Pro or Hyp; Xaa at residue 5 is Tyr
 , 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho
 -Ty

<400> 316
 Gly Cys Cys Xaa Xaa Met Cys Thr Xaa Cys Phe Xaa Cys Cys Phe Arg
 1 5 10 15

<210> 317
 <211> 295
 <212> DNA
 <213> *Conus ammiralis*

<400> 317
 caagagggat cgatagcagt tcatgatgtc taaactggga gtcttgttga ccatctgtct 60
 gcttctgttt ccccttactg ctcttccgct ggatggagat caacctgcag accaagctgc 120

91

agagcgtatg caggccgagc agcatccctt gtttgatcag aaaagacggt gttgcagggt 180

tccatgcccc gatacttgca gacatttgtg ttgcgggtga tgataacgtg ctgatgaccc 240

actttgtcat cacggctacg tcaagtgtct aatgaataag taaaatgatt gcagt 295

<210> 318

<211> 65

<212> PRT

<213> Conus ammiralis

<400> 318

Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
1 5 10 15

Pro Leu Thr Ala Leu Pro Leu Asp Gly Asp Gln Pro Ala Asp Gln Ala
20 25 30

Ala Glu Arg Met Gln Ala Glu Gln His Pro Leu Phe Asp Gln Lys Arg
35 40 45

Arg Cys Cys Arg Phe Pro Cys Pro Asp Thr Cys Arg His Leu Cys Cys
50 55 60

Gly

65

<210> 319

<211> 16

<212> PRT

<213> Conus ammiralis

<220>

<221> PEPTIDE

<222> (1)..(16)

<223> Xaa at residue 6 and 8 is Pro or Hyp

<400> 319

Arg Cys Cys Arg Phe Xaa Cys Xaa Asp Thr Cys Arg His Leu Cys Cys
1 5 10 15

<210> 320

<211> 267

<212> DNA

<213> Conus ammiralis

<400> 320

caagagggat cgatagcagt tcatgatgtt taaactggga gtcttgctga ccatctgtct 60

acttctgttt tcccttaatg ctgttccgct ggatggagat caacctgcag accaacctgc 120

agagcgtctg ctggacgaca tttcatctga aaataatccc ttttatgatc ccgccaaacg 180

gtgttgcatg acttgcttcg gttgcacacc ttgttggtga tgaccagcct catcaagtgt 240

ctaacgaata agtaaaacga ttgcagt 267

<210> 321

<211> 66

<212> PRT

<213> Conus ammiralis

<400> 321

Met Met Phe Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
1 5 10 15

Ser Leu Asn Ala Val Pro Leu Asp Gly Asp Gln Pro Ala Asp Gln Pro
20 25 30

Ala Glu Arg Leu Leu Asp Asp Ile Ser Ser Glu Asn Asn Pro Phe Tyr
35 40 45

Asp Pro Ala Lys Arg Cys Cys Met Thr Cys Phe Gly Cys Thr Pro Cys
50 55 60

Cys Gly
65

<210> 322
<211> 12
<212> PRT
<213> Conus ammiralis

<220>
<221> PEPTIDE
<222> (1)..(12)
<223> Xaa at residue 10 is Pro or Hyp

<400> 322
Cys Cys Met Thr Cys Phe Gly Cys Thr Xaa Cys Cys
1 5 10

<210> 323
<211> 294
<212> DNA
<213> Conus ammiralis

<400> 323
caagaaggat c gatagcagt tcatgatgtc taaactggga gccttggtga ccatctgtct 60
acttctgttt tcccttactg ctgttccgct ggatggagat caacatgcag accaacctgc 120
agagcgtctg caggaccgcc ttccaactga aaatcatccc ttatatgatc ccgtcaaacg 180
gtgttgcgat gattcggaat ggcactattc ttgctggcct tgctgtattt tttcataacc 240
tttgttatcg cggcctcatc ctagtgtcaa atgaataagt aaaacgattg cagt 294

<210> 324
<211> 71
<212> PRT
<213> Conus ammiralis

<400> 324
Met Met Ser Lys Leu Gly Ala Leu Leu Thr Ile Cys Leu Leu Leu Phe
1 5 10 15

Ser Leu Thr Ala Val Pro Leu Asp Gly Asp Gln His Ala Asp Gln Pro
20 25 30

Ala Glu Arg Leu Gln Asp Arg Leu Pro Thr Glu Asn His Pro Leu Tyr
35 40 45

Asp Pro Val Lys Arg Cys Cys Asp Asp Ser Glu Cys Asp Tyr Ser Cys
50 55 60

Trp Pro Cys Cys Ile Phe Ser
65 70

<210> 325
<211> 18

<212> PRT
 <213> Conus ammiralis

<220>
 <221> PEPTIDE
 <222> (1)..(18)
 <223> Xaa at residue 6 is Glu or gamma-carboxy Glu; Xaa at residue 13 is Pro or Hyp; Xaa at residue 12 is Trp or bromo-Trp; Xaa at residue 9 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 325
 Cys Cys Asp Asp Ser Xaa Cys Asp Xaa Ser Cys Xaa Xaa Cys Cys Ile
 1 5 10 15

Phe Ser

<210> 326
 <211> 284
 <212> DNA
 <213> Conus ammiralis

<400> 326
 caagagggat cgatagcagt tcatgatgtt taaactcgga gtcttgctga ccatctgtct 60
 acttctgttt tccctaattg ctgttccgct ggatggagat caacatgcag accaacctgc 120
 agagcgtctg caggaccgcc ttccaactga aaatcatccc ttatatgatc ccgtcaaacg 180
 gtgttgccagg ttgttatgcc tcagttgcaa cccttgttgt ggatgaccag ctttgttatc 240
 acggcctcat caagtgtcta atgaataagt aaaacgattg cagt 284

<210> 327
 <211> 67
 <212> PRT
 <213> Conus ammiralis

<400> 327
 Met Met Phe Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
 1 5 10 15

Ser Leu Ile Ala Val Pro Leu Asp Gly Asp Gln His Ala Asp Gln Pro
 20 25 30

Ala Glu Arg Leu Gln Asp Arg Leu Pro Thr Glu Asn His Pro Leu Tyr
 35 40 45

Asp Pro Val Lys Arg Cys Cys Arg Leu Leu Cys Leu Ser Cys Asn Pro
 50 55 60

Cys Cys Gly
 65

<210> 328
 <211> 13
 <212> PRT
 <213> Conus ammiralis

<220>
 <221> PEPTIDE
 <222> (1)..(13)
 <223> Xaa at residue 11 is Pro or Hyp

<400> 328

94

Cys Cys Arg Leu Leu Cys Leu Ser Cys Asn Xaa Cys Cys
 1 5 10

<210> 329
 <211> 289
 <212> DNA
 <213> Conus ammiralis

<400> 329
 caagaaggat cgatagcagt tcatgatgtc taaactggga gccttggtga ccatctgtct 60
 acttctgttt tcccttactg ctgttccgct ggatggagat caacatgcag accaacctgc 120
 agagcgtctg caggaccgca ttccaactga agatcatccc ttatttgatc ccaacaaacg 180
 gtgttgcgat gattcggaat gcggctattc atgctggcct tgctgttatg gataagcttt 240
 gttatcgcgg cctcatccag tgtcaacgaa taagtaaaac gattgcagt 289

<210> 330
 <211> 70
 <212> PRT
 <213> Conus ammiralis

<400> 330
 Met Met Ser Lys Leu Gly Ala Leu Leu Thr Ile Cys Leu Leu Leu Phe
 1 5 10 15
 Ser Leu Thr Ala Val Pro Leu Asp Gly Asp Gln His Ala Asp Gln Pro
 20 25 30
 Ala Glu Arg Leu Gln Asp Arg Ile Pro Thr Glu Asp His Pro Leu Phe
 35 40 45
 Asp Pro Asn Lys Arg Cys Cys Asp Asp Ser Glu Cys Gly Tyr Ser Cys
 50 55 60
 Trp Pro Cys Cys Tyr Gly
 65 70

<210> 331
 <211> 16
 <212> PRT
 <213> Conus ammiralis

<220>
 <221> PEPTIDE
 <222> (1)..(16)
 <223> Xaa at residue6 is Glu or gamma-carboxy Glu; Xaa at residue 13 is Pro or Hyp; Xaa at residue 12 is Trp or bromo-Trp; Xaa at residue 9 and 16 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 331
 Cys Cys Asp Asp Ser Xaa Cys Gly Xaa Ser Cys Xaa Xaa Cys Cys Xaa
 1 5 10 15

<210> 332
 <211> 272
 <212> DNA
 <213> Conus spurius

<400> 332
 caagaaggat cgatagcagt tcatgatgtc taaactggga gtcttgctga ccatctgtct 60

95

gcttctgttt ccacgtactt ctcttccgct ggatggagat caacctgcag tccgatctgc 120
 aaagcgtatg cattcatcta tacagcgctg tttctttgat cccgtcaaac ggtgttgccc 180
 tagatgcagc gagtgaacc cttgttggtg atgaccagct ttgtcatcgc ggcctcatta 240
 agtgtctaata gaataagtaa aatgattgca gt 272

<210> 333
 <211> 63
 <212> PRT
 <213> Conus spurius

<400> 333
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
 1 5 10 15
 Pro Arg Thr Ser Leu Pro Leu Asp Gly Asp Gln Pro Ala Val Arg Ser
 20 25 30
 Ala Lys Arg Met His Ser Ser Ile Gln Arg Arg Phe Phe Asp Pro Val
 35 40 45
 Lys Arg Cys Cys Pro Arg Cys Ser Glu Cys Asn Pro Cys Cys Gly
 50 55 60

<210> 334
 <211> 12
 <212> PRT
 <213> Conus spurius

<220>
 <221> PEPTIDE
 <222> (1)..(12)
 <223> Xaa at residue 7 is Glu or gamma-carboxy Glu; Xaa at residue 3 and 10 is Pro or Hy

<400> 334
 Cys Cys Xaa Arg Cys Ser Xaa Cys Asn Xaa Cys Cys
 1 5 10

<210> 335
 <211> 293
 <212> DNA
 <213> Conus omaria

<400> 335
 caagagggat cgatagcagt tcatgatgtc taaactggga gtctcgttga ccatctgtct 60
 acttctatatt tcccttactg ctgttccgct tgatggagat caacatgcag accaacctgc 120
 agagcgtctg cagggcgaca ttttatctga aaagcatccc ttatttaatc cccgtcaaacg 180
 gtgttgcatg gaggaagaat gcagcagtgc atgctggcct tgttggttggg ggtgatcagc 240
 tttgttatcg cggcctcatc aagtgtctaa tgaataagta aatgattgc agt 293

<210> 336
 <211> 70
 <212> PRT
 <213> Conus omaria

<400> 336
 Met Met Ser Lys Leu Gly Val Ser Leu Thr Ile Cys Leu Leu Leu Phe
 1 5 10 15

Ser Leu Thr Ala Val Pro Leu Asp Gly Asp Gln His Ala Asp Gln Pro
 20 25 30
 Ala Glu Arg Leu Gln Gly Asp Ile Leu Ser Glu Lys His Pro Leu Phe
 35 40 45
 Asn Pro Val Lys Arg Cys Cys Asp Glu Glu Glu Cys Ser Ser Ala Cys
 50 55 60
 Trp Pro Cys Cys Trp Gly
 65 70

<210> 337
 <211> 16
 <212> PRT
 <213> Conus omaria
 <220>
 <221> PEPTIDE
 <222> (1)..(16)
 <223> Xaa at residue 4, 5 and 6 is Glu or gamma-carboxy Glu; Xaa at residue 13 is Pro or Hyp; Xaa at residue 12 and 16 is Trp or bromo-Tr

<400> 337
 Cys Cys Asp Xaa Xaa Xaa Cys Ser Ser Ala Cys Xaa Xaa Cys Cys Xaa
 1 5 10 15

<210> 338
 <211> 293
 <212> DNA
 <213> Conus omaria

<400> 338
 caagaaggat cgatagcagt tcatgatgtc taaactggga gtcttggtga tcatctgtct 60
 acttctgtgt ccccttactg ctgttctgga ggatggagat caacctgcag accgacctgc 120
 agagcgtatg caggacgaca tttcaactga gcatcatccc ttttatgatc ccgtcaaacg 180
 gtgttgcaag tacgggtgga catgcttgct aggatgcact ccttggtgatt gttgaccagt 240
 tttgttatcg cggcctcgtc aagtgtctaa tgaataagta aaacgattgc agt 293

<210> 339
 <211> 70
 <212> PRT
 <213> Conus omaria

<400> 339
 Met Met Ser Lys Leu Gly Val Leu Leu Ile Ile Cys Leu Leu Leu Cys
 1 5 10 15

Pro Leu Thr Ala Val Leu Glu Asp Gly Asp Gln Pro Ala Asp Arg Pro
 20 25 30

Ala Glu Arg Met Gln Asp Asp Ile Ser Thr Glu His His Pro Phe Tyr
 35 40 45

Asp Pro Val Lys Arg Cys Cys Lys Tyr Gly Trp Thr Cys Leu Leu Gly
 50 55 60

Cys Thr Pro Cys Asp Cys
 65 70

<210> 340
 <211> 17
 <212> PRT
 <213> Conus omaria

<220>
 <221> PEPTIDE
 <222> (1)..(17)
 <223> Xaa at residue is 14 Pro or Hyp; Xaa at residue 6 is Trp or bromo-
 -Trp; Xaa at residue 4 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr,
 O-sulpho-Tyr or O-phospho-Ty

<400> 340
 Cys Cys Lys Xaa Gly Xaa Thr Cys Leu Leu Gly Cys Thr Xaa Cys Asp
 1 5 10 15

Cys

<210> 341
 <211> 290
 <212> DNA
 <213> Conus omaria

<400> 341
 caagagggat cgatagcagt tcatgatgtc tatactggga gtcttggtga tcatctgtct 60
 acttctgtgt ccccttactg ctgttctgga ggatggagat caacctgcag accgacctgc 120
 agagcgtatg caggacggca tttcatctga acatcatccc tttttggatc ccgtcaaacg 180
 gtgttgccat ctattggcat gccgctttgg atgctcgctt tgttggttgg gaccagcttt 240
 gttatcgagg cctcatcaag tgtctaataa ataagtaaaa cgattgcagt 290

<210> 342
 <211> 69
 <212> PRT
 <213> Conus omaria

<400> 342
 Met Met Ser Ile Leu Gly Val Leu Leu Ile Ile Cys Leu Leu Leu Cys
 1 5 10 15
 Pro Leu Thr Ala Val Leu Glu Asp Gly Asp Gln Pro Ala Asp Arg Pro
 20 25 30

Ala Glu Arg Met Gln Asp Gly Ile Ser Ser Glu His His Pro Phe Leu
 35 40 45

Asp Pro Val Lys Arg Cys Cys His Leu Leu Ala Cys Arg Phe Gly Cys
 50 55 60

Ser Pro Cys Cys Trp
 65

<210> 343
 <211> 16
 <212> PRT
 <213> Conus omaria

<220>
 <221> PEPTIDE
 <222> (1)..(16)
 <223> Xaa at residue 13 is Pro or Hyp; Xaa at residue 16 is Trp or bromo-
 o-Tr

<400> 343

Cys Cys His Leu Leu Ala Cys Arg Phe Gly Cys Ser Xaa Cys Cys Xaa
 1 5 10 15

<210> 344

<211> 293

<212> DNA

<213> Conus omaria

<400> 344

caagaaggat cgatagcagt tcatgatgtc taaactggga gtcttgttga tcatctgtct 60
 acttctttgt ccccttactg ctgttccgca ggatggagat caacctgcag accgacctgc 120
 agagcgtatg cagggcggca tttcatctga acatcatccc ttttttgatc ccgtcaaacg 180
 gtgttgcagg tacgggtgga catgctggct aggatgcact ccctgtgggt gttgaccagc 240
 tttgttatcg cggcctcatc aagtgtctaa tgaataagta aaacgattgc agt 293

<210> 345

<211> 70

<212> PRT

<213> Conus omaria

<400> 345

Met Met Ser Lys Leu Gly Val Leu Leu Ile Ile Cys Leu Leu Leu Cys
 1 5 10 15

Pro Leu Thr Ala Val Pro Gln Asp Gly Asp Gln Pro Ala Asp Arg Pro
 20 25 30

Ala Glu Arg Met Gln Gly Gly Ile Ser Ser Glu His His Pro Phe Phe
 35 40 45

Asp Pro Val Lys Arg Cys Cys Arg Tyr Gly Trp Thr Cys Trp Leu Gly
 50 55 60

Cys Thr Pro Cys Gly Cys
 65 70

<210> 346

<211> 17

<212> PRT

<213> Conus omaria

<220>

<221> PEPTIDE

<222> (1)..(17)

<223> Xaa at residue 14 is Pro or Hyp; Xaa at residue 6 and 9 is Trp or
 bromo-Trp; Xaa at residue 4 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-
 iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 346

Cys Cys Arg Xaa Gly Xaa Thr Cys Xaa Leu Gly Cys Thr Xaa Cys Gly
 1 5 10 15

Cys

<210> 347

<211> 293

<212> DNA

<213> Conus episcopatus

99

<400> 347
 caagaaggat cgatagcagt tcatgatgtc taaactggga gtcttggtga ccatctgtct 60
 acttctgttt tcccttattg ctgttccgct tgatggagat caacatgcag accaacctgc 120
 agagcgtctg cagggcgaca ttttatctga aaagcatccc ttatttatgc ctgtcaaacg 180
 gtgttgcgat gaggacgaat gcaacagttc atgctggcct tgttggtggg ggtgatcagc 240
 tttgttatcg cggcctgatc aagtgtataa tgaataagta aaacgattgc agt 293

<210> 348
 <211> 70
 <212> PRT
 <213> Conus episcopatus

<400> 348
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
 1 5 10 15
 Ser Leu Ile Ala Val Pro Leu Asp Gly Asp Gln His Ala Asp Gln Pro
 20 25 30
 Ala Glu Arg Leu Gln Gly Asp Ile Leu Ser Glu Lys His Pro Leu Phe
 35 40 45
 Met Pro Val Lys Arg Cys Cys Asp Glu Asp Glu Cys Asn Ser Ser Cys
 50 55 60
 Trp Pro Cys Cys Trp Gly
 65 70

<210> 349
 <211> 16
 <212> PRT
 <213> Conus episcopatus

<220>
 <221> PEPTIDE
 <222> (1)..(16)
 <223> Xaa at residue 4 and 6 is Glu or gamma-carboxy Glu; Xaa at residue 13 is Pro or Hyp; Xaa at residue 12 and 16 is Trp or bromo-Trp

<400> 349
 Cys Cys Asp Xaa Asp Xaa Cys Asn Ser Ser Cys Xaa Xaa Cys Cys Xaa
 1 5 10 15

<210> 350
 <211> 293
 <212> DNA
 <213> Conus episcopatus

<400> 350
 caagagggat cgatagcagt tcatgatgtc taaactggga gtcttggtga ccatctgtct 60
 acttctgttt tcccttattg ctgttccgct tgatggagat caacatgcag accaacctgc 120
 agagcgtctg cagggcgaca ttttatctga aaagcatccc ttatttatgc ctgtcaaacg 180
 gtgttgcgat gaggacgaat gcagcagttc atgctggcct tgttggtggg gatgagcagc 240
 tttgttatcg cggcctcatc aagtgtataa tgaataagta aaacgattgc agt 293

<210> 351
 <211> 70

100

<212> PRT

<213> Conus episcopatus

<400> 351

Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
 1 5 10 15

Ser Leu Ile Ala Val Pro Leu Asp Gly Asp Gln His Ala Asp Gln Pro
 20 25 30

Ala Glu Arg Leu Gln Gly Asp Ile Leu Ser Glu Lys His Pro Leu Phe
 35 40 45

Met Pro Val Lys Arg Cys Cys Asp Glu Asp Glu Cys Ser Ser Ser Cys
 50 55 60

Trp Pro Cys Cys Trp Gly
 65 70

<210> 352

<211> 16

<212> PRT

<213> Conus episcopatus

<220>

<221> PEPTIDE

<222> (1)..(16)

<223> Xaa at residue 4 and 6 is Glu or gamma-carboxy Glu; Xaa at residue 13 is Pro or Hyp; Xaa at residue 12 and 16 is Trp or bromo-Trp

<400> 352

Cys Cys Asp Xaa Asp Xaa Cys Ser Ser Ser Cys Xaa Xaa Cys Cys Xaa
 1 5 10 15

<210> 353

<211> 290

<212> DNA

<213> Conus episcopatus

<400> 353

caagagggat cgatagcagt tcatgatgtc taaactggga gtcttggtga ccatctgtct 60

acttctgttt tcccttactg ctgttccgct tgatggagat caacatgcag accaacctgc 120

agagcgtctg cagggcgaca ttttatctga aaagcatccc ttatttaatc ccgtcaaacy 180

gtgttgcccg gcggcgcat gtgccatggg atgcaagcct tgttggtgat gagcagcttt 240

gttatcgtgg cctcatcaag tgtctaatga ataagtaaaa cgattgcagt 290

<210> 354

<211> 69

<212> PRT

<213> Conus episcopatus

<400> 354

Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
 1 5 10 15

Ser Leu Thr Ala Val Pro Leu Asp Gly Asp Gln His Ala Asp Gln Pro
 20 25 30

Ala Glu Arg Leu Gln Gly Asp Ile Leu Ser Glu Lys His Pro Leu Phe
 35 40 45

101

Asn Pro Val Lys Arg Cys Cys Pro Ala Ala Ala Cys Ala Met Gly Cys
 50 55 60

Lys Pro Cys Cys Gly
 65

<210> 355
 <211> 15
 <212> PRT
 <213> *Conus episcopatus*

<220>
 <221> PEPTIDE
 <222> (1)..(15)
 <223> Xaa at residue 3 and 13 is Pro or Hyp

<400> 355
 Cys Cys Xaa Ala Ala Ala Cys Ala Met Gly Cys Lys Xaa Cys Cys
 1 5 10 15

<210> 356
 <211> 295
 <212> DNA
 <213> *Conus aulicus*

<400> 356
 caagagggat cgatagcagt tcatgatgtc taaactggga gtcttggtga ccattctgtct 60
 gcttctgttt tccgttactg ctcttccgcc ggatggagat caacctgcag accgagctgc 120
 agagcgtagg caggtcgagc agcatcccggt gtttgatcat gaaagaggggt gttgctcgcc 180
 accatgccac agtatttgcg ctgctttctg ttgcgggtga tgataacgtg ttgatgaccc 240
 actttgtcat cacggctgcg tcaagtgtct aatgaataag taaaatgatt gcagt 295

<210> 357
 <211> 65
 <212> PRT
 <213> *Conus aulicus*

<400> 357
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
 1 5 10 15

Ser Val Thr Ala Leu Pro Pro Asp Gly Asp Gln Pro Ala Asp Arg Ala
 20 25 30

Ala Glu Arg Arg Gln Val Glu Gln His Pro Val Phe Asp His Glu Arg
 35 40 45

Gly Cys Cys Ser Pro Pro Cys His Ser Ile Cys Ala Ala Phe Cys Cys
 50 55 60

Gly
 65

<210> 358
 <211> 16
 <212> PRT
 <213> *Conus aulicus*

<220>
 <221> PEPTIDE
 <222> (1)..(16)
 <223> Xaa at residue 5 and 6 is Pro or Hyp

102

<400> 358

Gly Cys Cys Ser Xaa Xaa Cys His Ser Ile Cys Ala Ala Phe Cys Cys
 1 5 10 15

<210> 359

<211> 290

<212> DNA

<213> Conus aulicus

<400> 359

caagagggat cgatagcagt tcatgatgtc taaactggga gtcttggtga ccatctgtct 60
 acttctgttt tcccttactg ctgttccgct tgatggagat caacatgcag accaacctgc 120
 agagcgtctg cagggcgaca ttttatctga aaagcatccc ttatttaatc ccgtcaaacg 180
 gtgttgccga ccggtggcat gtgccatggg atgcaagcct tgttggtgat gaggagcttt 240
 gttatcgtgg cctcatcaag tgtctaataa ataagtaaaa tgattgcagt 290

<210> 360

<211> 69

<212> PRT

<213> Conus aulicus

<400> 360

Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
 1 5 10 15

Ser Leu Thr Ala Val Pro Leu Asp Gly Asp Gln His Ala Asp Gln Pro
 20 25 30

Ala Glu Arg Leu Gln Gly Asp Ile Leu Ser Glu Lys His Pro Leu Phe
 35 40 45

Asn Pro Val Lys Arg Cys Cys Arg Pro Val Ala Cys Ala Met Gly Cys
 50 55 60

Lys Pro Cys Cys Gly
 65

<210> 361

<211> 15

<212> PRT

<213> Conus aulicus

<220>

<221> PEPTIDE

<222> (1)..(15)

<223> Xaa at residue 4 and 13 is Pro or Hyp

<400> 361

Cys Cys Arg Xaa Val Ala Cys Ala Met Gly Cys Lys Xaa Cys Cys
 1 5 10 15

<210> 362

<211> 290

<212> DNA

<213> Conus aulicus

<400> 362

caagagggat cgatagcagt tcatgatgtc taaactggga gtcttggtga tcatctgtct 60
 acttctgtct ccccttactg ctgttccgct ggatggagat caacctgcag accgacctgc 120

103

agagcgtatg caggacgaca tttcatctga acatcaaccc atgtttgatg ccatcagaca 180
 gtgttgcccg gcggtggcat gcgccatggg atgcgagcct tgttgtggat gaccagcttt 240
 gttatcgcg cctcatcaag tgtctaataa ataagtaaaa tgattgcagt 290

<210> 363
 <211> 69
 <212> PRT
 <213> Conus aulicus

<400> 363
 Met Met Ser Lys Leu Gly Val Leu Leu Ile Ile Cys Leu Leu Leu Ser
 1 5 10 15
 Pro Leu Thr Ala Val Pro Leu Asp Gly Asp Gln Pro Ala Asp Arg Pro
 20 25 30
 Ala Glu Arg Met Gln Asp Asp Ile Ser Ser Glu His Gln Pro Met Phe
 35 40 45
 Asp Ala Ile Arg Gln Cys Cys Pro Ala Val Ala Cys Ala Met Gly Cys
 50 55 60
 Glu Pro Cys Cys Gly
 65

<210> 364
 <211> 16
 <212> PRT
 <213> Conus aulicus

<220>
 <221> PEPTIDE
 <222> (1)..(16)
 <223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 13 is Glu or
 gamma-carboxy Glu; Xaa at residue 4 and 14 is Pro or Hy

<400> 364
 Xaa Cys Cys Xaa Ala Val Ala Cys Ala Met Gly Cys Xaa Xaa Cys Cys
 1 5 10 15

<210> 365
 <211> 293
 <212> DNA
 <213> Conus aureus

<400> 365
 caagaaggat cgatagcagt tcatgatgtc taaactggga gccttggtga ccatctgtct 60
 acttctgttt tcccttactg ctgttccgct ggatggagat caacatgcag accaactgc 120
 agagcgtctg catgaccgcc ttccaactga aaatcatccc ttatatgatc ccgtcaaacg 180
 gtgttgcgat gattcggaat gcgactattc ttgctggcct tgctgtatct ttggataacc 240
 tttgttatcg cggcctcatc aagtgtcaaa tgaataagta aaacgattgc agt 293

<210> 366
 <211> 71
 <212> PRT
 <213> Conus aureus

<400> 366

104

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

<210> 367

<211> 17

<212> PRT

<213> Conus aureus

<220>

<221> PEPTIDE

<222> (1)..(17)

<223> Xaa at residue 6 is Glu or gamma-carboxy Glu; Xaa at residue 13 is
 Pro or Hyp; Xaa at residue 12 is Trp or bromo-Trp; Xaa at residue
 9 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or
 O-phospho-Ty

<400> 367

Cys Cys Asp Asp Ser Xaa Cys Asp Xaa Ser Cys Xaa Xaa Cys Cys Ile
 1 5 10 15

Phe

<210> 368

<211> 290

<212> DNA

<213> Conus aureus

<400> 368

caagaggggat cgatagcagt tcatgatgtc taaactggga gccttggtga ccatctgtct 60
 acttctgttt tccctaactg ctgttccgct ggatggagat caacatgcag accaacctgc 120
 agagcgtctg caggaccgca ttccaactga aaatcatccc ttatttgatc cgaacaaacg 180
 gtgttgcaat gattgggaat gcgacgattc atgctggcct tgctgttatg gataaccttt 240
 gttatcgcg cctcatcaag tgtcaaatga ataagtaaaa cgattgcagt 290

<210> 369

<211> 70

<212> PRT

<213> Conus aureus

<400> 369

Met Met Ser Lys Leu Gly Ala Leu Leu Thr Ile Cys Leu Leu Leu Phe
 1 5 10 15

Ser Leu Thr Ala Val Pro Leu Asp Gly Asp Gln His Ala Asp Gln Pro
 20 25 30

Ala Glu Arg Leu Gln Asp Arg Ile Pro Thr Glu Asn His Pro Leu Phe
 35 40 45

105

Asp Pro Asn Lys Arg Cys Cys Asn Asp Trp Glu Cys Asp Asp Ser Cys
 50 55 60

Trp Pro Cys Cys Tyr Gly
 65 70

<210> 370

<211> 16

<212> PRT

<213> Conus aureus

<220>

<221> PEPTIDE

<222> (1)..(16)

<223> Xaa at residue 6 is Glu or gamma-carboxy Glu; Xaa at residue 13 is Pro or Hyp; Xaa at residue 5 and 12 is Trp or bromo-Trp; Xaa at residue 16 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 370

Cys Cys Asn Asp Xaa Xaa Cys Asp Asp Ser Cys Xaa Xaa Cys Cys Xaa
 1 5 10 15

<210> 371

<211> 310

<212> DNA

<213> Conus consors

<400> 371

caagagggat cgatagcagt tcatgatgtc taaactggga gtcttggtga ccatctgttt 60
 gcttctgttt ccccttactg ctcttccaat ggatggagat caatctgtag accgacctgc 120
 agagcgtatg caggacgaca tttcatctga gctgcatccc ttgttcaatc agaaaagaat 180
 gtgttgccggc gaaggtgctc catgccccag ctatttcaga aacagtcaga tttgtcattg 240
 ttgttaaagt acaacgtgtc gatgaccaac ttcgttatca cgactaatga ataagtaaaa 300
 tgattgcagt 310

<210> 372

<211> 74

<212> PRT

<213> Conus consors

<400> 372

Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
 1 5 10 15

Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Ser Val Asp Arg Pro
 20 25 30

Ala Glu Arg Met Gln Asp Asp Ile Ser Ser Glu Leu His Pro Leu Phe
 35 40 45

Asn Gln Lys Arg Met Cys Cys Gly Glu Gly Ala Pro Cys Pro Ser Tyr
 50 55 60

Phe Arg Asn Ser Gln Ile Cys His Cys Cys
 65 70

<210> 373

<211> 22

<212> PRT

106

<213> Conus consors

<220>

<221> PEPTIDE

<222> (1)..(22)

<223> Xaa at residue 5 is Glu or gamma-carboxy Glu; Xaa at residue 8 and 10 is Pro or Hyp; Xaa at residue 12 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 373

Met Cys Cys Gly Xaa Gly Ala Xaa Cys Xaa Ser Xaa Phe Arg Asn Ser
 1 5 10 15

Gln Ile Cys His Cys Cys
 20

<210> 374

<211> 315

<212> DNA

<213> Conus consors

<400> 374

taagagggat cgatagcagt tcatgatgtc taaactggga gtcttggtga ccatctgtct 60
 gcttctgttt ccccttattg ctcttccaat ggatggagat caacctgcag accgacctgc 120
 agagcgtatg caggacgaca ttcatctca gcagcatccc ttgtttgata agagaggccg 180
 ctgttgcatg gtgccgaacg catgctccgg cagatgggtgc agagatcacg cacaatgttg 240
 cggatgacga taacgtgttg atgaccaact ttgtgatcac ggctacatca agtgaataag 300
 taaaacgatt gcagt 315

<210> 375

<211> 74

<212> PRT

<213> Conus consors

<400> 375

Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
 1 5 10 15

Pro Leu Ile Ala Leu Pro Met Asp Gly Asp Gln Pro Ala Asp Arg Pro
 20 25 30

Ala Glu Arg Met Gln Asp Asp Ile Ser Ser Gln Gln His Pro Leu Phe
 35 40 45

Asp Lys Arg Gly Arg Cys Cys Asp Val Pro Asn Ala Cys Ser Gly Arg
 50 55 60

Trp Cys Arg Asp His Ala Gln Cys Cys Gly
 65 70

<210> 376

<211> 22

<212> PRT

<213> Conus consors

<220>

<221> PEPTIDE

<222> (1)..(22)

<223> Xaa at residue 7 is Pro or Hyp; Xaa at residue 14 is Trp or bromo-Tr

107

<400> 376

Gly Arg Cys Cys Asp Val Xaa Asn Ala Cys Ser Gly Arg Xaa Cys Arg
 1 5 10 15

Asp His Ala Gln Cys Cys
 20

<210> 377

<211> 322

<212> DNA

<213> Conus consors

<400> 377

caagagggat c gatagcagt tcatgatgtc taaactggga gtcttggtga ctgtctgttt 60
 gcttctgttt ccccttactg ctcttccgat ggatggagat caacctgcag accaacctgc 120
 agagcgtatg caggacgaca tttcatctga gcagcatccc ttgtttgata agagacaaag 180
 gtgttgcaact gggaagaagg ggtcatgctc cggtaaagca tgcaaaagtc tcaaatgttg 240
 ctctggacga taacgtgttg atgaccaact ttgttatcac ggctacgtca agtgtctagt 300
 gaataagtaa aacgattgca gt 322

<210> 378

<211> 76

<212> PRT

<213> Conus consors

<400> 378

Met Met Ser Lys Leu Gly Val Leu Leu Thr Val Cys Leu Leu Leu Phe
 1 5 10 15

Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Pro Ala Asp Gln Pro
 20 25 30

Ala Glu Arg Met Gln Asp Asp Ile Ser Ser Glu Gln His Pro Leu Phe
 35 40 45

Asp Lys Arg Gln Arg Cys Cys Thr Gly Lys Lys Gly Ser Cys Ser Gly
 50 55 60

Lys Ala Cys Lys Ser Leu Lys Cys Cys Ser Gly Arg
 65 70 75

<210> 379

<211> 23

<212> PRT

<213> Conus consors

<220>

<221> PEPTIDE

<222> (1)..(23)

<223> Xaa at residue 1 is Gln or pyro-Glu

<400> 379

Xaa Arg Cys Cys Thr Gly Lys Lys Gly Ser Cys Ser Gly Lys Ala Cys
 1 5 10 15

Lys Ser Leu Lys Cys Cys Ser
 20

<210> 380

108

<211> 284
 <212> DNA
 <213> Conus emaciatus

<400> 380
 caagagggat cgatagcagt tcatgatgtc taaactggga gtcttgctga ccatctgtct 60
 gcttctgttt ccccttactg ttcttccgat ggatggagat caacctgcag acctacctgc 120
 attgctgctg cagttctttg cacctgaaca tagtccccgg ttgaccccg tcaaacgggtg 180
 ctgctcgctg gattgcagtg ttgcatccc ttgttgcccg tatggatcac cttgattatt 240
 gcggccacgt caagtgtcta atgaataagt aaaatgattg cagt 284

<210> 381
 <211> 70
 <212> PRT
 <213> Conus emaciatus

<400> 381
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
 1 5 10 15
 Pro Leu Thr Val Leu Pro Met Asp Gly Asp Gln Pro Ala Asp Leu Pro
 20 25 30
 Ala Leu Arg Ala Gln Phe Phe Ala Pro Glu His Ser Pro Arg Phe Asp
 35 40 45
 Pro Val Lys Arg Cys Cys Ser Arg Asp Cys Ser Val Cys Ile Pro Cys
 50 55 60
 Cys Pro Tyr Gly Ser Pro
 65 70

<210> 382
 <211> 18
 <212> PRT
 <213> Conus emaciatus

<220>
 <221> PEPTIDE
 <222> (1)..(18)
 <223> Xaa at residue 11, 14 and 18 is Pro or Hyp; Xaa at residue 15 is
 Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phos
 pho-Ty

<400> 382
 Cys Cys Ser Arg Asp Cys Ser Val Cys Ile Xaa Cys Cys Xaa Xaa Gly
 1 5 10 15
 Ser Xaa

<210> 383
 <211> 13
 <212> PRT
 <213> Conus aurisiacus

<400> 383
 Cys Cys Lys Val Gln Cys Glu Ser Cys Thr Pro Cys Cys
 1 5 10

<210> 384
 <211> 15

109

<212> PRT

<213> Conus atlanticus

<400> 384

Cys	Cys	Glu	Leu	Pro	Cys	Gly	Pro	Gly	Phe	Cys	Val	Pro	Cys	Cys
1				5					10					15

<210> 385

<211> 14

<212> PRT

<213> Conus arentus

<400> 385

Cys	Cys	Glu	Arg	Pro	Cys	Asn	Ile	Gly	Cys	Val	Pro	Cys	Cys
1				5					10				

<210> 386

<211> 16

<212> PRT

<213> Conus bandus

<400> 386

Cys	Cys	Asn	Trp	Pro	Cys	Ser	Met	Gly	Cys	Ile	Pro	Cys	Cys	Tyr	Tyr
1				5					10					15	

<210> 387

<211> 15

<212> PRT

<213> Conus betulinus

<400> 387

Cys	Cys	Glu	Leu	Pro	Cys	His	Gly	Cys	Val	Pro	Cys	Cys	Trp	Pro
1				5					10					15

<210> 388

<211> 16

<212> PRT

<213> Conus betulinus

<400> 388

Cys	Cys	Gly	Leu	Pro	Cys	Asn	Gly	Cys	Val	Pro	Cys	Cys	Trp	Pro	Ser
1				5					10					15	

<210> 389

<211> 18

<212> PRT

<213> Conus betulinus

<400> 389

Cys	Cys	Ser	Arg	Asn	Cys	Ala	Val	Cys	Ile	Pro	Cys	Cys	Pro	Asn	Trp
1				5					10					15	

Pro Ala

<210> 390

<211> 14

<212> PRT

<213> Conus betulinus

<400> 390

Cys	Cys	Lys	Gln	Ser	Cys	Thr	Thr	Cys	Met	Pro	Cys	Cys	Trp
1				5					10				

<210> 391

<211> 14

110

<212> PRT
 <213> Conus betulinus

<220>
 <221> PEPTIDE
 <222> (1)..(14)
 <223> Xaa is Glu or gamma-carboxy Glu

<400> 391
 Ala Cys Cys Xaa Gln Ser Cys Thr Thr Cys Met Pro Cys Cys
 1 5 10

<210> 392
 <211> 14
 <212> PRT
 <213> Conus betulinus

<400> 392
 Cys Cys Glu Gln Ser Cys Thr Thr Cys Met Pro Cys Cys Trp
 1 5 10

<210> 393
 <211> 18
 <212> PRT
 <213> Conus characteristicus

<400> 393
 Arg Cys Cys Arg Tyr Pro Cys Pro Asp Ser Cys His Gly Ser Cys Cys
 1 5 10 15

Tyr Lys

<210> 394
 <211> 15
 <212> PRT
 <213> Conus characteristicus

<400> 394
 Cys Cys Pro Pro Val Ala Cys Asn Met Gly Cys Lys Pro Cys Cys
 1 5 10 15

<210> 395
 <211> 17
 <212> PRT
 <213> Conus characteristicus

<400> 395
 Cys Cys Asp Asp Ser Glu Cys Asp Tyr Ser Cys Trp Pro Cys Cys Met
 1 5 10 15

Phe

<210> 396
 <211> 14
 <212> PRT
 <213> Conus characteristicus

<400> 396
 Cys Cys Arg Arg Cys Tyr Met Gly Cys Ile Pro Cys Cys Phe
 1 5 10

<210> 397
 <211> 16
 <212> PRT
 <213> Conus textile

111

<400> 397

Cys	Cys	Pro	Pro	Val	Ala	Cys	Asn	Met	Gly	Cys	Lys	Pro	Cys	Cys	Gly
1				5					10					15	

<210> 398

<211> 19

<212> PRT

<213> Conus marmoreus

<220>

<221> PEPTIDE

<222> (1)..(19)

<223> Xaa is Hyp

<400> 398

Ser	Lys	Gln	Cys	Cys	His	Leu	Ala	Ala	Cys	Arg	Phe	Gly	Cys	Thr	Xaa
1				5					10					15	

Cys Cys Asn

<210> 399

<211> 15

<212> PRT

<213> Conus capitaneus

<400> 399

Ser	Cys	Cys	Arg	Asp	Cys	Gly	Glu	Asp	Cys	Val	Gly	Cys	Cys	Arg
1				5					10					15

<210> 400

<211> 16

<212> PRT

<213> Conus coronatus

<400> 400

Cys	Cys	Asp	Trp	Pro	Cys	Ile	Pro	Gly	Cys	Thr	Pro	Cys	Cys	Leu	Pro
1				5					10					15	

<210> 401

<211> 18

<212> PRT

<213> Conus dalli

<400> 401

Cys	Cys	Asp	Asp	Ser	Glu	Cys	Asp	Tyr	Ser	Cys	Trp	Pro	Cys	Cys	Ile
1				5					10					15	

Leu Ser

<210> 402

<211> 17

<212> PRT

<213> Conus dalli

<400> 402

Glx	Gln	Cys	Cys	Pro	Pro	Val	Ala	Cys	Asn	Met	Gly	Cys	Glu	Pro	Cys
1				5					10					15	

Cys

<210> 403

<211> 16

<212> PRT

<213> Conus dalli

112

<400> 403

Cys	Cys	Asn	Ala	Gly	Phe	Cys	Arg	Phe	Gly	Cys	Thr	Pro	Cys	Cys	Trp
1				5					10					15	

<210> 404

<211> 14

<212> PRT

<213> Conus distans

<400> 404

Glx	Cys	Cys	Val	His	Pro	Cys	Pro	Cys	Thr	Pro	Cys	Cys	Arg
1				5					10				

<210> 405

<211> 14

<212> PRT

<213> Conus figulinus

<400> 405

Cys	Cys	Pro	Trp	Pro	Cys	Asn	Ile	Gly	Cys	Val	Pro	Cys	Cys
1				5					10				

<210> 406

<211> 14

<212> PRT

<213> Conus figulinus

<400> 406

Cys	Cys	Ser	Lys	Asn	Cys	Ala	Val	Cys	Ile	Pro	Cys	Cys	Pro
1				5					10				

<210> 407

<211> 15

<212> PRT

<213> Conus figulinus

<400> 407

Cys	Cys	Arg	Trp	Pro	Cys	Pro	Ala	Arg	Cys	Gly	Ser	Cys	Cys	Leu
1				5					10					15

<210> 408

<211> 16

<212> PRT

<213> Conus figulinus

<400> 408

Cys	Cys	Glu	Leu	Ser	Arg	Cys	Leu	Gly	Cys	Val	Pro	Cys	Cys	Thr	Ser
1				5					10					15	

<210> 409

<211> 16

<212> PRT

<213> Conus figulinus

<400> 409

Cys	Cys	Glu	Leu	Ser	Lys	Cys	His	Gly	Cys	Val	Pro	Cys	Cys	Ile	Pro
1				5					10					15	

<210> 410

<211> 16

<212> PRT

<213> Conus generalis

<400> 410

113

Glx Cys Cys Thr Phe Cys Asn Phe Gly Cys Gln Pro Cys Cys Val Pro
 1 5 10 15

<210> 411
 <211> 16
 <212> PRT
 <213> Conus generalis

<400> 411
 Glx Cys Cys Thr Phe Cys Asn Phe Gly Cys Gln Pro Cys Cys Leu Thr
 1 5 10 15

<210> 412
 <211> 16
 <212> PRT
 <213> Conus generalis

<400> 412

Glx Cys Cys Thr Phe Cys Asn Phe Gly Cys Gln Pro Cys Cys Val Pro
 1 5 10 15

<210> 413
 <211> 17
 <212> PRT
 <213> Conus gloriamaris

<400> 413
 Cys Cys Asp Asp Ser Glu Cys Asp Tyr Ser Cys Trp Pro Cys Cys Met
 1 5 10 15

Phe

<210> 414
 <211> 17
 <212> PRT
 <213> Conus gloriamaris

<400> 414
 Gly Cys Cys His Leu Leu Ala Cys Arg Phe Gly Cys Ser Pro Cys Cys
 1 5 10 15
 Trp

<210> 415
 <211> 16
 <212> PRT
 <213> Conus gloriamaris

<400> 415
 Cys Cys Ser Trp Asp Val Cys Asp His Pro Ser Cys Thr Cys Cys Gly
 1 5 10 15

<210> 416
 <211> 13
 <212> PRT
 <213> Conus laterculatus

<400> 416
 Cys Cys Asp Trp Pro Cys Ser Gly Cys Ile Pro Cys Cys
 1 5 10

<210> 417
 <211> 19
 <212> PRT
 <213> Conus leopardus

114

<400> 417

Glx	Ile	Asn	Cys	Cys	Pro	Trp	Pro	Cys	Pro	Ser	Thr	Cys	Arg	His	Gln
1				5					10					15	

Cys Cys His

<210> 418

<211> 19

<212> PRT

<213> Conus lividus

<400> 418

Glx	Ile	Asn	Cys	Cys	Pro	Trp	Pro	Cys	Pro	Asp	Ser	Cys	His	Tyr	Gln
1				5					10					15	

Cys Cys His

<210> 419

<211> 14

<212> PRT

<213> Conus marmoreus

<400> 419

Cys	Cys	Arg	Leu	Ser	Cys	Gly	Leu	Gly	Cys	His	Pro	Cys	Cys
1				5					10				

<210> 420

<211> 17

<212> PRT

<213> Conus marmoreus

<400> 420

Glu	Cys	Cys	Gly	Ser	Phe	Ala	Cys	Arg	Phe	Gly	Cys	Val	Pro	Cys	Cys
1				5					10					15	

Val

<210> 421

<211> 19

<212> PRT

<213> Conus marmoreus

<400> 421

Ser	Lys	Gln	Cys	Cys	His	Leu	Pro	Ala	Cys	Arg	Phe	Gly	Cys	Thr	Pro
1				5					10					15	

Cys Cys Trp

<210> 422

<211> 17

<212> PRT

<213> Conus marmoreus

<400> 422

Met	Gly	Cys	Cys	Pro	Phe	Pro	Cys	Lys	Thr	Ser	Cys	Thr	Thr	Leu	Cys
1				5					10					15	

Cys

<210> 423

<211> 14

<212> PRT

<213> Conus musicus

<400> 423

115

Ala Cys Cys Glu Gln Ser Cys Thr Thr Cys Phe Pro Cys Cys
 1 5 10

<210> 424
 <211> 15
 <212> PRT
 <213> Conus nobilis

<400> 424
 Cys Cys Glu Leu Pro Cys Gly Pro Gly Phe Cys Val Pro Cys Cys
 1 5 10 15

<210> 425
 <211> 14
 <212> PRT
 <213> Conus pulicarius

<400> 425
 Cys Cys Asn Ser Cys Tyr Met Gly Cys Ile Pro Cys Cys Phe
 1 5 10

<210> 426
 <211> 17
 <212> PRT
 <213> Conus quercinus

<400> 426
 Glx Arg Cys Cys Gln Trp Pro Cys Pro Gly Ser Cys Arg Cys Cys Arg
 1 5 10 15

Thr

<210> 427
 <211> 18
 <212> PRT
 <213> Conus quercinus

<400> 427
 Glx Arg Cys Cys Arg Trp Pro Cys Pro Gly Ser Cys Arg Cys Cys Arg
 1 5 10 15

Tyr Arg

<210> 428
 <211> 18
 <212> PRT
 <213> Conus quercinus

<400> 428
 Arg Cys Cys Arg Tyr Pro Cys Pro Asp Ser Cys His Gly Ser Cys Cys
 1 5 10 15

Tyr Lys

<210> 429
 <211> 15
 <212> PRT
 <213> Conus quercinus

<220>
 <221> PEPTIDE
 <222> (1)..(15)
 <223> Xaa is Hyp

<400> 429

116

Cys Cys Ser Gln Asp Cys Leu Val Cys Ile Xaa Cys Cys Pro Asn
 1 5 10 15

<210> 430
 <211> 15
 <212> PRT
 <213> Conus quercinus

<220>
 <221> PEPTIDE
 <222> (1)..(15)
 <223> Xaa is Hyp

<400> 430
 Cys Cys Ser Arg His Cys Trp Val Cys Ile Xaa Cys Cys Pro Asn
 1 5 10 15

<210> 431
 <211> 16
 <212> PRT
 <213> Conus rattus

<400> 431
 Glx Thr Cys Cys Ser Asn Cys Gly Glu Asp Cys Asp Gly Cys Cys Gln
 1 5 10 15

<210> 432
 <211> 20
 <212> PRT
 <213> Conus striatus

<400> 432
 Glx Asn Cys Cys Asn Gly Gly Cys Ser Ser Lys Trp Cys Arg Asp His
 1 5 10 15

Ala Arg Cys Cys
 20

<210> 433
 <211> 12
 <212> PRT
 <213> Conus textile

<220>
 <221> PEPTIDE
 <222> (1)..(12)
 <223> Xaa is Hyp

<400> 433
 Cys Cys Arg Thr Cys Phe Gly Cys Thr Xaa Cys Cys
 1 5 10

<210> 434
 <211> 14
 <212> PRT
 <213> Conus tessulatus

<400> 434
 Cys Cys His Lys Cys Tyr Met Gly Cys Ile Pro Cys Cys Ile
 1 5 10

<210> 435
 <211> 18
 <212> PRT
 <213> Conus tessulatus

117

<400> 435

Lys	Cys	Cys	Arg	Pro	Pro	Cys	Ala	Met	Ser	Cys	Gly	Met	Ala	Arg	Cys
1				5					10					15	

Cys Tyr

<210> 436

<211> 23

<212> PRT

<213> Conus betulinus

<400> 436

Arg	Cys	Cys	Arg	Trp	Pro	Cys	Pro	Ser	Ile	Cys	Gly	Met	Ala	Arg	Cys
1				5					10					15	

Cys	Phe	Val	Met	Ile	Thr	Cys
			20			

<210> 437

<211> 23

<212> PRT

<213> Conus betulinus

<400> 437

Arg	Cys	Cys	Arg	Trp	Pro	Cys	Pro	Ser	Arg	Cys	Gly	Met	Ala	Arg	Cys
1				5					10					15	

Cys	Phe	Val	Met	Ile	Thr	Cys
			20			

<210> 438

<211> 15

<212> PRT

<213> Conus textile

<400> 438

Phe	Cys	Cys	Asp	Ser	Asn	Trp	Cys	His	Asp	Cys	Glu	Cys	Cys	Tyr
1				5					10					15

<210> 439

<211> 16

<212> PRT

<213> Conus marmoreus

<400> 439

Cys	Cys	His	Trp	Asn	Trp	Cys	Asp	His	Leu	Cys	Ser	Cys	Cys	Gly	Ser
1				5					10					15	

<210> 440

<211> 16

<212> PRT

<213> Conus marmoreus

<220>

<221> PEPTIDE

<222> (1)..(16)

<223> Xaa is Hyp

<400> 440

Asp	Cys	Cys	Xaa	Leu	Pro	Ala	Cys	Pro	Phe	Gly	Cys	Asn	Xaa	Cys	Cys
1				5					10					15	

<210> 441

<211> 16

118

<212> PRT
 <213> Conus marmoreus

<220>
 <221> PEPTIDE
 <222> (1)..(16)
 <223> Xaa is Hyp

<400> 441
 Cys Cys Ala Pro Ser Ala Cys Arg Leu Gly Cys Arg Xaa Cys Cys Arg
 1 5 10 15

<210> 442
 <211> 16
 <212> PRT
 <213> Conus marmoreus

<220>
 <221> PEPTIDE
 <222> (1)..(16)
 <223> Xaa is Hyp

<400> 442
 Cys Cys Ala Xaa Ser Ala Cys Arg Leu Gly Cys Arg Xaa Cys Cys Arg
 1 5 10 15

<210> 443
 <211> 16
 <212> PRT
 <213> Conus marmoreus

<400> 443
 Cys Cys Ala Pro Ser Ala Cys Arg Leu Gly Cys Arg Pro Cys Cys Arg
 1 5 10 15

<210> 444
 <211> 17
 <212> PRT
 <213> Conus marmoreus

<220>
 <221> PEPTIDE
 <222> (1)..(17)
 <223> Xaa is Hyp

<400> 444
 Gly Cys Cys Gly Ser Phe Ala Cys Arg Phe Gly Cys Val Xaa Cys Cys
 1 5 10 15

Val

<210> 445
 <211> 15
 <212> PRT
 <213> Conus textile

<400> 445
 Cys Cys Ser Trp Asp Val Cys Asp His Pro Ser Cys Thr Cys Cys
 1 5 10 15

<210> 446
 <211> 16
 <212> PRT
 <213> Conus textile

119

<400> 446

Arg	Cys	Cys	Lys	Phe	Pro	Cys	Pro	Asp	Ser	Cys	Arg	Tyr	Leu	Cys	Cys
1				5					10					15	

<210> 447

<211> 17

<212> PRT

<213> Conus aureus

<400> 447

Cys	Cys	Asp	Asp	Ser	Glu	Cys	Asp	Tyr	Ser	Cys	Trp	Pro	Cys	Cys	Ile
1				5					10					15	

Phe

<210> 448

<211> 16

<212> PRT

<213> Conus aureus

<400> 448

Cys	Cys	Asn	Asp	Trp	Glu	Cys	Asp	Asp	Ser	Cys	Trp	Pro	Cys	Cys	Tyr
1				5					10					15	

<210> 449

<211> 16

<212> PRT

<213> Conus ammiralis

<400> 449

Arg	Cys	Cys	Arg	Phe	Pro	Cys	Pro	Asp	Thr	Cys	Arg	His	Leu	Cys	Cys
1				5					10					15	

<210> 450

<211> 12

<212> PRT

<213> Conus ammiralis

<400> 450

Cys	Cys	Met	Thr	Cys	Phe	Gly	Cys	Thr	Pro	Cys	Cys
1				5					10		

<210> 451

<211> 18

<212> PRT

<213> Conus ammiralis

<400> 451

Cys	Cys	Asp	Asp	Ser	Glu	Cys	Asp	Tyr	Ser	Cys	Trp	Pro	Cys	Cys	Ile
1				5					10					15	

Phe Ser

<210> 452

<211> 13

<212> PRT

<213> Conus ammiralis

<400> 452

Cys	Cys	Arg	Leu	Leu	Cys	Leu	Ser	Cys	Asn	Pro	Cys	Cys
1				5					10			

<210> 453

<211> 16

<212> PRT

120

<213> Conus ammiralis

<400> 453

Cys	Cys	Asp	Asp	Ser	Glu	Cys	Gly	Tyr	Ser	Cys	Trp	Pro	Cys	Cys	Tyr
1				5					10					15	

<210> 454

<211> 16

<212> PRT

<213> Conus aulicus

<400> 454

Gly	Cys	Cys	Ser	Pro	Pro	Cys	His	Ser	Ile	Cys	Ala	Ala	Phe	Cys	Cys
1				5					10					15	

<210> 455

<211> 15

<212> PRT

<213> Conus aulicus

<400> 455

Cys	Cys	Arg	Pro	Val	Ala	Cys	Ala	Met	Gly	Cys	Lys	Pro	Cys	Cys
1				5					10					15

<210> 456

<211> 16

<212> PRT

<213> Conus aulicus

<400> 456

Glx	Cys	Cys	Pro	Ala	Val	Ala	Cys	Ala	Met	Gly	Cys	Glu	Pro	Cys	Cys
1				5					10					15	

<210> 457

<211> 18

<212> PRT

<213> Conus emaciatus

<400> 457

Cys	Cys	Ser	Arg	Asp	Cys	Ser	Val	Cys	Ile	Pro	Cys	Cys	Pro	Tyr	Gly
1				5					10					15	

Ser Pro

<210> 458

<211> 16

<212> PRT

<213> Conus episcopatus

<400> 458

Cys	Cys	Asp	Glu	Asp	Glu	Cys	Asn	Ser	Ser	Cys	Trp	Pro	Cys	Cys	Trp
1				5					10					15	

<210> 459

<211> 16

<212> PRT

<213> Conus episcopatus

<400> 459

Cys	Cys	Asp	Glu	Asp	Glu	Cys	Ser	Ser	Ser	Cys	Trp	Pro	Cys	Cys	Trp
1				5					10					15	

<210> 460

<211> 15

<212> PRT

121

<213> *Conus episcopatus*

<400> 460

Cys	Cys	Pro	Ala	Ala	Ala	Cys	Ala	Met	Gly	Cys	Lys	Pro	Cys	Cys
1				5					10					15

<210> 461

<211> 16

<212> PRT

<213> *Conus omaria*

<400> 461

Cys	Cys	Asp	Glu	Glu	Glu	Cys	Ser	Ser	Ala	Cys	Trp	Pro	Cys	Cys	Trp
1				5					10					15	

<210> 462

<211> 16

<212> PRT

<213> *Conus omaria*

<400> 462

Cys	Cys	His	Leu	Leu	Ala	Cys	Arg	Phe	Gly	Cys	Ser	Pro	Cys	Cys	Trp
1				5					10					15	

<210> 463

<211> 12

<212> PRT

<213> *Conus spurius*

<400> 463

Cys	Cys	Pro	Arg	Cys	Ser	Glu	Cys	Asn	Pro	Cys	Cys
1				5					10		

<210> 464

<211> 16

<212> PRT

<213> *Conus pennaceus*

<400> 464

Arg	Cys	Cys	Lys	Phe	Pro	Cys	Pro	Asp	Ser	Cys	Lys	Tyr	Leu	Cys	Cys
1				5					10					15	

<210> 465

<211> 19

<212> PRT

<213> *Conus flavidus*

<400> 465

Arg	Cys	Cys	Arg	Trp	Pro	Cys	Pro	Ser	Ile	Cys	Gly	Met	Ala	Arg	Cys
1				5					10					15	

Cys Ser Ser

<210> 466

<211> 14

<212> PRT

<213> *Conus pulicarius*

<400> 466

Cys	Cys	Lys	Leu	Leu	Cys	Gly	Cys	Thr	Pro	Cys	Cys	His	Ile
1				5					10				

<210> 467

<211> 15

<212> PRT

122

<213> Conus ebraceus

<400> 467

Cys	Cys	Glu	Gln	Pro	Cys	Tyr	Met	Gly	Cys	Ile	Pro	Cys	Cys	Phe
1				5					10					15

<210> 468

<211> 15

<212> PRT

<213> Conus ebraceus

<400> 468

Cys	Cys	Ala	Gln	Pro	Cys	Tyr	Met	Gly	Cys	Ile	Pro	Cys	Cys	Phe
1				5					10					15

<210> 469

<211> 14

<212> PRT

<213> Conus pulicarius

<400> 469

Cys	Cys	Val	Ser	Cys	Tyr	Met	Gly	Cys	Ile	Pro	Cys	Cys	Phe
1				5					10				

<210> 470

<211> 16

<212> PRT

<213> Conus miliaris

<400> 470

Cys	Cys	Asp	Trp	Pro	Cys	Ser	Ala	Gly	Cys	Tyr	Pro	Cys	Cys	Phe	Pro
1				5					10					15	

<210> 471

<211> 16

<212> PRT

<213> Conus miliaris

<400> 471

Gly	Cys	Cys	Pro	Pro	Met	Cys	Thr	Pro	Cys	Phe	Pro	Cys	Cys	Phe	Arg
1				5					10					15	

<210> 472

<211> 23

<212> PRT

<213> Conus rattus

<400> 472

Arg	Gly	Cys	Cys	Ala	Pro	Pro	Arg	Lys	Cys	Lys	Asp	Arg	Ala	Cys	Lys
1				5					10					15	

Pro	Ala	Arg	Cys	Cys	Gly	Pro
			20			

<210> 473

<211> 22

<212> PRT

<213> Conus stercusmuscarum

<400> 473

Glx	Arg	Cys	Cys	Asn	Gly	Arg	Arg	Gly	Cys	Ser	Ser	Arg	Trp	Cys	Arg
1				5					10					15	

Asp	His	Ser	Arg	Cys	Cys
			20		

123

<210> 474
 <211> 22
 <212> PRT
 <213> Conus consors

<400> 474
 Gly Arg Cys Cys Asp Val Pro Asn Ala Cys Ser Gly Arg Trp Cys Arg
 1 5 10 15
 Asp His Ala Gln Cys Cys
 20

<210> 475
 <211> 23
 <212> PRT
 <213> Conus consors

<400> 475
 Glx Arg Cys Cys Thr Gly Lys Lys Gly Ser Cys Ser Gly Lys Ala Cys
 1 5 10 15
 Lys Ser Leu Lys Cys Cys Ser
 20

<210> 476
 <211> 22
 <212> PRT
 <213> Conus aurisiacus

<400> 476
 Met Cys Cys Gly Glu Gly Arg Lys Cys Pro Ser Tyr Phe Arg Asn Ser
 1 5 10 15
 Gln Ile Cys His Cys Cys
 20

<210> 477
 <211> 19
 <212> PRT
 <213> Conus aurisiacus

<400> 477
 Cys Cys Arg Trp Pro Cys Pro Arg Gln Ile Asp Gly Glu Tyr Cys Gly
 1 5 10 15
 Cys Cys Leu

<210> 478
 <211> 22
 <212> PRT
 <213> Conus bullatus

<400> 478
 Arg Cys Cys Gly Glu Gly Leu Thr Cys Pro Arg Tyr Trp Lys Asn Ser
 1 5 10 15
 Gln Ile Cys Ala Cys Cys
 20

<210> 479
 <211> 21
 <212> PRT
 <213> Conus characteristicus

<400> 479

124

Cys Cys Gly Pro Gly Gly Ser Cys Pro Val Tyr Phe Arg Asp Asn Phe
 1 5 10 15

Ile Cys Gly Cys Cys
 20

<210> 480
 <211> 23
 <212> PRT
 <213> Conus circumciscus

<400> 480
 Arg Lys Cys Cys Gly Lys Asp Gly Pro Cys Pro Lys Tyr Phe Lys Asp
 1 5 10 15

Asn Phe Ile Cys Gly Cys Cys
 20

<210> 481
 <211> 20
 <212> PRT
 <213> Conus ermineus

<400> 481
 Cys Cys Ser Trp Pro Cys Pro Arg Tyr Ser Asn Gly Lys Leu Val Cys
 1 5 10 15

Phe Cys Cys Leu
 20

<210> 482
 <211> 21
 <212> PRT
 <213> Conus magus

<400> 482
 Cys Cys Gly Pro Gly Gly Ser Cys Pro Val Tyr Phe Arg Asp Asn Phe
 1 5 10 15

Ile Cys Gly Cys Cys
 20

<210> 483
 <211> 22
 <212> PRT
 <213> Conus magus

<400> 483
 Met Cys Cys Gly Glu Ser Ala Pro Cys Pro Ser Tyr Phe Arg Asn Ser
 1 5 10 15

Gln Ile Cys His Cys Cys
 20

<210> 484
 <211> 22
 <212> PRT
 <213> Conus magus

<400> 484
 Glx Lys Cys Cys Gly Pro Gly Gly Ser Cys Pro Val Tyr Phe Thr Asp
 1 5 10 15

Asn Phe Ile Cys Gly Cys
 20

125

<210> 485
 <211> 23
 <212> PRT
 <213> Conus magus

<400> 485
 Glx Lys Cys Cys Gly Pro Gly Gly Ser Cys Pro Val Tyr Phe Arg Asp
 1 5 10 15
 Asn Phe Ile Cys Gly Cys Cys
 20

<210> 486
 <211> 23
 <212> PRT
 <213> Conus striatus

<400> 486
 Glx Lys Cys Cys Gly Glu Gly Ser Ser Cys Pro Lys Tyr Phe Lys Asn
 1 5 10 15
 Asn Phe Ile Cys Gly Cys Cys
 20

<210> 487
 <211> 22
 <212> PRT
 <213> Conus magus

<400> 487
 Glx Lys Cys Cys Ser Gly Gly Ser Cys Pro Leu Tyr Phe Arg Asp Arg
 1 5 10 15
 Leu Ile Cys Pro Cys Cys
 20

<210> 488
 <211> 23
 <212> PRT
 <213> Conus stercusmuscarum

<400> 488
 Glx Lys Cys Cys Gly Pro Gly Ala Ser Cys Pro Arg Tyr Phe Lys Asp
 1 5 10 15
 Asn Phe Ile Cys Gly Cys Cys
 20

<210> 489
 <211> 22
 <212> PRT
 <213> Conus consors

<400> 489
 Met Cys Cys Gly Glu Gly Ala Pro Cys Pro Ser Tyr Phe Arg Asn Ser
 1 5 10 15
 Gln Ile Cys His Cys Cys
 20

<210> 490
 <211> 23
 <212> PRT
 <213> Conus aurisiacus

126

<400> 490

Glx	Lys	Cys	Cys	Thr	Gly	Lys	Lys	Gly	Ser	Cys	Ser	Gly	Lys	Ala	Cys
1				5					10					15	

Lys	Asn	Leu	Lys	Cys	Cys	Ser
			20			

<210> 491

<211> 23

<212> PRT

<213> Conus aurisiacus

<400> 491

Glx	Lys	Cys	Cys	Thr	Gly	Arg	Lys	Gly	Ser	Cys	Ser	Gly	Lys	Ala	Cys
1				5					10					15	

Lys	Asn	Leu	Lys	Cys	Cys	Ser
			20			

<210> 492

<211> 23

<212> PRT

<213> Conus bullatus

<400> 492

Val	Thr	Asp	Arg	Cys	Cys	Lys	Gly	Lys	Arg	Glu	Cys	Gly	Arg	Trp	Cys
1				5					10					15	

Arg	Asp	His	Ser	Arg	Cys	Cys
			20			

<210> 493

<211> 23

<212> PRT

<213> Conus bullatus

<400> 493

Val	Gly	Asp	Arg	Cys	Cys	Lys	Gly	Lys	Arg	Gly	Cys	Gly	Arg	Trp	Cys
1				5					10					15	

Arg	Asp	His	Ser	Arg	Cys	Cys
			20			

<210> 494

<211> 24

<212> PRT

<213> Conus bullatus

<400> 494

Val	Gly	Glu	Arg	Cys	Cys	Lys	Asn	Gly	Lys	Arg	Gly	Cys	Gly	Arg	Trp
1				5					10					15	

Cys	Arg	Asp	His	Ser	Arg	Cys	Cys
			20				

<210> 495

<211> 26

<212> PRT

<213> Conus bullatus

<400> 495

Ile	Val	Asp	Arg	Cys	Cys	Asn	Lys	Gly	Asn	Gly	Lys	Arg	Gly	Cys	Ser
1				5					10					15	

Arg	Trp	Cys	Arg	Asp	His	Ser	Arg	Cys	Cys
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

127

20

25

<210> 496
 <211> 25
 <212> PRT
 <213> Conus bullatus

<400> 496
 Val Gly Cys Cys Arg Pro Lys Pro Asn Gly Gln Met Met Cys Asp Arg
 1 5 10 15

Trp Cys Glu Lys Asn Ser Arg Cys Cys
 20 25

<210> 497
 <211> 22
 <212> PRT
 <213> Conus characteristicus

<400> 497
 Arg Asp Cys Cys Thr Pro Pro Lys Lys Cys Lys Asp Arg Gln Cys Lys
 1 5 10 15

Pro Gln Arg Cys Cys Ala
 20

<210> 498
 <211> 23
 <212> PRT
 <213> Conus lynceus

<400> 498
 Gly Arg Asp Cys Cys Thr Pro Pro Arg Lys Cys Arg Asp Arg Ala Cys
 1 5 10 15

Lys Pro Gln Arg Cys Cys Gly
 20

<210> 499
 <211> 22
 <212> PRT
 <213> Conus lynceus

<400> 499
 Glx Arg Leu Cys Cys Gly Phe Pro Lys Ser Cys Arg Ser Arg Gln Cys
 1 5 10 15

Lys Pro His Arg Cys Cys
 20

<210> 500
 <211> 22
 <212> PRT
 <213> Conus laterculatus

<400> 500
 Arg Asp Cys Cys Thr Pro Pro Lys Lys Cys Arg Asp Arg Gln Cys Lys
 1 5 10 15

Pro Ala Arg Cys Cys Gly
 20

<210> 501
 <211> 22
 <212> PRT

128

<213> Conus laterculatus

<400> 501

Arg	Pro	Pro	Cys	Cys	Thr	Tyr	Asp	Gly	Ser	Cys	Leu	Lys	Glu	Ser	Cys
1				5					10					15	

Met	Arg	Lys	Ala	Cys	Cys
			20		

<210> 502

<211> 22

<212> PRT

<213> Conus laterculatus

<400> 502

Arg	Pro	Pro	Cys	Cys	Thr	Tyr	Asp	Gly	Ser	Cys	Leu	Lys	Glu	Ser	Cys
1				5					10					15	

Lys	Arg	Lys	Ala	Cys	Cys
			20		

<210> 503

<211> 22

<212> PRT

<213> Conus geographus

<220>

<221> PEPTIDE

<222> (1)..(22)

<223> Xaa is Hyp

<400> 503

Arg	Asp	Cys	Cys	Thr	Xaa	Xaa	Lys	Lys	Cys	Lys	Asp	Arg	Gln	Cys	Lys
1				5					10					15	

Xaa	Gln	Arg	Cys	Cys	Ala
			20		

<210> 504

<211> 22

<212> PRT

<213> Conus geographus

<220>

<221> PEPTIDE

<222> (1)..(22)

<223> Xaa is Hyp

<400> 504

Arg	Asp	Cys	Cys	Thr	Xaa	Xaa	Arg	Lys	Cys	Lys	Asp	Arg	Arg	Cys	Lys
1				5					10					15	

Xaa	Met	Lys	Cys	Cys	Ala
			20		

<210> 505

<211> 22

<212> PRT

<213> Conus geographus

<220>

<221> PEPTIDE

<222> (1)..(22)

<223> Xaa is Hyp

129

<400> 505

Arg	Asp	Cys	Cys	Thr	Xaa	Xaa	Lys	Lys	Cys	Lys	Asp	Arg	Arg	Cys	Lys
1				5					10					15	

Xaa	Leu	Lys	Cys	Cys	Ala
			20		

<210> 506

<211> 22

<212> PRT

<213> Conus purpurascens

<220>

<221> PEPTIDE

<222> (1)..(22)

<223> Xaa is Hyp

<400> 506

Glx	Arg	Leu	Cys	Cys	Gly	Phe	Xaa	Lys	Ser	Cys	Arg	Ser	Arg	Gln	Cys
1				5					10					15	

Lys	Xaa	His	Arg	Cys	Cys
			20		

<210> 507

<211> 22

<212> PRT

<213> Conus magus

<400> 507

Arg	Asp	Cys	Cys	Thr	Pro	Pro	Lys	Lys	Cys	Lys	Asp	Arg	Gln	Cys	Lys
1				5					10					15	

Pro	Gln	Arg	Cys	Cys	Ala
			20		

<210> 508

<211> 24

<212> PRT

<213> Conus marmoreus

<400> 508

Arg	Gly	Gly	Cys	Cys	Thr	Pro	Pro	Arg	Lys	Cys	Lys	Asp	Arg	Ala	Cys
1				5					10					15	

Lys	Pro	Ala	Arg	Cys	Cys	Gly	Pro
				20			

<210> 509

<211> 23

<212> PRT

<213> Conus nobilis

<400> 509

Glx	Lys	Cys	Cys	Thr	Gly	Lys	Lys	Gly	Ser	Cys	Ser	Gly	Lys	Ala	Cys
1				5					10					15	

Lys	Asn	Leu	Lys	Cys	Cys	Ser
			20			

<210> 510

<211> 24

<212> PRT

<213> Conus parius

130

<400> 510

Arg Gly Gly Cys Cys Thr Pro Pro Lys Lys Cys Lys Asp Arg Ala Cys
 1 5 10 15

Lys Pro Ala Arg Cys Cys Gly Pro
 20

<210> 511

<211> 23

<212> PRT

<213> Conus parius

<400> 511

Arg Gly Cys Cys Thr Pro Pro Arg Lys Cys Lys Asp Arg Ala Cys Lys
 1 5 10 15

Pro Ala Arg Cys Cys Gly Pro
 20

<210> 512

<211> 24

<212> PRT

<213> Conus radiatus

<220>

<221> PEPTIDE

<222> (1)..(24)

<223> Xaa is Hyp

<400> 512

Leu Xaa Ser Cys Cys Ser Leu Asn Leu Arg Leu Cys Xaa Val Xaa Ala
 1 5 10 15

Cys Lys Arg Asn Xaa Cys Cys Thr
 20

<210> 513

<211> 24

<212> PRT

<213> Conus radiatus

<220>

<221> PEPTIDE

<222> (1)..(24)

<223> Xaa is Hyp

<400> 513

Glx Gln Arg Cys Cys Thr Val Lys Arg Ile Cys Xaa Val Xaa Ala Cys
 1 5 10 15

Arg Ser Lys Xaa Cys Cys Lys Ser
 20

<210> 514

<211> 24

<212> PRT

<213> Conus radiatus

<400> 514

Arg Gly Gly Cys Cys Thr Pro Pro Arg Lys Cys Lys Asp Arg Ala Cys
 1 5 10 15

Lys Pro Ala Arg Cys Cys Gly Pro
 20

131

<210> 515
 <211> 23
 <212> PRT
 <213> Conus stercusmuscarum

<400> 515
 Glx Lys Cys Cys Thr Gly Lys Lys Gly Ser Cys Ser Gly Lys Ala Cys
 1 5 10 15
 Lys Asn Leu Lys Cys Cys Ser
 20

<210> 516
 <211> 21
 <212> PRT
 <213> Conus tulipa

<220>
 <221> PEPTIDE
 <222> (1)..(21)
 <223> Xaa is Hyp

<400> 516
 His Gly Cys Cys Lys Gly Xaa Glu Gly Cys Ser Ser Arg Glu Cys Arg
 1 5 10 15
 Xaa Gln His Cys Cys
 20

<210> 517
 <211> 21
 <212> PRT
 <213> Conus tulipa

<400> 517
 His Gly Cys Cys Glu Gly Pro Lys Gly Cys Ser Ser Arg Glu Cys Arg
 1 5 10 15
 Pro Gln His Cys Cys
 20

<210> 518
 <211> 23
 <212> PRT
 <213> Conus wittigi

<400> 518
 Leu Pro Ser Cys Cys Asp Phe Glu Arg Leu Cys Val Val Pro Ala Cys
 1 5 10 15
 Ile Arg His Gln Cys Cys Thr
 20

<210> 519
 <211> 17
 <212> PRT
 <213> Conus omaria

<400> 519
 Cys Cys Lys Tyr Gly Trp Thr Cys Leu Leu Gly Cys Thr Pro Cys Asp
 1 5 10 15

Cys

<210> 520

132

<211> 17

<212> PRT

<213> Conus omaria

<400> 520

Cys	Cys	Arg	Tyr	Gly	Trp	Thr	Cys	Trp	Leu	Gly	Cys	Thr	Pro	Cys	Gly
1				5					10					15	

Cys